

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
9 August 2001 (09.08.2001) ---

PCT

(10) International Publication Number
WO 01/57275 A2

(51) International Patent Classification⁷: **C12Q 1/68**,
G06F 19/00, C07K 14/47

94043 (US). RANK, David, R. [US/US]; 117 El Dorado
Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00667

(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharma-
cia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ
08855 (US).

(22) International Filing Date: 30 January 2001 (30.01.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/180,312 4 February 2000 (04.02.2000) US
60/207,456 26 May 2000 (26.05.2000) US
09/608,408 30 June 2000 (30.06.2000) US
09/632,366 3 August 2000 (03.08.2000) US
60/234,687 21 September 2000 (21.09.2000) US
60/236,359 27 September 2000 (27.09.2000) US
0024263.6 4 October 2000 (04.10.2000) GB

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): MOLEC-
ULAR DYNAMICS, INC. [—/US]; 928 East Arques Av-
enue, Sunnyvale, CA 94086 (US).

Published:

— without international search report and to be republished
upon receipt of that report

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PENN, Sharron,
G. [GB/US]; 617 South Delaware Street, San Mateo, CA
94402 (US). HANZEL, David, K. [US/US]; 988 Loma
Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wen-
sheng [CN/US]; 210 Easy Street #25, Mountain View, CA

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

WO 01/57275 A2

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the
brain and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5
The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20
The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BRAIN.txt, created
25 24 January 2001, having 25,840,972 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30
The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

brain and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.:

12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

15 wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

30 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
35 ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
10 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

15

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary
35 planar substrate, as is described, *inter alia*, in Brenner

et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick
10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
20 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
30 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
35 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100
5 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a
10 required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome
15 ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown
20 that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer
25 than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of
30 sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus,
35 as further described in Examples 1 and 2, *infra*, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the
5 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously
10 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily
15 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other
20 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity
25 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10)
30 ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query
35 criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable
5 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,
10 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and
15 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual
20 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
25 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known
30 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be
35 removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating
35 transcription, regulating message transport after

transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
35 secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
35 amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the
5 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and
Maniatis et al., Molecular Cloning : A Laboratory Manual,
10 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

15 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,
20 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes
25 not only provide adequate signal, but have substantial advantages, as herein described.

 After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single
30 exon probe) is disposed in an array upon a support substrate.

 Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
35 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or

32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
35 throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
30 libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST, microarrays".

Such EST microarrays by definition can measure
35 expression only of those genes found in EST libraries,

shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
10 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
15 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, 5 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric 10 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome- 15 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present 20 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the 25 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically 30 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector 35 sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-
25 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large

percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
35 nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
35 alignment search tool"). The results of such query -

including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence -- can then be passed directly to process 500, or used to
5 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data
10 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or
15 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or
20 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence
25 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic
30 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
35 the number of nucleotides typically represented in an

annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from

GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
10 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
15 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to
35 indicate expression intensity. As discussed *infra*, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of
5 the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon
15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these
20 ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in
25 brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness
30 of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades
35 Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5 Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and
25 internal neurofibrillary tangles.

Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

30 At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing

- 5 (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

- 10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological
15 transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed
20 optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

- As early as 1965, McAlpine, in Multiple
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general population, but could discern no definite genetic pattern
30 of inheritance.

- Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet. 7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to
35 the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2
different sites, as have sites on the X chromosome. Wei et
al., Nature Genet. 25:376-377 (2000) report more
specifically that the NOTCH4 locus is associated with
5 susceptibility to schizophrenia.

In general, however, it is believed that
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.
8:1729-1739 (1999) undertook a systematic search for
10 linkage in 196 affected sib pairs (ASPs) with
schizophrenia. Using 229 microsatellite markers at an
average intermarker distance of 17.26 cM, followed in a
second stage by a further 54 markers allowing the regions
identified in stage 1 to be typed at an average spacing of
15 5.15 cM, Williams et al. considered results on chromosomes
4p, 18q, and Xcen as suggestive; however, given the scores,
Williams et al. interpreted their results as suggesting
that common genes of major effect (susceptibility ratio
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.
81(5):364-76 (1998), in a genome-wide search for
schizophrenia susceptibility genes, found that twelve
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and
22) had at least one region with a nominal P value <0.05,
25 that two of these chromosomes had a nominal P value <0.01
(chromosomes 13 and 16), and that five chromosomes (1, 2,
4, 11, and 13) had at least one marker with a lod score
>2.0, suggesting the existence of multiple loci that
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,
paroxysmal disorders of cerebral function (seizures); that
is, by sudden, brief attacks of altered consciousness,
35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion diseases (Creutzfeld-Jakob, Gerstmann-Strausler-Shenker,
10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-telangiectasia, amyotrophic lateral sclerosis, bulbo-spinal
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease,
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man-syndrome and Von Hippel-Lindau
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma,
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous
35 system that likely have genetic components include the

various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease,

5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10 The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single

15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known

25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the

30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating

35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme,

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 – 25,434, respectively, for probe SEQ ID NOS. 1 – 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

- 5 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a
10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization
15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
20 temperature (approximately 25°C).

- When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single
25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

- Thus, each single exon probe will include no more
30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more
35 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®].

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in

Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 -
5 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as
10 protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New
15 England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide
20 Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles
25 of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino
30 acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a
35 further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of
5 illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

10

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
15 GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
20 The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
25 heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
30 genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
35 GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit
35 subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments

from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

- 5 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and
10 standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some
15 submitted sequence data.

 Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression
20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not
25 shown).

 The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII
30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

35 Each of the probe sequences was BLASTed against

the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

30

100 μ M dATP, 100 μ M dGTP, 100 μ M dTTP, 50 μ M dCTP, 50 μ M
Cy3-dCTP or Cy5-dCTP 50 μ M, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
Speedvac, resuspended in 30 μ l hybridization solution
containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2
 μ g/ μ l human c₀t1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a
coverslip, with the array placed in a humid oven at 42°C
overnight. Before scanning, slides were washed in 1X SSC,
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%
SDS, at 55°C for 20 minutes. Slides were briefly dipped in
20 water and dried thoroughly under a gentle stream of
nitrogen.

Slides were scanned using a Molecular Dynamics
Gen3 scanner, as described. Schena (ed.), Microarray
Biochip: Tools and Technology, Eaton Publishing
25 Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference
permitted the survey of a large number of tissues, it
attenuates the measurement of relative gene expression,
30 since every highly expressed gene in the tissue/cell type-
specific fluorescence channel will be present to a level of
at least 10% in the control channel. Because of this fact,
both signal and expression ratios (the latter hereinafter,
"expression" or "relative expression") for each probe were
35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic" expression (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray
 5 hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
------------	-----	--	------	--

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
5 AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain
were a ferritin heavy chain protein, which is reported in
10 the literature to be found in brain and liver (Joshi et
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
duplicated with the array. Other highly expressed chip
sequences included a translation elongation factor 1 α
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
15 chromosome RNA-binding motif (Chai et *al.*, *Genomics*
49(2):283-89 (1998))(AC007320-3). A low homology analog
(AP00123-1/2) to a gene, DSCR1, thought to be involved in
trisomy 21 (Down's syndrome), showed high expression in
both brain and heart, in agreement with the literature
20 (Fuentes et *al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we
selected the BAC AC006064 to be included on the array.
This BAC was known to contain the GAPDH gene, and thus
could be used as a control for the ORF selection process.
25 The gene finding and exon selection algorithms resulted in
choosing 25 exons from BAC AC006064 for spotting onto the
array, of which four were drawn from the GAPDH gene. Table
3 shows the comparison of the average expression ratio for
the 4 exons from BAC006064 compared with the average
30 expression ratio for 5 different dilutions of a
commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOs.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified
5 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were
35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes:
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

16. A single exon nucleic acid probe as claimed in any one.
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

- 5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

- 15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the brain of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

- 30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 25,434 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 25,434.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID NOS: 25,435 - 37,811.

Page 1 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	29898	6.47				
889	13638	26308	15.92				
1022	13782		2.16				
1278	14029	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1609	14355	27044	3.19				
1633	14378	27069	6.1				
1718	14481	27160	3.31				
1743	14485	27184	1.44				
1750	14492	27182	6.78				
1884	14621	27331	1.44				
1971	14707	27425	2.14				
2182	14892	27627	2.7				
2277	15003	27743	2.91				
2578	15282	28028	1				
2578	15282	28029	1				
3181	15944	28505	2.83				
3442	16198	28648	1.42				
3505	16201	28915	12.04				
3549	16304		1				
3549	16402	29042	1.67				
3628	16578		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29813	0.97				
4248	16989	29814	0.97				
4303	17042		1.07				
4381	17089	29734	0.76				
4784	17518	30138	0.99				
4983	17706	30310	5.38				
4995	17718	30323	1.3				
5176	17985	30500	1.57				
5176	17985	30501	1.57				

Page 2 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5536	18130		4.3				
5510	18308		8.14				
5593	18139		3.97				
5648	18443	31368	0.6				
5654	18449	31362	3.28				
5922	25082	31673	1.62				
5958	18740	31689	1.76				
6322	19082		1.27				
6454	19222	32220	1.1				
6454	19222	32221	1.1				
7026	19717	32774	1				
7026	19717	32775	1				
7311	19984	33071	1.76				
7311	19984	33072	1.76				
7712	20376		0.81				
7960	20655	33780	1.4				
8384	21077	34214	1.49				
8759	21451	34598	0.59				
8759	21451	34599	0.59				
8434	22112	35287	2.67				
9586	22318	35515	0.77				
9782	22493	36638	1.24				
9922	22570	35787	0.94				
10328	22975	36194	0.82				
10328	22975	36195	0.82				
10562	23277		2.83				
10749	25131	36879	1.34				
10952	23829		2.2				
11030	23701	36868	1.84				
11352	24023	37328	2.02				
11485	24088		2.47				
12313	24735		1.52				
12609	24916	31006	2.36				
5061	18743	31703	17.79	0.9E+00 AJ239028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18

Page 3 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7905	20600	33790	1.74	9.4E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9843	22295	35489	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9843	22295	35490	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
6901	19639	32884	0.73	9.8E+00	AF065830.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
6901	19639	32885	0.73	9.8E+00	AF065830.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22668	36187	1.17	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2H2) genes, complete cds
10321	22668	36188	1.17	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2H2) genes, complete cds
2871	15381	28119	1	9.4E+00	L11433.1	NT	Dengua virus type 3 membrane protein (pMm)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2871	15381	28120	1	9.4E+00	L11433.1	NT	Dengua virus type 3 membrane protein (pMm)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2924	15500	28534	2.87	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
7997	20692	33820	0.91	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8901	21592	34733	3.08	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.46	9.1E+00	AF095609.1	NT	Leuiciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5214	18022	30646	2.46	9.1E+00	AF095609.1	NT	Leuiciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
8330	21697		0.83	9.0E+00	P08241	SWISSPROT	RHODOPSIN
5945	18727	31685	5.55	8.9E+00	BE871808.1	EST HUMAN	601651038R1 NIH_JMG. 81 Homo sapiens cDNA clone IMAGE:3934592 3'
6287	18060	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cptb33 premature mRNA, partial cds
6287	18060	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cptb33 premature mRNA, partial cds
430	13216	25881	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6355	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (oea2a)
11122	23791		2	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8051	20745		0.89	7.9E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	15931		1.9	7.5E+00	AL445063.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8259	20553	34090	1.81	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20553	34091	1.81	7.5E+00	P35441	SWISSPROT	THROMOSPONDIN 1 PRECURSOR
5711	18504	31428	2.66	7.4E+00	BF700517.1	EST HUMAN	602128876F1 NIH_JMG. 98 Homo sapiens cDNA clone IMAGE:4285508 5'
9051	21343	34487	2.7	7.4E+00	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Page 4 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15743	28390	3.58	7.2E+00	L12051.1	NT	Lycopodium seculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.58	7.2E+00	L12051.1	NT	Lycopodium seculentum Mill. GTPase (SAR2) mRNA, complete cds
6931	19687	32713	0.71	7.2E+00	BE176900.1	EST_HUMAN	RCB-H10513-200300-031-1407 HT0513 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22151		8.93	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN URDA-PHPB INTERGENIC REGION
9882	22932	35729	3.37	7.0E+00	P48910	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8161	20875	34011	1.92	6.9E+00	P35979	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scores melanocyte 2NH-M Homo sapiens cDNA IMAGE:291860 6'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scores melanocyte 2NH-M Homo sapiens cDNA IMAGE:291860 5'
9031	21721		1.26	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8
10109	22757	35989	3.24	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 167.0 KDA PROTEIN C36C10.5 IN CHROMOSOME III
5202	18010		0.72	6.8E+00	Q68028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6450	16218	32216	0.81	6.8E+00	BF67212.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
8974	22622	35827	2.36	6.8E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8974	22622	35828	2.36	6.8E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11073	23743		1.97	6.8E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9078	21768	34831	7	6.8E+00	P03374	SWISSPROT	ENT POLYPROTEIN (CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36)
10203	22251	35057	0.49	6.8E+00	BE960001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:396089 5'
9942	22284	35488	1.55	6.2E+00	AY110901.1	NT	Schizosaccharomyces commune unknown mRNA
10460	23108	36337	0.5	6.2E+00	8754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
6930	19871	32717	1.48	6.0E+00	BE760163.1	EST_HUMAN	601488031F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3871303 5'
9716	22367	35555	0.48	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1486000 nt, position (877)
10411	23057	36274	0.87	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36275	0.87	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6428	19186	32103	7.32	5.8E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlck3) and two pore domain K ⁺ channel subunit (Kcnk6) genes, complete cds
3514	16270		0.99	6.8E+00	7661557	NT	Homo sapiens DESCT1 protein (DESCT1), mRNA
7081	19752	32819	0.95	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

Page 5 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7091	19752	32817	0.95	5.7E+00	AF302049.1	NT	Mus musculus Immunoglobulin scavenger receptor (gR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11456	23223	36458	2.59	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
6157	18334	31801	0.95	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10678	23089		1.28	5.3E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11454	23221	36455	3.09	5.5E+00	P11960	SWISSPROT	PNEUMOLYSIN (THIOALACTIVATED CYTOLYSIN)
6930	19462	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
6930	19462	32515	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7769	20465		1.54	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8958	21390	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8958	21390	34535	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
5938	22594	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
5938	22594	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17466	30102	1.32	5.3E+00	L43726.1	NT	Bovine Immunodeficiency virus surface envelope gene, 5' end of cds
7978	20673		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
11628	24225		3.2	5.3E+00	Q27805	SWISSPROT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
8982	21573		0.49	5.3E+00	AB034980.1	NT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5371	16177	37548	0.91	5.2E+00	BE184940.1	EST_HUMAN	QV4-HT10601-270400-186-009 HT10891 Homo sapiens cDNA
10271	22919		0.95	5.2E+00	AF248070.1	SWISSPROT	Drosophila crinifera R1B retinoblastoma element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10138	SWISSPROT	HYPOTHECAL 61.1: KD PROTEIN C23E2.03C IN CHROMOSOME 1
8951	21562	34598	0.9	5.1E+00	O16005	SWISSPROT	RHODOPSIN
6725	22378	35577	1.19	5.1E+00	P09162	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6193	18593	31944	0.72	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.99	5.0E+00	BF308961.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22977	36197	3.07	5.0E+00	AF162445.2	NT	Carla famillaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11250	23922		8.95	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
10132	22780		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RORC gene, and sodium phosphate transporter (NPT3) gene, complete cds
4039	16784		10.86	4.8E+00	AF185255.1	NT	Eucite australis histone H3 (H3) gene, partial cds
8054	20449	33878	0.47	4.8E+00	BF387809.1	EST_HUMAN	RC3-GN0042-100800-071-c10 GN0042 Homo sapiens cDNA
8439	21131		5.28	4.8E+00	AW150087.1	EST_HUMAN	PMB-B10547-310100-002-004 BT0547 Homo sapiens cDNA
283	13080	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'

Page 6 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
264	13090	25731	1.89	4.7E+00	BF240552.1	EST_HUMAN	601873654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3288	16030	28679	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9095	21783	34948	1.18	4.9E+00	BE64437.1	EST_HUMAN	7e8g10.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 075140 KIA0046 PROTEIN, contains element PTR5 repetitive element;
9095	21783	34949	1.18	4.9E+00	BE64437.1	EST_HUMAN	7e8g10.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 075140 KIA0046 PROTEIN, contains element PTR5 repetitive element;
10287	22935		0.61	4.9E+00	AF240789.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11054	23724		2.31	4.9E+00	D83989.1	NT	Synchocytis sp. PCC6803 complete genome, 18/27, 2267260-2392728
11605	24204	37526	2.59	4.9E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11782	24353	37985	1.78	4.9E+00	BF6684.1	EST_HUMAN	602123235F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280216 5'
3035	16801	28447	0.89	4.4E+00	BF530893.1	EST_HUMAN	602072595F1 NCI_CGAP_Bln87 Homo sapiens cDNA clone IMAGE:4216284 5'
3035	16801	28448	0.88	4.4E+00	BF530893.1	EST_HUMAN	602072595F1 NCI_CGAP_Bln87 Homo sapiens cDNA clone IMAGE:4216284 5'
6109	18886		1.85	4.4E+00	X13414.1	NT	Muthe 1 gene for MHC class II (a) associated invariant chain
6027	18807		0.68	4.3E+00	AF056978.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7238	20019	33097	2.03	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
7515	20188	33280	0.85	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
10769	23453	36696	7.64	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5507	18305	31206	0.87	4.2E+00	P51828	SWISSPROT	IAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6874	18691	32827	2.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6974	18991	32828	2.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8859	21550	34697	4.68	4.2E+00	AJ09013.1	EST_HUMAN	wf67g03.x1 Soares_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360682 3'
6818	22469	35672	1.08	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (FOU DOMAIN PROTEIN 1) (FDM-1) (DFOU-19) (DOOCT1)
10048	22697		0.48	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
5846	25079	31569	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P63
5846	25079	31570	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P63
7012	19704	32780	0.84	4.1E+00	BE256668.1	EST_HUMAN	601107272F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351534 5'
7111	19789	32893	0.85	4.1E+00	BF247939.1	EST_HUMAN	60169030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069788 5'
7659	20229	33332	8.73	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7691	20345		0.82	4.1E+00	AB041523.1	NT	Pathoquery: yescensilis miRNA for calcineurin A, complete cds
7683	20347	33459	4.32	4.1E+00	P28864	SWISSPROT	GENE 66 PROTEIN

Page 7 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20347	33480	4.32	4.1E+00	P25954	SWISSPROT	GENE 68 PROTEIN
7817	20512	33038	2.53	4.1E+00	U57603.1	NT	Penicillin-binding novel repetitive sdo LTR element in the RNU2 locus
9440	22118	35295	0.67	4.1E+00	P11283	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.48	4.1E+00	BF692435.1	EST_HUMAN	60247683F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
							CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10206	22853		0.48	4.1E+00	P46414	SWISSPROT	(P27KIP1)
10800	23483		3.05	4.1E+00	P08716	SWISSPROT	HYPOTHETICAL PROTEIN RVLF1
10892	23572		11.69	4.1E+00	BE885880.1	EST_HUMAN	001607610F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908051 5'
3533	16289		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	19500	32524	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5372	19500	32525	0.77	4.0E+00	O52653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6938	19500	32524	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6938	19500	32525	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7039	19776	32943	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21494	34611	0.45	4.0E+00	O14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
8843	22404	35695	0.44	4.0E+00	O51309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10095	22713	35631	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 50 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
							GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11637	24137	37444	2.27	4.0E+00	P07564	SWISSPROT	
							GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07564	SWISSPROT	
3494	10280	28904	4.61	3.9E+00	X64518.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
4287	17026		8.24	3.9E+00	AF065468.1	NT	
5572	15369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5572	15369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6591	19354	32367	0.55	3.9E+00	U01328.1	NT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
6774	19518	32546	4.92	3.9E+00	P39299	SWISSPROT	

Page 8 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7282	18948	33022	4.3	3.9E+00	M23007.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8216	20910	34049	1.88	3.9E+00	X58965.1	NT	X. laevis mRNA for MA muscarinic receptor
11365	23178	36403	3.3	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2656	16347		0.9	3.9E+00	AE001582.1	NT	Helicobacter pylori, strain 189, section 123 of 132 of the complete genome
6297	18070	32054	0.96	3.9E+00	Q37830	SWISSPROT	HYPOPHYSAL PROTEIN MJ0385
6673	19580	32626	0.96	3.9E+00	AA93849.1	EST_HUMAN	q25107.x1 NCI_OGAP_Kid1 Human sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34161	1.1	3.9E+00	DA4725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
8694	22345		0.62	3.9E+00	AL390061.1	NT	Streptococcus cricetus partial xat gene for xanthine phosphoribosyltransferase, strain NGT C7884
4001	16748	26379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7066	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 316
8609	21301		0.95	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9076	21765	34828	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24057	37953	2.23	3.7E+00	BF66279.1	EST_HUMAN	602120551FT NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24057	37354	2.23	3.7E+00	BF66278.1	EST_HUMAN	602120551FT NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
576	13359	26986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4746	17477		1.06	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17893	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	601801866FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131018 5'
8460	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000T098 Liver HepG2 cell line. Homo sapiens cDNA clone 1608
8460	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000T1008 Liver HepG2 cell line. Homo sapiens cDNA clone 1608
8543	21235	34378	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gfpE), the translation start site has been verified (gfpC), and repressor protein (gfpR) genes, complete cds
10759	23444		4.07	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3241	16003	28652	1.1	3.5E+00	AF221533.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
5911	18695		1.17	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 250115) outer surface protein (ospC) gene, partial cds
5118	18696	31864	1.18	3.5E+00	R10745.1	EST_HUMAN	3940208.r1 Soera infant brain IN1B Homo sapiens cDNA clone IMAGE:34940 5'
8383	21076		0.96	3.5E+00	P24657	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8930	21021	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86604.at Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
8930	21621	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86604.at Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
8393	22055	35227	0.96	3.6E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10417	28063	36283	0.46	3.4E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	26933	2.64	3.4E+00	AF264577.1	NT	Breskian naps RPB5d mRNA, complete cds
7261	18945	33021	2.64	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7601	20267	33374	0.68	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8571	21289		0.7	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channel ROMK1, ROMK2, ROMK3, ROMK4, ROMK5, and ROMK6 (KCNK1) gene, complete cds
8972	21662	34813	0.87	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9010	21700	34850	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10164	22812	36030	2.97	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11518	24119	37429	1.88	3.4E+00	L77570.1	NT	Homo sapiens Digeorge syndrome critical region, centromeric end
5971	18769	31722	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5971	18759	31723	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7764	20489	33611	0.79	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
488	13273	25808	1.64	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4004	13273	25808	0.9	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4679	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5461	18280	31176	1.08	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5461	18280	31177	1.08	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12763	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12763	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18998	31664	1.78	3.2E+00	P16691	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
9214	18998	31965	1.78	3.2E+00	P16691	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7505	20176	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13955.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ysf4, ysf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13955.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ysf4, ysf3, rps18 genes
8926	21618		4.31	3.2E+00	P13061	SWISSPROT	PERPLASMIC [NFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENYLASE SMALL CHAIN)
9430	22108	33283	0.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LVT) gene, complete cds
10041	22609	36907	2.03	3.2E+00	AB016081.2	NT	Oryzias latipes DIC68 gene for guanylyl cyclase C, complete cds
11948	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.48	3.1E+00	O10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C2E2.02 IN CHROMOSOME 1
7197	18970	33047	0.93	3.1E+00	P62178	SWISSPROT	TRIOSE PHOSPHATE PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (C1P1)

Page 10 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7627	20293		0.94	3.1E+00	AF503225.1	NT	Beclitea dicolophus pectate lyase (cdE) gene, complete cds
7698	20881	33507	0.48	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LEASE HUL4
8500	21192	34333	4.36	3.1E+00	P46884	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
8500	21192	34334	4.35	3.1E+00	P46884	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
9188	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9798	22447	35652	0.59	3.1E+00	7524759	NT	Chloridia vulgaris chloroplast, complete genome
9898	22538		0.83	3.1E+00	Q10125	SWISSPROT	HYPOPHYSAL 58.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10234	22882	36065	5.52	3.1E+00	P49365	SWISSPROT	DEOXYHYPOSINE SYNTHASE (DHS)
11440	23207		2.86	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A, AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS3); retinoid acid nuclear receptor isoform beta 2 [nile, embryonal carcinoma cell line, PCCT-MZ1, mRNA, 2971 nt]
11463	24066		3.28	3.1E+00	S56660.1	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
2842	15810	28259	1.09	3.0E+00	8023984	NT	S. aureus genes encoding Sae98I DNA methyltransferase and Sae98I restriction endonuclease
5294	18060	30689	1.32	3.0E+00	X53098.1	NT	Corynebacterium glutamicum trnC gene for threonine synthase (EC 4.2.99.2)
6491	19228	32228	0.83	3.0E+00	X59037.1	NT	Corynebacterium glutamicum trnC gene for threonine synthase (EC 4.2.99.2)
6491	19228	32229	0.83	3.0E+00	X59037.1	NT	CYR61 PROTEIN PRECURSOR (3CH61)
7055	19746		0.09	3.0E+00	P18408	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
7056	19765		0.8	3.0E+00	Q13201	SWISSPROT	B. napus DNA for myosinase
8605	21497		1.2	3.0E+00	X37538.1	NT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10192	22840	36055	0.62	3.0E+00	Q68605	SWISSPROT	GDCT0 PROTEIN HOMOLOG
10544	23240	36474	1.57	3.0E+00	Q16181	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-2)
10931	23611	36880	8.44	3.0E+00	P61842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-2)
10931	23611	36961	6.44	3.0E+00	P61842	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
11578	24177	37462	2.72	3.0E+00	P34184	SWISSPROT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
2004	14740	27464	2.28	2.9E+00	A6002225.2	NT	F-primed gcpA gene for P-protein of the glycine cleavage system
6809	19470	32483	1.74	2.9E+00	Z39878.1	NT	BRIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7110	19768	32981	5.21	2.9E+00	Q14514	SWISSPROT	

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7110	19788	32882	5.21	2.8E+00	014514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	8.84	2.8E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.87	2.8E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.87	2.8E+00	P06844	SWISSPROT	NONSTRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7805	20591	33819	1.03	2.8E+00	BF344171.1	EST HUMAN	602017413F1 NCL CGAP Brn68 Homo sapiens cDNA clone IMAGE:4169589 5'
1440	14187	26572	4.41	2.8E+00	AF196358.1	EST HUMAN	Buxus hartiensis malvaceae K (malik) gene, partial cds; chloroplast gene for chloroplast product
1629	14375		2.74	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32988	5.72	2.8E+00	8393724	NT	Mus musculus endomucin (LOC83423), mRNA
8513	22168		0.94	2.8E+00	BE565182.1	EST HUMAN	601342768F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3884807 5'
10588	16892	32968	1.32	2.8E+00	8393724	NT	Mus musculus endomucin (LOC83423), mRNA
224	13036	25672	13.51	2.7E+00	6678308	NT	Mus musculus per-hexamer repeat gene 3 (Phox3), mRNA
224	13036	25673	13.51	2.7E+00	6678308	NT	Mus musculus per-hexamer repeat gene 3 (Phox3), mRNA
5484	18283	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apoa4 polymorphism (Kingle IV gene, exons 1 and 2)
8045	20739		0.6	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8907	21558		1.83	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation xc88412.x1 NCL CGAP Brn35 Homo sapiens cDNA clone IMAGE:2891374 3' similar to gbl:M17733
9332	20403	33516	0.73	2.7E+00	AW088101.1	EST HUMAN	THYMOSIN BETA-4 (HUMAN);
10397	23043		1.75	2.7E+00	BE063527.1	EST HUMAN	GM-BT0281-031159-087-H04 BT0281 Homo sapiens cDNA
4626	17361	26984	5.15	2.6E+00	AF068749.1	NT	GM-BT0281-031159-087-H04 BT0281 Homo sapiens cDNA
5480	18259	31149	1.08	2.6E+00	6766601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5480	18259	31150	1.98	2.6E+00	6766601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5736	18528		0.89	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	25424		0.82	2.6E+00	AJ224630.1	NT	Mycobacterium fortuitum furA II gene
7600	20266		0.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7958	20553	33776	1.13	2.6E+00	AJ132180.1	NT	Mus musculus SH-2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7958	20553	33777	1.13	2.6E+00	AJ132180.1	NT	feba been necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9057	22210	33585	2.83	2.6E+00	AL161540.2	NT	feba been necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10253	22901		1.87	2.6E+00	6056103	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10583	23530	36876	1.32	2.6E+00	AF143676.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12560	25304		3.17	2.6E+00	11418220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14185	26878	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
							Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1448	14195	26679	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6397	18515	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6397	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6530	19392	32406	0.84	2.5E+00	D30052.1	NT	Vibrio cholerae cdaA gene and cdaB gene for cholera toxins, complete cds
7659	20323	33431	0.99	2.5E+00	AW049168.1	EST_HUMAN	QY4-FT0005-110500-205-407 FT0003 Homo sapiens cDNA
7700	20363	33477	0.69	2.5E+00	4502802	NT	Rice DNA for aldolase C-1, complete cds
9001	21691	34941	1.53	2.5E+00	D60307.1	NT	60117579F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531080 5'
9752	22403	35608	0.67	2.5E+00	BE207758.1	EST_HUMAN	DNABJ PROTEIN
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	Mus musculus E1F4H gene, partial cds; LINK1 gene, complete cds; and ELN gene, partial cds
11943	24498		3.08	2.5E+00	AF265665.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
3012	16778	29428	1.73	2.4E+00	M24282.1	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
4849	17578	30203	6.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN1 PRECURSOR (YOLK PROTEIN 1)
5920	18705	31957	4.16	2.4E+00	BF687502.1	EST_HUMAN	602120855F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	18694	33040	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120855F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	18694	33041	0.78	2.4E+00	BF687502.1	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
9039	20734	33985	2.4	2.4E+00	P28942	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
9039	20734	33985	2.4	2.4E+00	P28942	SWISSPROT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8110	20804		2.63	2.4E+00	AE001486.1	NT	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
8549	21241		1.81	2.4E+00	AW875128.1	EST_HUMAN	ENDOGUTININASE B PRECURSOR (CHN-B)
8727	21419	34553	7.36	2.4E+00	P24091	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9938	22598	35768	2.66	2.4E+00	P13973	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9938	22598	35769	2.66	2.4E+00	P13973	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10037	22655	35988	1.86	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10143	22761		6.65	2.4E+00	P09069	SWISSPROT	XYLOLASE KINASE (XYLUKINASE)
10220	22868	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	h6306.01 NCI CCAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22868	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	h6306.01 NCI CCAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10490	23136	36384	0.87	2.4E+00	Q31481	SWISSPROT	DEMYELINATION REGULATORY PROTEIN NRQ
11331	24022	37327	2.16	2.4E+00	AF156552.2	NT	Fregeria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-e allele, complete cds
1231	13980	26550	13.6	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4102	16845		1.35	2.3E+00	AJ401081.1	NT	Bos taurus partial cyb gene for cytochrome b

Page 13 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5744	18598		0.65	2.3E+00	N88245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYL-CARBOXYPEPTIDASE
7354	20035	33113	2.47	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7495	25425		3.07	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	1.01	2.3E+00	X50255.1	NT	Mus mus domestica and dnas genes homologues coding for DnaK and DnaJ
8008	21698	34949	0.64	2.3E+00	5833317	NT	Polyporus cratipennis mitochondrion, complete genome
8068	21757	34919	1.8	2.3E+00	Q11127	SWISSPROT	ALPHA-1,3-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
10704	23395	36632	3.83	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11782	24373	37703	3.03	2.3E+00	BF541987.1	EST_HUMAN	602059121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11782	24373	37704	3.03	2.3E+00	BF541987.1	EST_HUMAN	602059121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24642	31099	8.84	2.3E+00	BE995237.1	EST_HUMAN	607438373F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
3699	16746	29378	0.95	2.2E+00	AF205228.1	NT	Magnaporthe oryzae Class IV chitin synthase (chs4) gene, complete cds
4278	17017	29644	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4278	17017	29645	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)(>)
5258	18084	30692	12.73	2.2E+00	O98307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)(>)
5258	18084	30693	12.73	2.2E+00	O98307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)(>)
5763	18554	31478	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5763	18554	31479	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5971	18753	31714	9.84	2.2E+00	BE250393.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6261	19035	32010	3.87	2.2E+00	Q00393	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6502	19287	32269	3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8851	17598		3.84	2.2E+00	AA594574.1	EST_HUMAN	in59502.s1 NC1 CGAP_Cg10 Homo sapiens cDNA clone IMAGE:1058379 3'
7217	18802	32975	0.9	2.2E+00	AA137027.1	EST_HUMAN	2967704.1 Straligene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565143 5'
7507	20178	33272	19.2	2.2E+00	AA448012.1	EST_HUMAN	2005g10.1 Soares_fetal_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:785834 5'
7698	20257	33365	0.72	2.2E+00	P64918	SWISSPROT	ALANINE RACEMASE
							b677h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2983207 3' similar to gb:D45936 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8001	20696	33823	0.58	2.2E+00	BE301580.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8001	20698	33824	0.68	2.2E+00	BE301580.1	EST_HUMAN	b57h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2663207.3 similar to gb:D46836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE).
8241	21920		11.02	2.2E+00	BE741678.1	EST_HUMAN	601694733.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3848561.5
9468	25124		2.28	2.2E+00	Q04705	SWISSPROT	TRANSPUSON TY1 PROTEIN A
9653	22601	35804	1.1	2.2E+00	A1290373.1	EST_HUMAN	qm59003.x1 Soares_Placenta_869weeks_2NHHP869W Homo sapiens cDNA clone IMAGE:1893965.3 similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN)
9953	22601	35805	1.1	2.2E+00	A1290373.1	EST_HUMAN	qm59003.x1 Soares_Placenta_869weeks_2NHHP869W Homo sapiens cDNA clone IMAGE:1893965.3 similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN)
9998	22644	35858	2.68	2.2E+00	BF246782.1	EST_HUMAN	601694733.F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075391.5
10333	23000	36217	3.11	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 KDa protein hGR74 homolog mRNA, complete cds
11418	23185	36415	3.47	2.2E+00	P07811	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11616	24214	37539	5.89	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
556	15545	25867	8.3	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region end upstream region
3576	16330		1.08	2.1E+00	AW 446368.1	EST_HUMAN	U1H-813-aid-e-08-0-U1.s1 NCL_CGAP_Sub05 Homo sapiens cDNA clone IMAGE:2734850.3
6041	18821		0.89	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
9710	18925	32669	3.95	2.1E+00	Q70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6846	19428	32443	5.72	2.1E+00	N29575.1	EST_HUMAN	Y08a10.s1 Soares_melanocytes_2NHIM Homo sapiens cDNA clone IMAGE:270818.3 similar to gb:M56554
8395	21088		1.97	2.1E+00	AU129630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	AU129630 NT 2RM2 Homo sapiens cDNA clone NT2RM2000671.5
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p220kdel (DOKDEL) mRNA, complete cds
1312	14060	26735	0.97	2.0E+00	AF204927.1	NT	Homo sapiens p220kdel (DOKDEL) mRNA, complete cds
1559	14318		2.61	2.0E+00	P25582	SWISSPROT	Onchocerca cuticularis Nt-K-A1Pase beta 1 subunit mRNA, complete cds
2145	14875	27609	5.98	2.0E+00	Z78279.1	NT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2145	14875	27610	5.98	2.0E+00	Z78279.1	NT	R.novgolicus mRNA for collagen alpha1 type 1
4080	16824	29450	2.2	2.0E+00	AW664498.1	EST_HUMAN	h13d05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168.3 similar to gb:X01677
4080	16824	29451	2.2	2.0E+00	AW664498.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7449	20125		0.92	2.0E+00	P07568	SWISSPROT	h13d05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168.3 similar to gb:X01677
7923	20618	33745	3.17	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7923	20618	33746	3.17	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds

Page 15 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8820	21512	34556	3.15	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12461	26285	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.9E+00	6754359	NT	Mus musculus Insulin 1,4,6-triphosphate receptor 1 (Iipr1), mRNA
5511	18309	31210	4.77	1.9E+00	6754359	NT	Mus musculus Insulin 1,4,6-triphosphate receptor 1 (Iipr1), mRNA
6009	18780	31753	1.32	1.9E+00	BE969595.1	EST_HUMAN	601679836F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6556	19321		0.75	1.9E+00	AW845899.1	EST_HUMAN	MRO-CT0083-071099-002-g02 CT0083 Homo sapiens cDNA
6650	19412		2.48	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34190	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21246		2.94	1.9E+00	BF390208.1	EST_HUMAN	CM3-MT0114-010800-323-h12 MT0114 Homo sapiens cDNA
8782	21484		1.33	1.9E+00	O51761	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9530	22183	35397	0.69	1.9E+00	AA669125.1	EST_HUMAN	ad54604.6t Stratagene lung (M937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element/contains element L1 L4 repetitive element ;
10462	23108	36339	0.62	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pod precursor protein gene, partial cds
3056	15854	28466	1.3	1.9E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3118	15883	28522	1.57	1.8E+00	U04355.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3178	15883	28523	1.57	1.8E+00	U04355.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5717	16598		1.91	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6013	18794		1.32	1.8E+00	BF311589.1	EST_HUMAN	601687854F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4123364 5'
6306	19077		1.12	1.8E+00	BF683327.1	EST_HUMAN	602193470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:428272 5'
8041	19403	32418	1.84	1.8E+00	BF305652.1	EST_HUMAN	601683469F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
6958	19440	32455	1.76	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8388	21081	34201	0.44	1.8E+00	P46634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8388	21081	34202	0.44	1.8E+00	P46634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8388	21081	34203	0.44	1.8E+00	P46634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8753	21446	34593	1.98	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9073	21792	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	JH72208.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	QVO-070303-070303-148-a03 OT0030 Homo sapiens cDNA

Page 16 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9748	22400	35805	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PR00630 mRNA, complete cds
10452	23098		0.63	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12276	28236		6.28	1.8E+00	AF314284.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	8509404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
1086	13844	26502	2.21	1.7E+00	C60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27334	2.28	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2372	15094	27833	2.66	1.7E+00	AI141067.1	EST_HUMAN	oz33105.x1 Soares_NIHMPu_S11 Homo sapiens cDNA clone IMAGE:1078137 3'
4426	17162	29782	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31223	1.77	1.7E+00	BE063548.1	EST_HUMAN	CMD-BT0282-171295-127-c05 BT0282 Homo sapiens cDNA
5525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMD-BT0282-171295-127-c05 BT0282 Homo sapiens cDNA
5927	18711	31668	3.28	1.7E+00	CG1778	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7118	19906	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 39.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19906	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 39.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7763	20449	33578	0.91	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7832	20527	33758	1.13	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall1), mRNA
7861	20566	33761	0.59	1.7E+00	BF330630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bri87 Homo sapiens cDNA clone IMAGE:4214669 5'
8440	21132	34268	0.5	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8805	21297	34440	0.59	1.7E+00	X69063.1	NT	Mus musculus Ank-1 mRNA for erythroid enkyrin
8605	21297	34441	0.69	1.7E+00	X69063.1	NT	Mus musculus Ank-1 mRNA for erythroid enkyrin
9047	25123	34892	2.18	1.7E+00	C60478	SWISSPROT	HOMEBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	C60478	SWISSPROT	HOMEBOX PROTEIN DLX-3
9506	22159		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10071	22719		0.48	1.7E+00	AW963881.1	EST_HUMAN	EST365761 IMAGE:rescues, MAGC Homo sapiens cDNA
11596	24169	37514	2.57	1.7E+00	WZ2424.1	EST_HUMAN	9787 Human retina cDNA Tsp508-cleaned sublibrary/Homo sapiens cDNA not directional
12231	24684	31074	1.9	1.7E+00	AI678443.1	EST_HUMAN	tsu2207.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2267549 3' similar to contains MSR1.11
12717	24990	30970	1.84	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element;
2027	14762	27491	18.51	1.6E+00	AF199339.1	NT	q150b01.x1 Soares_1estis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element;
							(Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2036	14771	27500	3.75	1.6E+00	AF07374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27506	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2282	15007		1.24	1.6E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
2881	15727	28377	1.61	1.6E+00	W68428.1	EST_HUMAN	225601.1 Soares fetal heart_NH4H18W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb0286905 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4011	16757		5.66	1.6E+00	BF570077.1	EST_HUMAN	60218605611 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	29682	1.9	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SVARCA6) mRNA, complete cds
4319	17058	29683	1.9	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SVARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	AF075394.1	NT	Urethralis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17669	30278	0.84	1.6E+00	AF075394.1	NT	Urethralis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5737	18529	31450	2.16	1.6E+00	LQ4608.1	NT	Brachyidius reno MHC class II D-beta-2701 gene, 3' end
5823	18612	31543	0.79	1.6E+00	AF005631.1	NT	IL2-UT0073-090900-145-E02 UT0073 Homo sapiens cDNA
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	U14-H12-ah-b-04-DJ1.1 NCL DGAP Sub4 Homo sapiens cDNA clone IMAGE:2727811 3'
6510	19373	32387	1.08	1.6E+00	AW264881.1	EST_HUMAN	RCO-CT0416-20700-032-c10 CT0416 Homo sapiens cDNA
7145	19632	32801	2.73	1.6E+00	BE697287.1	EST_HUMAN	VRULENCE FACTOR WVIN HOMOLOG
7829	20624		1.19	1.6E+00	Q46378	SWISSPROT	Mus musculus SIL_MAP_17_CYP_a_SCL & CYP_b genes
8277	20971	34112	3.28	1.6E+00	AJ297131.1	NT	Homo sapiens hypodermal protein PRO0971 (PRO0971), mRNA
8798	21490	34636	0.83	1.6E+00	11437222	NT	Homo sapiens hypodermal protein PRO0971 (PRO0971), mRNA
8798	21490	34637	0.83	1.6E+00	11437222	NT	Homo sapiens hypodermal protein PRO0971 (PRO0971), mRNA
8970	21660	34910	0.47	1.6E+00	BE386835.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9360	25121	33549	1.84	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha1
9360	25121	33550	1.84	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha1
9437	22140		0.68	1.6E+00	AF043468.1	NT	Thermoplasma acidophilum D-xylose-binding protein (xyf) gene, complete cds
9634	22265	35480	1.32	1.6E+00	141250.1	EST_HUMAN	ph8B_16/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph8B_16/1TV
10047	22695		0.5	1.6E+00	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase (AL), end
10035	22733	35947	1.15	1.6E+00	AF121381.1	EST_HUMAN	Zinc finger protein (UNZ1) genes, complete cds
10095	22733	35948	1.15	1.6E+00	AF121381.1	EST_HUMAN	QV4-L10016-090200-100-407 LT0016 Homo sapiens cDNA
10242	22860	36102	0.47	1.6E+00	AF037352.1	EST_HUMAN	QV4-L10016-090200-100-407 LT0016 Homo sapiens cDNA
10461	23137	36385	0.45	1.6E+00	AF162084.1	NT	Mus musculus cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
							Gluga pleoclonis beta-tubulin 2 (btub2) gene, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10670	23351	36602	1.95	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN [nc16002.61 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008267 similar to contains element MER4 repetitive element];
10728	23416	36657	1.27	1.6E+00	AJ271687.1	EST_HUMAN	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
10747	18812	31643	5.27	1.6E+00	AF006931.1	NT	Homo sapiens unknown mRNA
11705	24300	37626	3.46	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12859	25476	5.31	1.5E+00	U63449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25574	2.2	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AK39, section 32 of 84 of the complete genome
608	13384		2.03	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (melagidin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato Virus A RNA complete genome, isolate U
2519	16236	27975	2	1.5E+00	6678360	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tlimt1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato Virus A RNA complete genome, isolate U
3388	16127	28785	0.72	1.5E+00	AE001845.1	NT	Dainiboccus radiodurans R1 section 82 of 228 of the complete chromosome 1
5842	18437	31350	0.83	1.5E+00	AI655301.1	EST_HUMAN	h1210.x1 NCL_CGAP_GC05 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
5842	18437	31351	0.83	1.5E+00	AI655301.1	EST_HUMAN	h1210.x1 NCL_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
6312	19093	32068	3.02	1.5E+00	RI17879.1	EST_HUMAN	Y019602.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:311693 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	G01478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3687555 5'
7060	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOPHYSICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7060	18751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOPHYSICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7245	19930	35066	0.61	1.5E+00	A4889259.1	EST_HUMAN	h26210.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7468	20166	35257	0.78	1.5E+00	AI003254.1	EST_HUMAN	h07611.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684863 3' similar to gb:595936 SEROTRANSFERRIN PRECURSOR (HUMAN);
7727	20390		0.64	1.5E+00	AB039887.1	NT	Homo sapiens WD44 gene for WD repeat protein, complete cds
8021	20716	33848	0.89	1.5E+00	BE587446.1	EST_HUMAN	G0150586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02138.1	NT	Mouse gamma IgM chain gene, mu-delta region
8814	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens NGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34876	0.48	1.5E+00	BF217818.1	EST_HUMAN	G01882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9093	22045	35217	0.64	1.5E+00	R91928.1	EST_HUMAN	Y03801.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147697 5'
9335	22186	35374	1.39	1.5E+00	AW375967.1	EST_HUMAN	G03-CT0192.261099-008-008 CT0192 Homo sapiens cDNA
9760	22411	35618	8.39	1.5E+00	BF376764.1	EST_HUMAN	RC0-TN0078-150000-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF337644.1	EST_HUMAN	G02035771F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
10096	22744	35958	1.66	1.5E+00	AA017666.1	EST_HUMAN	z93803.g11 Soares retina N28-4HR Homo sapiens cDNA clone IMAGE:361308 5'

Page 19 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10068	22744	35659	1.09	1.5E+00	AA017689.1	EST_HUMAN	2a38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11375	23982	37282	4.46	1.5E+00	AL134197.1	EST_HUMAN	DKFZP547P243_s1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZP547P243 3'
11530	24130		0.65	1.5E+00	X07380.1	NT	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11626	24226	37549	2.1	1.5E+00	AI400788.1	EST_HUMAN	ig94d09.x1 NCI CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2116433 3'
11628	24226	37550	2.1	1.5E+00	AI400788.1	EST_HUMAN	ig94d09.x1 NCI CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2116433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12445	24815		3.93	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
28	12858	25472	2.78	1.4E+00	7661685	NT	Homo sapiens DKFZP568M0122 protein (DKFZP568M0122), mRNA
28	12858	25473	2.78	1.4E+00	7661685	NT	Homo sapiens DKFZP568M0122 protein (DKFZP568M0122), mRNA
2333	15057		0.92	1.4E+00	U67822.1	NT	Ovis aries prion protein gene, complete cds
2675	15384	28125	2.21	1.4E+00	X74483.1	NT	Human papillomavirus type 7 genomic DNA
2776	15481	28221	2.61	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2778	15481	28222	2.61	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4543	17280		1.81	1.4E+00	BF081547.1	EST_HUMAN	6021688B7F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4287566 5'
5288	18053	30754	1.61	1.4E+00	AW054976.1	EST_HUMAN	wk45g07.x1 NCI CGAP_Pant Homo sapiens cDNA clone IMAGE:2510460 3'
5441	18240		5.67	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6168	18653	31838	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0505 protein, complete cds
6318	19089	32074	2.67	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II
6318	19089	32075	2.67	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II
7188	19872	32946	2.07	1.4E+00	AJ132589.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7201	19887	32962	1.17	1.4E+00	AW467760.1	EST_HUMAN	hep3105.x1 NCI CGAP_GML1 Homo sapiens cDNA clone IMAGE:2918973 3' similar to contains Alu repetitive element;
7258	19942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7258	19942	33019	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8293	20927		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN (GLUCOHYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8891	21681	34629	1.73	1.4E+00	R20459.1	EST_HUMAN	y93f312.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:34345 5'
9097	21765	34951	4.65	1.4E+00	BE094667.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9131	21819	34955	0.51	1.4E+00	AF134844.1	NT	Scoloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds

Page 20 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10108	22756	35688	0.79	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:428187 5'
10151	22759	36015	0.81	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT10186-291099-008-C04 HT0168 Homo sapiens cDNA
10151	22769	36016	0.81	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT10186-291099-008-C04 HT0168 Homo sapiens cDNA
10424	23070	36281	1.08	1.4E+00	D63441.1	NT	Pandorina colonensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	36282	1.05	1.4E+00	D63441.1	NT	Pandorina colonensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23675	36831	1.34	1.4E+00	AA195528.1	EST_HUMAN	233609.1 Soares_NHHPMU_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;
11188	23653	37139	6.16	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11381	23088	37283	4.42	1.4E+00	BE982107.2	EST_HUMAN	60165154R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11381	23088	37283	4.42	1.4E+00	BE982107.2	EST_HUMAN	60165154R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.48	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. rattii guanine nucleotide binding protein alpha subunit (pgt1) gene, complete cds
11404	24053	37358	3.46	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. rattii guanine nucleotide binding protein alpha subunit (pgt1) gene, complete cds
12079	25256		1.48	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
667	13339		1.81	1.3E+00	Z73840.1	NT	Mnucodo gene encoding 4-Dihydroxyethyl-trisoprate dehydrogenase
892	13651	26320	3.42	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1107	13864		20.26	1.3E+00	Y18213.1	NT	Homo sapiens putative psbH-bA pseudogene for hair keratin, exons 2 to 7
1274	14024	26592	13.71	1.3E+00	4507968	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1274	14024	26593	13.71	1.3E+00	4507968	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Cox acetylme-coA dihydrodipicolinate synthase (dipa) gene, complete cds
1605	14351		2.27	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2239	14967		1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPs and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2405	15126	27862	1.27	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2553	15268		1.75	1.3E+00	BE966736.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2840	15705	28354	0.73	1.3E+00	6755921	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
3594	16339	28584	0.89	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), avianlike vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5427	18226	30838	1.09	1.3E+00	F19132	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5622	18418	31330	0.6	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
5903	18500	31590	0.81	1.3E+00	BF603825.1	EST_HUMAN	60214524F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4306095 5'
5928	18712	31697	7.57	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-281199-004-f08 CT0289 Homo sapiens cDNA

Page 21 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5828	18712	31868	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMB-CT0289-291169-004-08 CT0289 Homo sapiens cDNA
6323	18053	32081	1.34	1.3E+00	M33486.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6652	18414		0.76	1.3E+00	Q00156	SWISSPROT	HYPOPHOSPHATE
6739	18573	32506	0.82	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
6834	18554	32584	1.17	1.3E+00	BE538919.1	EST_HUMAN	60108142031 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7000	16892	32743	0.81	1.3E+00	BE243571.1	EST_HUMAN	TCBAP100959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project CBA Homo sapiens cDNA clone TCBAP0959
7358	20039	33117	1.01	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8197	20891	34029	1.28	1.3E+00	AJ009912.1	NT	Sua acd4a pip gene
8348	21039	34176	2.78	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3968195 3'
8459	21151	34294	0.86	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303		1.78	1.3E+00	5910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8659	21381	34525	0.79	1.3E+00	AJ927029.1	EST_HUMAN	w655a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
8415	22063		5.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-acetylaseN-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.55	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for phobylase
9424	22102	35274	2.56	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for phobylase
9524	22177	35361	0.85	1.3E+00	AF059260.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9559	22222	35407	1.56	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9631	22303	35498	1.14	1.3E+00	AJ927629.1	EST_HUMAN	w655a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
9726	22377	35578	0.79	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremicis NCDO-hv1 chromosomal inversion junction DNA
9726	22377	35579	0.79	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremicis NCDO-hv1 chromosomal inversion junction DNA
9768	22417	35624	4.53	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3968195 3'
9826	22477		0.48	1.3E+00	AJ659944.1	EST_HUMAN	ig77a12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gbX14723
10050	22698	35913	0.46	1.3E+00	AF081251.1	NT	CLUSTERIN PROTEIN (HUMAN);
10050	22698	35914	0.46	1.3E+00	AF081251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	35974	1.82	1.3E+00	AJ600430.2	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10130	22778	35991	1.35	1.3E+00	AJ600430.2	NT	Vibrio cholerae chromosome II, section 48 of 68 of the complete chromosome
10483	23129		0.82	1.3E+00	AL18302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10511	23157	36383	0.45	1.3E+00	AJ690846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C102
10522	23265		4.6	1.3E+00	Q14117	SWISSPROT	w632a10.x1 NCI_CGAP_GG8 Homo sapiens cDNA clone IMAGE:2486922 3' similar to SW:TRXB_HUMAN Q18891 THIOREDOXIN REDUCTASE ;
							Q18891 THIOREDOXIN REDUCTASE ;
							DIHYDROXYIMINASE (DHPASE) (HYDANTOINASE) (DHP)

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	36744	1.93	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNAT5
10846	23528	36772	2.01	1.3E+00	Z18922.2	NT	Mus musculus desmin gene
11307	23986		1.8	1.3E+00	AW214791.1	EST_HUMAN	XP00603.x1 NCJ CGAP HN9 Homo sapiens cDNA clone IMAGE:2739693 3'
11527	24127	37433	3.21	1.3E+00	DA2042.1	NT	Human mRNA for KIAA0035 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z86982.1	NT	Bacillus subtilis genomic DNA 23.8kDa fragment
12210	24675		2.64	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12358	24780	31035	6.3	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCJ CGAP Bm67 Homo sapiens cDNA clone IMAGE:4158462 5'
12397	25153		2.73	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	26848		2.15	1.3E+00	AF187035.1	NT	Stimula ilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
635	13414	26050	11.05	1.2E+00	AA876248.1	EST_HUMAN	Z22208.s1 Soares fetal liver spleen 1NF1LS S1 Homo sapiens cDNA clone IMAGE:431535 3'
804	13576	26239	0.87	1.2E+00	P06223	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
804	13576	26240	0.87	1.2E+00	P06223	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26241	0.87	1.2E+00	P06223	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
659	13627		1.35	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077). mRNA
1138	13893	26554	5.94	1.2E+00	AF060246.2	NT	Eleis oclifera sesquiterpene synthase mRNA, complete cds
1183	13935	26800	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26801	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140531.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15873	28512	1.24	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15926	28573	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15926	28574	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3280	16041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3659	16452	29091	0.68	1.2E+00	U75022.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3957	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MRQ-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4268	18110	28768	1.11	1.2E+00	AF188740.1	NT	Homo sapiens LH3 gene, intron 2
4438	17174		1.67	1.2E+00	M87060.1	NT	Rattus rattus cardiac AEs gene, exons 1-23
4487	17222	28850	0.66	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17258	28862	1.89	1.2E+00	AF158485.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4549	17293		6.43	1.2E+00	Y06200.1	NT	T. phaeum chloroplast bcd gene, partial
5351	18154	30836	1.1	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5467	18268	31158	1.91	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016062.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6000	18840	31801	2.51	1.2E+00	XT4885.1	NT	Dhysl av1 repeat cluster DNA, fragment D
6119	18897	31855	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-160-a03 BN0080 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6188	18974	31951	1.54	1.2E+00	X83984.1	NT	C. glutamicum pla gene and ackA gene
6188	18974	31952	1.54	1.2E+00	X83984.1	NT	C. glutamicum pla gene and ackA gene
6241	19015	31989	39.54	1.2E+00	AA759254.1	EST_HUMAN	ab84g12.at Scores, testis, NIH Homo sapiens cDNA clone 1322374 3'
6342	19112	32101	0.55	1.2E+00	N33295.1	EST_HUMAN	y63b12.at Scores melanocyte 2N3HM Homo sapiens cDNA clone IMAGE:273599 3' similar to g51487935.HUMAAALU472 Human carcinoma cell-derived Alu RNA transcript, (fRNA); gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6408	19177	32175	0.88	1.2E+00	P17671	SWISSPROT	ECDSYONE-INDUCIBLE PROTEIN E75-A
6412	19180	32179	2.06	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-005 ST0191 Homo sapiens cDNA
6815	19478	32498	1.77	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
6929	19840	32512	3.11	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7153	19840		0.84	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7292	25109	33044	4.96	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cDAAFH03 5'
7590	20220	33223	2.49	1.2E+00	XZ4267.1	NT	L. lactis pyrD and pyrF genes
7603	20269	33376	0.58	1.2E+00	J05278.1	NT	Chicken muscarinic acetylcholine receptor (m4 mAChR) gene, complete cds
7715	20378	33492	0.59	1.2E+00	BE787648.1	EST_HUMAN	g01481761.F1 NIH_JMGC_58 Homo sapiens cDNA clone IMAGE:3884270 5'
8467	21159	34302	3.32	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8591	21253	34391	0.68	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-GLUCOSEPHOSPHATE (TREHALOSE-6-PHOSPHATE PHOSPHATASE)
8776	21497		0.51	1.2E+00		NT	GLUCOSYLTRANSFERASE
8923	21614	34756	1.87	1.2E+00	AW37720.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9138	21826	34991	0.5	1.2E+00	H48589.1	EST_HUMAN	MR2-CT0222-207099-001-007 CT0222 Homo sapiens cDNA
9298	21955	35138	3.75	1.2E+00	D32850.1	NT	y62a06.1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202066 6'
9506	22168	35339	1.81	1.2E+00	D1745.1	EST_HUMAN	R. communis gene for pyrophosphatase-dependent phosphofructokinase beta subunit
9631	22482	35684	2.86	1.2E+00	X59832.1	NT	HUMH01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10224	22872		0.73	1.2E+00	AB009595.1	NT	H. sapiens ENO3 gene for muscle specific enolase
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	Homo sapiens kld10 gene, exon 1
11357	24045		10.82	1.2E+00	BE160781.1	EST_HUMAN	PMO-ST0294-161159-001-001 ST0294 Homo sapiens cDNA
11455	23202	36434	4.36	1.2E+00	BE160781.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
12178	29227	30817	17.06	1.2E+00	AL163203.2	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12196	24667		2.8	1.2E+00	AF001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
451	13237	25876	1.63	1.1E+00	D89990.1	NT	Homo sapiens chromosome 21 segment HS21C003
1767	14499	27200	1.33	1.1E+00	AW095303.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
1892	14629	27339	0.68	1.1E+00	AW578995.1	EST_HUMAN	Q10A-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
						EST_HUMAN	UHFH-BR09-ajk-4-02-0-UI-61 NIH_JMGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

Page 24 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3450	16236	28992	1.11	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3557	16322	28970	1.01	1.1E+00	AB003680.1	EST HUMAN	wf4h11.x1 Sources, NFL.T. GBC.S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3707	16460	28098	1.05	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3707	16460	28099	1.05	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3798	16550		1.02	1.1E+00	X83374.1	NT	Hypocleodolus hohli(MA), hohli(MG), hphIR and menB genes
4190	16931		5.89	1.1E+00	5835331	NT	R. unicornis complete mitochondrial genome
4634	17366		0.81	1.1E+00	U34982.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
4934	17662	30272	3.45	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
4935	17663	30273	1.05	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5128	17847	30494	1.07	1.1E+00	6650360	NT	Homo sapiens putative GRG protein (GRG), mRNA
5224	18031	30557	1.39	1.1E+00	6978530	NT	Relus norvegicus Aquaporin 4 (Aqp4), mRNA
5528	18324	31225	15.75	1.1E+00	BE960184.1	EST HUMAN	G01652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5545	18342	31250	1.2	1.1E+00	AI19592.1	EST HUMAN	q8B603.x1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6001	18782	31743	1.1	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6161	18958	31932	0.82	1.1E+00	AF187861.1	NT	Macgregaria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6313	19084	32069	0.82	1.1E+00	R06037.1	EST HUMAN	y894903.r1 Scores fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:124924 5'
6616	19379	32394	0.72	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7145	19842		0.59	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 28 through 28
7156	19882	32958	0.72	1.1E+00	X55981.1	NT	Maize mRNA for endo-1,2-phospho-D-glycerate hydrolase
7369	20068	33148	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7369	20068	33147	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7411	20088	33172	8.84	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7480	25115	33247	0.8	1.1E+00	11987960	NT	Mus musculus elient mating type information regulator 2, (S.cerevisiae, homolog) like (Sir2), mRNA
8032	20727	33950	3.01	1.1E+00	BF693968.1	EST HUMAN	G02082382F NIH_MGC_81 Homo sapiens cDNA clone IMAGE:124628 5'
8120	20814	33950	0.64	1.1E+00	AI478339.1	EST HUMAN	tn38R11.XT NCLCGAP_XMT7 Homo sapiens cDNA clone IMAGE:2160549 3'
8636	21328	34471	0.71	1.1E+00	AB003088.1	NT	Acetabularia calliculus mitochondrial COX-like gene
8714	21408	34549	0.75	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	21518	34887	0.45	1.1E+00	A1075946.1	EST_HUMAN	023405.1 Soares NIH/MPU_S1 Homo sapiens cDNA clone IMAGE:1677246 3'
9337	20408		0.59	1.1E+00	BE384878.1	EST_HUMAN	601278276F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35565	0.53	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9580	22233		1.2	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9972	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psae, psaeF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22363	35585	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
9837	22468	35690	4.59	1.1E+00	AL161615.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus glutamine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36760	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23150	36375	0.73	1.1E+00	AI878921.1	EST_HUMAN	au51c11.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb.D10522
10547	23243	36478	2.25	1.1E+00	11067364	EST_HUMAN	Human mRNA for 80K-L protein, complete cds. (HUMAN)
10608	23300		3.1	1.1E+00	AF086942.1	NT	Klebschmidium fulvum cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11023	23685	36659	1.28	1.1E+00	11438396	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11026	23698	36661	1.85	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P4502C9 (GYP2C9) gene, 5' flank and exon 1
11042	17801		5.23	1.1E+00	8822673	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36688	3.88	1.1E+00	AF012852.1	NT	Petroselinum crispum cytosolic glucose-5-phosphate dehydrogenase 1 (cGSDH1) mRNA, complete cds
11048	23718	36689	3.69	1.1E+00	AF012852.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cGSDH1) mRNA, complete cds
11328	24016	37523	4.59	1.1E+00	AI809699.1	EST_HUMAN	wf70a11.T_Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361549 3'
11561	24160	37470	1.63	1.1E+00	DB9501.1	NT	Human PBI gene, complete cds
11561	24160	37471	1.63	1.1E+00	DB9501.1	NT	Human PBI gene, complete cds
12153	24639		3.69	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12250	24697	31078	1.93	1.1E+00	AF216696.1	NT	Taeniaris solium immunogenic protein T670 mRNA, partial cds
12378	25225		2.09	1.1E+00	AF234169.1	NT	Dicystosium discoidum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
12388	25200		1.44	1.1E+00	8393196	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Cp), mRNA
97	12923		2.46	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
111	12932	25569	0.73	1.0E+00	DB8425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
409	13164		2.25	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 6S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
562	13344	25971	1.2	1.0E+00	AI251660.1	NT	Glandia sigmna mRNA for homeodomain transcription factor (so gene)
662	13438	26078	4.38	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment H621C018

Page 26 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
683	13439		0.95	1.0E+00	AF125084.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1385	15657		3.03	1.0E+00	X80410.1	NT	V. carchariae Agat-CAM mRNA
1751	14493	27163	0.93	1.0E+00	AB006531.1	NT	Plautia stali Intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2469	15208	27947	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2489	15208	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2878	15645	28287	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15645	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2887	15723		1.17	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN GBF12.08C IN CHROMOSOME I
3194	15957	28509	1.24	1.0E+00	AA628453.1	EST_HUMAN	af26908.t1 Soares, total, fetal, N62-HF8, 9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WIP-C42D8.3 CE04204, contains element MER22 MER22 repetitive element :
3585	12923		1.24	1.0E+00	U23903.1	NT	Xenopus laevis rhodopsin gene, complete cds
3669	16422	28063	1.04	1.0E+00	AJ223816.1	NT	Agericus bisporus mRNA for tyrosinase
4050	16795	29424	0.76	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4242	16983		0.79	1.0E+00	8922243	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4954	17680		0.93	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
4975	17698	30306	0.74	1.0E+00	AF042505.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and prodomain Rump white inversion breakpoint
5200	18008	30529	3.83	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551	31472	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5769	18551	31473	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5987	18654	31595	1.53	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FGA contig fragment No. 9
6024	18904	31765	4.7	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	U1H-B13-abx4-05-Q-111st NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:306959 3'
6397	18166	32166	1.95	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LFC (PC7) gene, exons 1 to 8, partial cds
6447	18218	32213	0.91	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (P4204) gene, exons 2 through 5
6534	18300		1.06	1.0E+00	P48506	SWISSPROT	SRB-11 PROTEIN
6978	18566	32634	1.33	1.0E+00	Y11204.1	NT	V. carchariae gene encoding valoxopain

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9753	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9753	36610	36610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35676	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MIC3BF) mRNA
10012	22660	35676	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MIC3BF) mRNA
10104	22752	35966	0.81	1.0E+00	A077620.1	EST_HUMAN	cyt5d07.s1 Soares, senescent fibroblasts, NHBF Homo sapiens cDNA clone IMAGE:1655901 3'
10225	22873	36055	4.36	1.0E+00	A0759923.1	EST_HUMAN	A0759923 BM Homo sapiens cDNA clone BMFAW004 5'
10375	23021	36237	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:428900 5'
10375	23021	36238	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:428900 5'
10407	23053	36270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10983	23573	36523	4.57	1.0E+00	S60923.1	NT	PBR1=protein-rich protein (triton 3) (human, Genomic, 893 nt)
11025	23697	36660	1.49	1.0E+00	AA701494.1	EST_HUMAN	zf63b1.1.s1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:435493 3' similar to contains Alu repetitive element, contains element MER38 repetitive element ;
11522	24122	37613	1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18008	30529	1.55	1.0E+00	Z37022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11838	24422	37703	12.29	1.0E+00	Q60019	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11838	24452	37704	1.38	1.0E+00	9626187	NT	Human adenovirus type 5, complete genome
12048	24568	37704	3.01	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772	38097	2.32	1.0E+00	AW076184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
2843	16345	35951	1.18	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5547	16345	35951	0.87	9.9E-01	AFT174565.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5779	16370	31498	10.09	9.9E-01	P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
9160	21630	31498	0.93	9.9E-01	Q08632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9455	22005	36547	1.37	9.9E-01	U68567.1	NT	Lyoparation oculatum putative M1 copy 1 nematode-resistance gene
10614	23308	36547	2.18	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11562	24191	37509	2.3	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
11562	24191	37509	2.3	9.9E-01	Y11972.1	NT	Baphichia 16S rDNA (host T. suber)
510	13294	25826	1.14	9.9E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL GLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	16020	36547	1.21	9.9E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	16509	36547	1.01	9.9E-01	AFT174644.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
3781	16533	29171	0.92	9.9E-01	Q87551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEASE IV)
7059	19788	32862	4.97	9.9E-01	AJ302158.1	NT	Enterobacteriaceae sp. JH983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JH983

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7059	19788	32853	4.97	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groS gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33316	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7545	20215	33317	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8519	21311	34453	0.91	9.8E-01	P33952	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10335	22883	1	1.13	9.8E-01	AA825955.1	EST_HUMAN	605504.51 NCL CGAP G08T Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23596	38942	2.29	9.8E-01	BE256705.1	EST_HUMAN	601110289F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350780 5'
10919	23599	38943	2.29	9.8E-01	BE256705.1	EST_HUMAN	601110289F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350780 5'
11764	24355	37688	1.57	9.8E-01	A0830876.1	EST_HUMAN	1642c10x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
12258	24702		1.56	9.8E-01	U62111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
7058	19749	32812	2.28	9.7E-01	U26716.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr1D) gene, complete cds
8401	21094	34230	1.88	9.7E-01	AF149112.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (ret)
8407	21100	34236	1.3	9.7E-01	M00644.1	EST_HUMAN	UHH-B14-edt-e-07-G-U1st NCL_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3068140 3'
11123	23792		3.64	9.7E-01	BF511209.1	EST_HUMAN	PM2-UM0053-240300-005-12 UM0053 Homo sapiens cDNA
4425	17161	29791	1.5	9.6E-01	AW169674.1	EST_HUMAN	Panovirus B19 DNA, patient C, genome position 2448-2694
5657	18462	31376	3.77	9.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2694
5657	18462	31377	3.77	9.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2694
6848	19410	32424	0.81	9.6E-01	Z07341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8201	20985		2.33	9.6E-01	X66275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
8750	21442	34589	0.59	9.6E-01	L81138.1	NT	Relbia norvegicus (strain R21) Rps2r gene, complete cds
11903	24104	37416	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11903	24104	37417	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11952	24505		1.92	9.6E-01	11421722	NT	Homo sapiens centromeric protein 2 (CEP2), mRNA
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Sphynx fibro NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2480	15198	27638	1.05	9.5E-01	770556.1	NT	Homo sapiens CGH-125 protein (LOC51003), mRNA
2373	15582	28122	0.97	9.5E-01	Q02834	SWISSPROT	ENDO GLUCANASE [PRECURSOR (EGN) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE I)]
3762	16514	29150	2.04	9.5E-01	BE602340.1	EST_HUMAN	501675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
3762	16514	29151	2.04	9.5E-01	BE602340.1	EST_HUMAN	501675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
8699	21590	34730	0.69	9.5E-01	A1190162.1	EST_HUMAN	qd57d07.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1739581 3'
9003	21603	34843	1.05	9.5E-01	AW681102.1	EST_HUMAN	RG1-CT0285-241199-011-002 CT0285 Homo sapiens cDNA

Page 30 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11208	23872	37166	1.88	8.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11428	23196	36427	2.42	8.5E-01	AW263789.1	EST_HUMAN	UIH-H12-arp-C9-Q-UJ.s1 NCI_CGAP_Su04 Homo sapiens cDNA clone IMAGE:2727877 3'
11765	24385	37718	1.55	9.5E-01	T67204.1	EST_HUMAN	YAS5404.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66631 3'
3196	15959		3.33	9.4E-01	AF165960.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (pcb) gene, partial cds
3272	15975		2.06	9.4E-01	AF080585.1	NT	Pimpriella trachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34806	0.67	9.4E-01	M80724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
12202	24670		1.92	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
12557	26210		1.76	9.4E-01	11410857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1728	14468		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytoey-CoA hydroxylase (PHYH) gene, exon 5
2640	15351	28095	1.36	9.3E-01	BE071172.1	EST_HUMAN	RC8-BT0803-271199-071-B01 BT0803 Homo sapiens cDNA
4015	16761	29388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	29389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5505	18303	31204	1.56	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18398	31298	3.99	9.3E-01	L39789.1	NT	Spodoptera frugiperda methyltetrahydrofolate dehydrogenase mRNA, complete cds
7966	20861	33785	1.65	9.3E-01	AA847040.1	EST_HUMAN	oe09003.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061081.1	NT	Xenopus laevis CCGH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8835	21527	34673	0.95	9.3E-01	AL161634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24670		3.72	9.3E-01	AF271207.1	NT	Actes triseriatus putative large subunit ribosomal protein rL34 mRNA, complete cds
12802	25049		1.48	9.3E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cellactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1
3233	15895	28648	2.63	9.2E-01	BE622702.1	EST_HUMAN	601441335T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4822	17553		0.97	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5631	18428		1.15	9.2E-01	7108410	NT	Mus musculus soluble carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5888	18632	31631	7.36	9.2E-01	BF037586.1	EST_HUMAN	501461133F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3964681 5'
6537	19303	32306	0.61	9.2E-01	MG4703.1	NT	N crassa val1-RNA synthetase (GV-20/un-3) gene
9560	22213	35389	0.92	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9548	22801	35466	1.07	9.2E-01	6571677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22962	36176	1.9	9.2E-01	BF693251.1	EST_HUMAN	7658e06.x1 NCI_CGAP_K1D1 Homo sapiens cDNA clone IMAGE:3578219 5' similar to SW-NU5M_TRYBB
10543	23239	36473	1.83	9.2E-01	BE683811.1	EST_HUMAN	P04540 NADH+UBIQUINONE OXIDOREDUCTASE CHAIN 5
							601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3668714 5'

Page 31 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24316	37659	1.79	9.2E-01	BF132402.1	EST_HUMAN	601620312F1.N1F_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1621	14368	27057	1.88	9.1E-01	T98876.1	EST_HUMAN	yes201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121359 3' similar to contains Alu repetitive element
2120	14851		2.78	9.1E-01	8523053	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15983	28614	1.15	9.1E-01	T28418.1	EST_HUMAN	AB2000GBR Infant brain, LLNL array of Dr. M. Soares IN1B Homo sapiens cDNA clone LAB200G8 5'
3200	15983	28615	1.15	9.1E-01	T26418.1	EST_HUMAN	AB2000GBR Infant brain, LLNL array of Dr. M. Soares IN1B Homo sapiens cDNA clone LAB200G8 5'
6075	18954	31821	1.28	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6413	19181	32180	3.53	9.1E-01	Q81704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITIH3) (ITIH3)
7475	20148	33241	17.62	9.1E-01	AA086523.1	EST_HUMAN	cd7Tg08.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1339862 3'
7837	20302	33410	2.34	9.1E-01	U72956.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10075	22723	35940	0.45	9.1E-01	P38432	SWISSPROT	P80-COLIN
12281	25294		27.98	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4346	17085	29714	2.08	9.0E-01	AF069810.1	NT	Homo sapiens neuramin II-alpha gene, partial cds
7291	19974	33052	0.72	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lims) mRNA, complete cds
7321	20004		1.18	9.0E-01	D38921.1	NT	Xenopus laevis gene for aldolase, complete cds
9249	21928	35100	0.49	9.0E-01	AF086761.1	NT	Danio rerio sarinaphofin Z1a mRNA, complete cds
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5810	18408	31318	2.88	8.9E-01	AF026188.1	NT	Rabbit MHO fragment RLA-DF DNA
6154	18831		1.38	8.9E-01	X60866.1	NT	Olfithone nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
8325	21018	34154	0.71	8.9E-01	AF245957.1	NT	Xylella fastidiosa, section 80 of 228 of the complete genome
11787	24377	37707	2.51	8.9E-01	AE033844.1	NT	Chlamydomonas reinhardtii AF36, section 21 of 84 of the complete genome
12138	24627		2.86	8.9E-01	AE002186.2	NT	Chlamydomonas reinhardtii AF36, section 21 of 84 of the complete genome
12762	25343		2.51	8.9E-01	A1150835.1	EST_HUMAN	q664d08.x1 Soares fetal heart NBHH19HW Homo sapiens cDNA clone IMAGE:1704879 3'
4505	17240	29873	3.82	8.9E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5289	18094	30755	0.87	8.9E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22778	35922	0.93	8.9E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23590	36953	4.98	8.9E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PNA1
11968	25382		1.18	8.9E-01	D90911.1	NT	Synochococcus sp. PC66803 complete genome, 13/27, 1876593-1718843
432	13238	25917	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ("Top") Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15544	28238	5.05	8.7E-01	AA505863.1	EST_HUMAN	in0511.st NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1078877
4946	17673						Pseudomonas aeruginosa lipoproteinase (top), putative transcriptional regulatory protein OhR (ohR), ortho-halobenzoate 1,2-dioxygenase beta-SP protein OhA (ohA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-SP protein OhbB (ohbB), and put-
5102	17820		3.17	8.7E-01	AF121970.1	NT	Homo sapiens partial LOC459 gene for galectin-9, exon 3
7036	20634	33761	0.97	8.7E-01	AJ289085.1	NT	RC4-NN0057-12050-013-c07 NN0057 Homo sapiens cDNA
8828	21520	34655	0.69	8.7E-01	AF230455.1	EST_HUMAN	h35640.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
8828	21520	34668	0.69	8.7E-01	AF230455.1	EST_HUMAN	h35640.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9538	22290	35483	1.57	8.7E-01	AF230455.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10202	22850	36055	0.81	8.7E-01	BF570169.1	EST_HUMAN	80218554T11 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308906 3'
10202	22850	36055	0.81	8.7E-01	BF570169.1	EST_HUMAN	80218554T11 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308906 3'
10735	23422	36555	5.25	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-10080-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	5.47	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
492	13247		1.75	8.6E-01	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
538	13608	26279	3.45	8.6E-01	W65089.1	EST_HUMAN	zid44603.t Soares_fetal_NBHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2288	14694	27793	0.96	8.6E-01	4603210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrolendinous xanthanoketase), polypeptide 1 (CYP27A1b) mRNA
3503	16361	28003	0.85	8.6E-01	AL101565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3782	18534	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster melfin (Dmelfin) mRNA, complete cds
5806	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5803	18597	31526	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6609	19372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6609	19372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104		0.78	8.6E-01	AE000591.1	NT	Halobacter pylori 26895 section 69 of 134 of the complete genome
7828	20623		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 1214
7841	20536	33763	0.55	8.6E-01	AF077837.1	NT	Archaeophaga fulgidus section 128 of 172 of the complete genome
6985	22144		0.49	8.6E-01	AE000973.1	NT	Archaeophaga fulgidus section 128 of 172 of the complete genome
12518	25258		1.35	8.6E-01	AF112162.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
19328	32401		0.95	8.6E-01	AF165214.1	NT	Bacteriophage O3, complete genome
7426	20102	33189	2.51	8.5E-01	BE542812.1	EST_HUMAN	601097107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3443505 5'
8317	21010	34147	0.78	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8317	21010	34148	0.78	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Page 33 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22866	36105	1.17	8.5E-01	AB006799.1	NT	Cyandium calderium gene for SigC, complete cds
10249	22866	36106	1.17	8.5E-01	AB006799.1	NT	Cyandium calderium gene for SigC, complete cds
12278	25296		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 (HIV-1), mRNA
4702	17436	30067	0.73	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
6406	25068	30910	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25068	30911	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF051142.1	NT	Mammstra brassicae phenomene binding protein 2 precursor (PBP2) mRNA, complete cds
6959	22608		2.69	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
724	13498	29151	2.9	8.3E-01	M83437.1	NT	Thermus thermophilus cyclochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	18595	26467	2.99	8.3E-01	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3700	18542	29177	0.79	8.3E-01	AB010878.1	NT	Nicotiana glauca mRNA for chloroplast ribosomal protein L10, complete cds
3993	19741	29378	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17695	30511	2.41	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9569	22221		4.51	8.3E-01	AF061982.1	EST_HUMAN	nc0112.v3 NCI CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.L1 THR repetitive element
10010	22658	35872	1.27	8.3E-01	AF088070.1	NT	Drosophila melanogaster Ust1 homolog mRNA, complete cds
10118	22768	35978	3.46	8.3E-01	AF108133.1	NT	Mus musculus neuro-44 gene, exons 3 through 12 and partial cds
10572	23267	36505	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from basus 1270510 to 1283409 (section 109 of 146) of the complete genome
10590	23294		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	26865	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000486.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2693	15395		1.06	8.2E-01	AW376890.1	EST_HUMAN	IL3-CT0218-161189-031-C08 CT0219 Homo sapiens cDNA
6678	19593	32631	0.78	8.2E-01	AJ010142.1	EST_HUMAN	Ananias muscaria mRNA for SCIL125 protein
6797	19541	32569	3.49	8.2E-01	AW376433.1	EST_HUMAN	CNA4-HT0243-081159-037-e01 HT0243 Homo sapiens cDNA
7169	25106	32928	4.74	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (NH), and DNA polymerase alpha (partial)
8343	21038	34173	0.59	8.2E-01	BE263145.1	EST_HUMAN	501144855F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9924	22572	35770	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
6959	26907	33812	1.37	8.2E-01	AF052650.1	NT	Homo sapiens thiorodoxin-related protein mRNA, complete cds
10123	22771	35985	0.59	8.2E-01	AF223698.1	NT	Oncorhynchus kislayishcha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35988	0.59	8.2E-01	AF223698.1	NT	Oncorhynchus kislayishcha isolate T-20 somatolactin precursor gene, exon 1

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10283	22831	38145	3.85	8.2E-01	Q9J170	SWISSPROT	ICKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22931	38148	3.65	8.2E-01	Q9J170	SWISSPROT	ICKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11841	24238	37562	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328	37562	6.38	8.2E-01	P10393	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	8.02	8.2E-01	H87398.1	EST_HUMAN	jy1402.1 Scores: placenta_80cweeks_2NbpHP803W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb1M5972 605 RIBOSOMAL PROTEIN L7A (HUMAN);
12268	24723	31054	2.37	8.2E-01	AJ001291.1	NT	Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds
2762	18407		1.08	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds
3451	18207	28857	3.08	8.1E-01	AF055068.1	NT	Homo sapiens MYC class 1 region
3451	18207	28858	3.08	8.1E-01	AF055068.1	NT	Homo sapiens MYC class 1 region
4893	17592		0.74	8.1E-01	AF202834.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6223	18897	31973	0.84	8.1E-01	U18790.1	NT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6526	19292	32295	2.63	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
6526	19292	32296	2.68	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7229	18914	32857	0.78	8.1E-01	AB007877.1	NT	Homo sapiens KIA0417 mRNA, complete cds
7412	20069	33173	0.66	8.1E-01	O47477	SWISSPROT	CYTOSCHROME B
7811	20508	33828	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nech) and putative ankyrin-related protein (Amyel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
7811	20508	33629	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nech) and putative ankyrin-related protein (Amyel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
8507	21169	34344	0.93	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21169	34345	0.83	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8999	21380	34507	1.08	8.1E-01	AW242847.1	EST_HUMAN	xx01103.x1 NCL_GGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW1LYAR_MOUSE Q08298 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22 b1 PTR5, repetitive element
10025	22673	35888	0.7	8.1E-01	P06425	SWISSPROT	PROBABILE E4 PROTEIN
10311	22659	36174	0.5	8.1E-01	N84541.1	EST_HUMAN	KK6872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK6872 5' similar to EST(CLONE C-0PPE11)
11464	24007	37374	2.63	8.1E-01	BE638598.1	EST_HUMAN	RCO-TN0080-220800-025-r10 TN0080 Homo sapiens cDNA
11464	24007	37375	2.63	8.1E-01	BE638598.1	EST_HUMAN	RCO-TN0080-220800-025-r10 TN0080 Homo sapiens cDNA
12022	24550	31110	1.57	8.1E-01	AE001711.1	NT	Thermoplasma acidophilum section 23 of 138 of the complete genome
172	12865		3.49	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphatidyl transferase allele 15

Page 35 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus protease (proscame, macropan) 28 subunit, alpha (Psmet), mRNA
2029	14764		1.91	8.0E-01	BF530892.1	EST_HUMAN	602072473F1 NCI_OGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3075	15841	28484	1.2	8.0E-01	AF127897.1	NT	Salinix baltensis effector/receptor (SBO27) gene, partial cds
3307	16087	28716	1.35	8.0E-01	AB006193.1	NT	Mus musculus gene for orvidual glycoprotein, complete cds
3580	16433		1.32	8.0E-01	AL162768.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4496	17232	28882	6.05	8.0E-01	X83739.2	NT	Gallus gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7589	20584		2.25	8.0E-01	AW801489.1	EST_HUMAN	RC0-NN1012-270300-021-H06 NN1012 Homo sapiens cDNA
8423	21116	34264	0.98	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10876	23556	38803	2.78	8.0E-01	Q82793	SWISSPROT	CREB-BINDING PROTEIN
441	13227	29570	1.16	7.9E-01	DT1476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	13473		1.14	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1600	14346		22.69	7.8E-01	AB040835.1	NT	Homo sapiens mRNA for KIAA1482 protein, partial cds
1652	14388		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2269	14986	27726	5.68	7.9E-01	AB004516.1	NT	Oryzias latipes cDNA for misugumiz9, complete cds
2260	14987	27727	2.4	7.9E-01	AF130469.1	NT	Danio rerio Tpt4-associated protein Tpt4A (laptA) mRNA, complete cds
3505	16262	28976	3.01	7.9E-01	AF226694.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4288	17008		0.85	7.8E-01	BE263512.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4572	17307	29935	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4572	17307	29936	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
6252	19026	32000	0.57	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33931	2.79	7.9E-01	X00096.1	NT	P. aethiops GR gene
8447	21214	35304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein C3M-B (vapG3M-B) mRNA, partial cds
9549	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9591	22693	35849	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKCC Homo sapiens cDNA clone GKCCRE12 3'
10408	23064	36271	1.84	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-kaio-L-rhamnose reductase, complete cds
10519	23192	36359	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10529	23609		2.74	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	31123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
898	13623		2.24	7.8E-01	Z43785.1	EST_HUMAN	HSC70H041 normalized infant brain cDNA Homo sapiens cDNA clone c-18b04
2273	17397	31737	7.47	7.8E-01	AW806067.1	EST_HUMAN	EST137637 MAGGE resequences, MAGF Homo sapiens cDNA
4653	17987	30020	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5976	18760	31724	2.28	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endonase mRNA, partial cds

Page 36 of 636
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31871	0.88	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON
6371	19140	32136	0.93	7.8E-01	AL45008.1	NT	BEFA-2 (HYDRIDOMA GROWTH FACTOR)
8389	21082	34215	1.02	7.8E-01	BF108927.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5
9133	21821	34937	1.3	7.8E-01	Y10169.1	NT	7154305.X1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3225178 3'
9231	21910	35083	0.51	7.8E-01	4826873	NT	D discoidium recGAP gene
10024	22672		0.97	7.8E-01	Q25452	SWISSPROT	Homo sapiens nucleoside 214kD (GAIN) (NUP214), mRNA
12271	25275		2.5	7.8E-01	L29260.1	NT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
139	12054	25596	7.61	7.7E-01	AF184345.1	NT	Arabidopsis thaliana 1'-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
							Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	13483		2.28	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (A2beta) and major histocompatibility protein class II beta chain (E2beta) genes, complete cds;
2717	15424	28163	2.21	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG9), butyrophilin-4a
							CITRATE SYNTHASE
3351	16111		0.84	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactose 4-epimerase N-acetylglucosaminyltransferase 7
3688	16340	28985	3.88	7.7E-01	AF118085.1	NT	(GalNAc-T7) (GALNAC-T7), mRNA
4365	17103	29738	3.38	7.7E-01	AF199485.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4366	17103	29739	3.38	7.7E-01	AF199485.1	NT	Colutrix columbica japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31185	1.45	7.7E-01	P16553	SWISSPROT	Colutrix columbica japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31186	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6866	18653	31694	0.85	7.7E-01	R08600.1	EST_HUMAN	YF24002.S1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127755 3'
9744	22395	35600	0.51	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12161	24844		4.55	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
							Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6008	18789	31761	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6009	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6425	19193	32189	0.81	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6751	17920	30555	0.94	7.6E-01	AI253399.1	EST_HUMAN	seq14b12.X1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2630879
6751	17920	30555	0.94	7.6E-01	AI253399.1	EST_HUMAN	seq14b12.X1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2630879
6951	19433	32449	0.88	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-lactalbumin receptor mRNA, complete cds

Page 37 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7984	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPILP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8026	20721	33862	1.89	7.6E-01	6857752	NT	Mus musculus ecdilin (Acdil-pending), mRNA
8026	20721	33863	1.88	7.6E-01	6857752	NT	Mus musculus ecdilin (Acdil-pending), mRNA
8866	21587	34703	0.74	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9176	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11330	24021	37326	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11711	24305		3.64	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11931	24489		3.73	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
500	13284		1.44	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
570	13351	25978	1.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3354	18114	26769	0.95	7.6E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (86572) Homo sapiens cDNA clone GEN-037E11 5'
7421	20068	33186	1.01	7.5E-01	AF062730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11177	23844	37130	1.5	7.5E-01	AB047819.1	NT	Homo sapiens GCMa/GCM1 gene for chorion-specific transcription factor GCMa, complete cds
12228	24682		4.8	7.5E-01	AF163161.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12742	25008	30975	1.46	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328192 (section 29 of 148) of the complete genome
1108	13895	26622	1.78	7.4E-01	AI598146.1	EST_HUMAN	h14093.X1 NC1 CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2342	15095	27802	0.88	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
4276	17015	25842	4.78	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7743	20439	33662	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
7743	20439	33593	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
8931	21223	34365	0.83	7.4E-01	BF346266.1	EST_HUMAN	602018456FT NC1 CGAP_Brn57 Homo sapiens cDNA clone IMAGE:3164340 5'
8613	21305		0.76	7.4E-01	U87980.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
8894	21684	34634	0.95	7.4E-01	BE147803.1	EST_HUMAN	60157026FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9054	21743	34601	1.14	7.4E-01	AA187966.1	EST_HUMAN	z987101.s1 Striatagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPOQ_Mouse P42932 T-COMPLEX PROTEIN 1, THE TA SUBUNIT ;
10302	22949	39164	0.76	7.4E-01	11424633	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA

Page 38 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11666	24260	37582	1.65	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11665	24260	37583	1.65	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11800	24487		3.62	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12008	24542		1.78	7.4E-01	A1472641.1	EST_HUMAN	h33001.x1 NCI CGAP Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
2698	15765	28413	0.8	7.3E-01	P08710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (PRL1) (TRL1)
4575	17310	29938	0.7	7.3E-01	AE011166.1	NT	Borrelia burgdorferi (section 82 of 70) of the complete genome
4652	17759	30019	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5040	17366	30373	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6511	19276	32278	6.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6511	19276	32277	6.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6894	25103	32735	0.87	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7359	20040	33118	0.69	7.3E-01	Z14133.1	NT	D. melanogaster Chc mRNA for clathrin heavy chain
7445	20121	33210	7.84	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
7445	20121	33211	7.84	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
11407	24056	37851	3.83	7.3E-01	AA578019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:431769 3'
11407	24056	37852	3.83	7.3E-01	AA578018.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:431769 3'
812	13563		3.89	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1650	14653	27358	2.32	7.2E-01	X79140.1	NT	N. laibachii Nelf-4A13 mRNA
2483	15181	27620	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3083	15829	28473	1.38	7.2E-01	AF198100.1	NT	Powderbox virus, complete genome
3445	16201	28851	2.56	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp-417-6) gene, vsp417-6/A-1 allele, complete cds
3601	16364	28994	1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4040	16785		0.7	7.2E-01	AF108093.1	NT	Homo sapiens IIA-2 gene, intron 19
4718	17450	30083	2.65	7.2E-01	D90314.1	NT	Lincentin gene for sucrose phosphorylase (EC 2.4.1.7)
6075	17794	30410	0.74	7.2E-01	P30666	SWISSPROT	I)
7112	19800	32864	0.88	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8353	21046	34183	1.11	7.2E-01	AF236061.1	NT	Oryzopsis anticalyx RING-finger binding protein mRNA, partial cds
8892	21553		0.46	7.2E-01	AF743073.1	EST_HUMAN	AF743073 CB Homo sapiens cDNA clone G31AFD06 5'
10239	22887	36100	2.33	7.2E-01	BF670061.1	EST_HUMAN	302118381FT NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4276381 6'
10639	23330	36568	4.02	7.2E-01	U82623.1	NT	Rattus norvegicus cyclophilin mRNA, complete cds
11104	23774	37048	1.27	7.2E-01	S798338.1	NT	Dbs=Dbi guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]

Page 39 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12422	24768		2.9	7.2E-01	AF000003.1	NT	Aeropyrum pernix genomic DNA, section 67
676	13451	26094	12.73	7.1E-01	D21070.1	NT	Rana catabolism mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RYR1), complete cds
30562	18626	26470	11.76	7.1E-01	AJ207071.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 15-16
4184	18625	26555	3.18	7.1E-01	7305360	NT	Mus musculus osteonin (Olog), mRNA
4184	18625	26556	3.18	7.1E-01	7305360	NT	Mus musculus osteonin (Olog), mRNA
5858	18645	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4266344 5'
5858	18645	31586	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4266344 5'
6650	19550	32650	7.68	7.1E-01	U36232.1	NT	Discothelia melanogaster 5-pyruvyltetrahydropterin synthase (p7) gene, complete cds
8091	20786	33916	0.56	7.1E-01	H64244.1	EST_HUMAN	y49609.at Soares fetal liver spleen TNF15 Homo sapiens cDNA clone IMAGE:202861 3'
8035	21327	34408	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0587-301269-011-409 BT0587 Homo sapiens cDNA
8535	21327	34470	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0587-301269-011-409 BT0587 Homo sapiens cDNA
9755	22406	35613	1.43	7.1E-01	BE304405.1	EST_HUMAN	801496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE3638485 5'
10309	22456	36172	1.22	7.1E-01	M12361.1	NT	Human T-cell receptor gamma chain J2 gene
12211	25235		2.21	7.1E-01	AA427492.1	EST_HUMAN	z40611.at Soares testis_NHT Homo sapiens cDNA clone IMAGE:791109 3'
1207	13958	26624	0.99	7.0E-01	AB074514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1207	13958	26625	0.99	7.0E-01	AB074514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2450	15169	27607	1.13	7.0E-01	N62412.1	EST_HUMAN	y273407.at Soares multiple sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:268708 3' similar to contains Alu repetitive element
2450	15169	27608	1.13	7.0E-01	N62412.1	EST_HUMAN	y273407.at Soares multiple sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:268708 3' similar to contains Alu repetitive element
4968	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6862	18648		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8276	20670		11.76	7.0E-01	AE000233.1	NT	Escherichia coli K-12 MG1665 section 143 of 400 of the complete genome
9216	21895	35064	0.57	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mlaA, mliR, mliF, and mliD genes, complete cds
9216	21895	35065	0.57	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mlaA, mliR, mliF, and mliD genes, complete cds
10528	23172	35400	0.49	7.0E-01	U34682.1	NT	Danio rerio complement factor B mRNA, complete cds
11084	23734	37008	1.94	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCHC04 5'
11084	23734	37007	1.94	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCHC04 5'
949	13716	26380	11.02	6.9E-01	U69674.1	NT	Candida albicans epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds

Page 40 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
946	13715	26381	11.02	6.9E-01	U96974.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.9E-01	AA593330.1	EST_HUMAN	hnt2a00.s1 NCI_OGAP_Gast1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213	15976	28927	1.97	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5594	18488	31409	0.91	6.9E-01	AE035682.1	NT	Branched-chain belcheri BNA3 mRNA for notochord actin, complete cds
5900	18895	31633	0.82	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP50, partial
6277	19050	32027	1.36	6.9E-01	BE298188.1	EST_HUMAN	60177733.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3523228 5'
7679	20360	33474	0.65	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7879	20574	33701	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9089	21758	35431	0.79	6.9E-01	AF118048.1	NT	Entamoeba dispar cation transporting ATPase (dtpase) gene, partial cds
9594	22247	35432	0.59	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23886	37172	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11223	23886	37172	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11878	26197		3.01	6.9E-01	Q99969	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFK-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
937	13704	26368	1.05	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2680	15389		0.69	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2632	14356	27045	1.49	6.8E-01	AA854475.1	EST_HUMAN	g15a05.51 Soares parathyroid tumor NHPA Homo sapiens cDNA clone IMAGE:1402266 3' similar to gb-X58411.1 rat ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4533	17268	28901	1.45	6.8E-01	J00762.1	NT	Ratiodoped proteolysin gene: exon iii and flanks
9338	22161	33375	1.45	6.8E-01	AE037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23699	35962	1.92	6.8E-01	AJ276975.1	NT	Stenotaphrum secundatum bgl1 gene for beta-glucosidase, exons 1-4
11027	23699	35963	1.92	6.8E-01	AJ276975.1	NT	Stenotaphrum secundatum bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	AF039839.1	NT	Mus musculus zinc finger protein (Png3) mRNA, complete cds
11058	23728	37001	2.4	6.8E-01	AF039839.1	NT	Mus musculus zinc finger protein (Png3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Scem21 gene, partial>
11607	24205	37527	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Scem21 gene, partial>
11607	24205	37528	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Scem21 gene, partial>

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
291	13097	25738	44.11	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27608	1.73	6.7E-01	AA451884.1	EST_HUMAN	z1212.2.1 Scores: total feus_N62HF8_9w Homo sapiens cDNA, clone IMAGE786310 3' similar to contains element TART repetitive element;
2163	15587	27628	2.51	6.7E-01	AF186073.1	NT	Drosophila melanogaster Met85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2094	15760	28408	3.41	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29788	0.78	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30532	0.94	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30533	0.64	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	18005	31881	1.18	6.7E-01	6635038	NT	Gallid herpesvirus 2, complete genome
6231	18005	31882	1.18	6.7E-01	6635038	NT	Gallid herpesvirus 2, complete genome
7215	19900		4.34	6.7E-01	AE004608.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240	19925	33000	0.92	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.68	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23563	38900	2.07	6.7E-01	BF354648.1	EST_HUMAN	CH3-HT0768-010608-197-c03 HT0768 Homo sapiens cDNA
11435	23203	38435	3.59	6.7E-01	O14357	SWISSPROT	NCACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
11659	24235	37578	1.68	6.7E-01	AA342821.1	EST_HUMAN	EST48068 Fetal spleen Homo sapiens cDNA 3' end
2805	19222	27694	1.29	6.6E-01	AF076240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2704	16411	28148	1.44	6.6E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	16403	29043	4.57	6.6E-01	Y07689.1	NT	Calicheamicin random DNA marker, 282bp
4089	16832		0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5125	17843	30461	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 68
6240	18014	31688	4.29	6.6E-01	6860577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7583	20283	33389	3.76	6.6E-01	AY680806.1	EST_HUMAN	AY680806 GLC Homo sapiens cDNA clone GLCSD04 3'
8464	21195	34289	0.52	6.6E-01	AY704700.1	EST_HUMAN	AY704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9594	22217		2	6.6E-01	AL168278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470	24836	31033	1.48	6.6E-01	AE004382.1	NT	Vinco chloresis chromosome II, section 39 of 63 of the complete chromosome
610	13388	28019	18.23	6.5E-01	M75140.1	NT	H. vulgatus Na,K-ATPase alpha subunit mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
610	13388	28020	18.23	6.5E-01	M75140.1	NT	H vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3428	18183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	16890	29615	4.23	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-5
4277	17016	29643	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
5003	17726	30328	2.8	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25067	30843	1.77	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF1 (SWISNF COMPLEX COMPONENT SNF5)
5627	18424	31337	0.62	6.5E-01	AL168249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6025	18387	32400	1.8	6.5E-01	D88346.1	NT	Homo sapiens chromosome 21 segment HS21C049
7556	20236	33340	0.84	6.5E-01	A1769882.1	EST_HUMAN	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
9737	22388		0.8	6.5E-01	I78904.1	EST_HUMAN	wc46d02.x1 NC1 CGAP P28 Homo sapiens cDNA clone IMAGE:2321642 3'
10233	22881	36094	1.66	6.5E-01	AF118676.1	NT	xy421b04.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108947 3'
10529	23228	36460	2.68	6.5E-01	H87583.1	EST_HUMAN	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10585	23260	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	jw1708.r1 Scores placenta_81c9weeks_2NHP0b0W Homo sapiens cDNA clone IMAGE:262815 5'
10690	23381		3.93	6.5E-01	AU138078.1	EST_HUMAN	h01607.a1 NC1 CGAP Ph61 Homo sapiens cDNA clone IMAGE:1100748 3'
11596	24198	37518	2.42	6.5E-01	AF014115.1	NT	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
12267	24710						Pisum sativum berghel cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b
12504	25149		1.81	6.5E-01	Z714145.1	NT	genes, mitochondrial genes encoding mitochondrial proteins, complete cds
245	13054	28504	8.05	6.4E-01	U48948.1	NT	hw7441.x1 NC1 CGAP L224 Homo sapiens cDNA clone IMAGE:3179130 3'
2593	15307	28043	1.16	6.4E-01	AF161184.1	NT	S cerevisiae chromosome IV reading frame ORF YDL097c
3449	10205	28555	2.16	6.4E-01	U48554.2	NT	Drosophila melanogaster 8kd dyshen light chain mRNA, complete cds
3542	16553	29230	1.08	6.4E-01	AB048827.1	NT	Pseudomonas fluorescens tryptophan halogenase (pna) gene, complete cds
8510	12102	34347	1.82	6.4E-01	AE001247.1	NT	Mus musculus dyshen light chain 1 (DAG1) gene, exons 1 and 2 and complete cds
8989	22637	35948	8.6	6.4E-01	U28238.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
10004	22652	35964	1.22	6.4E-01	BF670405.1	EST_HUMAN	Troponin pallidum section 63 of 87 of the complete genome
12392	24771		5.69	6.4E-01	AV769212.1	EST_HUMAN	Homo sapiens axata telomerase (ATM) gene, complete cds
425	13211	29558	4.58	6.3E-01	P05228	SWISSPROT	8021.5028F2F NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4291126 5'
522	13306	29538	2.25	6.3E-01	U32889.1	NT	AV769212 MDS Homo sapiens cDNA clone MDSGCG03 5'
2159	14859	27623	2.02	6.3E-01	U41136.1	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFRP-III)
2593	15297	28035	3.51	6.3E-01	U75331.1	NT	Hemophilus influenzae Rd section 4 of 163 of the complete genome
2593	15297	28035	3.51	6.3E-01	U75331.1	NT	Shigella flexneri multi-antigen resistance locus
2593	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2593	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5873	18755	31716	0.94	6.3E-01	BE03908.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mig) gene, complete cds
6504	19269	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mig) gene, complete cds
8419	21112		3.44	6.3E-01	BE002044.1	EST_HUMAN	601678893F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE3956351 6'
8784	21476	34624	0.95	6.3E-01	S52927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216894.1	EST_HUMAN	601684050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE4102595 5'
9320	21987	35169	2.45	6.3E-01	9827521	NT	Varicella virus, complete genome
9320	21987	35160	2.45	6.3E-01	9827521	NT	Varicella virus, complete genome
9838	22489		0.67	6.3E-01	AE002326.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10326	22673	36163	1.47	6.3E-01	Z73003.1	NT	S cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36284	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1685 section 203 of 400 of the complete genome
10458	23102		0.45	6.3E-01	AW795395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
10593	23687	36924	2.21	6.3E-01	AA877715.1	EST_HUMAN	nr08106.a.1 NCL_OGAP_Co10 Homo sapiens cDNA clone IMAGE1161371 3' similar to TR:002916 002918 HLARK.1
11308	23987	37208	9.25	6.3E-01	AB04160.1	EST_HUMAN	CM-BT043-090269-048 BT043 Homo sapiens cDNA
11402	24051	37355	1.65	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11881	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 16.3 KD PROTEIN IN VMA12-APT INTERGENIC REGION
11898	25355	30607	4.37	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Kt2-6g), mRNA
12078	24587		1.45	6.3E-01	AF105227.1	NT	Homo sapiens 5-phosphoadenosine 5-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12283	25272		2.63	6.3E-01	X8328.1	NT	Clintocida pscd gene
5790	18571	31469	2.31	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN G35E2.02 IN CHROMOSOME I
7394	20073		3.44	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Cas-rs4) mRNA, partial cds and Zinc finger protein 185
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus chromosome X cartilagin, putative Magea8 gene, Callitrich, NAD(P) steroid dehydrogenase
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	ys01068.s1 Soares fetal liver spleen tNFI5 Homo sapiens cDNA clone IMAGE213542 3'
8765	21447	34595	0.52	6.2E-01	AF034411.1	NT	Lycopodium eculeum cytochrome CytZn superoxide dismutase (Sod) gene, partial cds; and dehydroquinolate dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9349	20420	33540	1.55	6.2E-01	BE562887.1	EST_HUMAN	601336146F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE3690010 5'
9410	22072		2.55	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9578	22626	35834	6.2	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35882	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNC1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNC1), mRNA

Page 44 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36306	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.39	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5449	18248	31137	1.15	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 Celyd-0 (hh-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM2 gene, complete cds
6820	19859	32702	0.84	6.1E-01	AW105953.1	EST_HUMAN	cd50103.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12871_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN)
7005	19697	32761	0.72	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8132	20826	33682	3.27	6.1E-01	AF033353.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8694	21389	34528	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21389	34529	1.09	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9315	21882	35183	18.74	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21882	35184	18.74	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22383	35597	0.93	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
9846	22594	35797	1.06	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11739	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30859	2.29	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for Type IV collagen alpha 5 chain, complete cds
12694	24977		1.57	6.1E-01	X85287.1	NT	M. mazei orfA, orfB, and orfC of archaeal ABC-transporter system
482	13267	25903	1.24	6.0E-01	D87975.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	13331		3.09	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20), mRNA
1341	14089	28795	1.91	6.0E-01	AF095253.1	NT	Human respiratory syncytial virus strain CH69-539 attachment protein (G) gene, complete cds
3765	16547	29130	0.82	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, NV, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF088966.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5199	18007	30828	2	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18196	30839	2.96	6.0E-01	AW139713.1	EST_HUMAN	U1H-B1-1a2-a-10-U1-st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
8445	19213	32210	2.78	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

Page 45 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6563	19228	32335	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7254	16938	33013	6.99	6.0E-01	AJ277681.1	NT	(CDW139) (CD136 ANTIGEN)
8023	20718	33850	4.39	6.0E-01	P02835	SWISSPROT	Homo sapiens partial LM01 gene for LIM domain only 1 protein, exon 1
8023	20718	33851	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22874	35574	1.81	6.0E-01	AB008169.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
10173	22821		1.46	6.0E-01	Q01487	SWISSPROT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10990	23664	36921	1.49	6.0E-01	AJ131892.1	NT	PEROXISOMAL MEMBRANE PROTEIN PEROXIN-3
10990	23664	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperon protein, 419 KD isoform
11540	24140	37449	3.77	6.0E-01	AJ420623.1	EST_HUMAN	Gallus gallus mRNA for Hyperon protein, 419 KD isoform
12554	24768	37060	2.25	6.0E-01	11421663	NT	H0807.XT NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
12455	24824		2.6	6.0E-01	AA706087.1	EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2) like 3 (NFE2L3), mRNA
12939	25208	30815	3.04	6.0E-01	8055303	NT	Homo sapiens cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12964	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	Mus musculus GMP-inhibited phosphodiesterase (Pde3a), mRNA
980	13745	28407	1.36	5.9E-01	U32701.1	NT	RC1-H10375-030500-015-03 H10375 Homo sapiens cDNA
3264	16026	28875	2.29	5.9E-01	AL163267.2	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3264	16026	28876	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4166	16937		4.21	5.9E-01	AF162756.1	NT	Homo sapiens chromosome 21 segment HS21C087
6373	19142	32189	1.55	5.9E-01	AF085440.2	NT	Rattus norvegicus casein 2 mRNA, partial cds
7166	19853	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7266	19876		0.61	5.9E-01	X68801.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7898	20563	33725	0.48	5.9E-01	D09811.1	NT	G gallus gene for skeletal alpha-actinin, exon EF2
8536	21228	34370	0.48	5.9E-01	D12922.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576563-1719543
8443	22120	35289	0.82	5.9E-01	AF063204.2	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
8813	22464		0.74	5.9E-01	P06463	SWISSPROT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds
10089	22736	35561	1.15	5.9E-01	P55284	SWISSPROT	EG PROTEIN
10569	23264	35502	2.5	5.9E-01	Q9X003	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10573	23271	35507	1.72	5.9E-01	AF19744.1	NT	THYMIDYLATE KINASE (TMP KINASE)
10881	23561	36808	2.91	5.9E-01	AF037175.1	EST_HUMAN	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11149	23816	37059	1.95	5.9E-01	AF064626.1	NT	PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA
11453	24082	37398	1.56	5.9E-01	P47135	SWISSPROT	Mus musculus strain SPRET/EJ CD48 antigen (Cd48) gene, partial cds
						SWISSPROT	JSNT PROTEIN

Page 46 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11468	24002	37869	1.66	5.9E-01	P47135	SWISSPROT	JSM1 PROTEIN
12021	24549	31109	2	5.9E-01	I42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 A1) gene, promoter region
12252	24698		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12465	24832		5.72	5.9E-01	P34928	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
13021	14639	27348	1.36	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2569	16283	28021	1.01	5.9E-01	Z305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	29838	4.37	5.9E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
5290	18095		0.82	5.9E-01	AE002162.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5444	18243	31131	0.82	5.8E-01	Q10869	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18669	31835	1.09	5.8E-01	D78659.1	EST_HUMAN	HUM500E08 Human placenta polyA* (Tfujivara) Homo sapiens cDNA clone GEN-500E08 5'
6220	18994	31970	0.66	5.8E-01	D50401.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6715	19630		2.48	5.8E-01	S85091.1	NT	Cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.81	5.8E-01	H41571.1	EST_HUMAN	Y91803.s1 Soares adult brain N264-H855Y Homo sapiens cDNA clone IMAGE:176787 3' similar to
7885	20580	33805	0.64	5.8E-01	AI280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
7985	20680	33806	0.64	5.8E-01	AI280061.1	EST_HUMAN	gb:S44010.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853778 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	gb:S44010.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853778 3'
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8789	21481	34628	8.97	5.8E-01	AJ270774.1	SWISSPROT	SPORE COAT PROTEIN SP96
8871	21562	34707	0.99	5.8E-01	Q27368	SWISSPROT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 6-11
8872	21562	34707	0.99	5.8E-01	Q27368	SWISSPROT	TRANSSCRIPTION FACTOR E2F
9466	22149	36837	0.51	5.8E-01	Q20471	SWISSPROT	POTENTIAL CASEIN KINASE F46P22 IN CHROMOSOME X
10811	23591	36837	7.56	5.8E-01	B9021608.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10962	23638		3.97	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11089	23769		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4294403 5'
1480	14227	26912	1.12	5.7E-01	P06727	SWISSPROT	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4294403 5'
1480	14227	26913	1.12	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.69	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3217	15900	28631	1.62	5.7E-01	Q8WTJ2	SWISSPROT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
						NT	POTENTIAL TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOTA)
3495	16281		2.92	5.7E-01	AB033503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopentane-1-carboxylate synthase, complete cds
6282	19036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	30145486FT NIH_MGC_56 Homo sapiens cDNA clone IMAGE:385860 5'
8911	19374	32388	0.81	5.7E-01	JA194201.1	EST_HUMAN	Z38c0611 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666674 5'
8783	17932	30658	1.33	5.7E-01	AL111440.1	NT	Bathyra cinerea strain 14 cDNA library under conditions of nitrogen deprivation

Page 47 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7694	20328	35438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR)(P5C REDUCTASE)
8770	20666		0.5	5.7E-01	AJ231835.1	NT	Mus musculus Kcnq1, Lirp5, Miah2, Tape-1, Tesc4 and Tesc6 genes, alternative transcripts
8279	20973		0.47	5.7E-01	A065081.1	EST_HUMAN	H0895 Human fetal liver cDNA library Homo sapiens cDNA
9698	22350	35544	1.19	5.7E-01	AL181832.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9698	22350	35544	1.19	5.7E-01	AL181832.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	38351	0.72	5.7E-01	BF640862.1	EST_HUMAN	60208712F1 NIH_MGC_58 Homo sapiens cDNA, contig fragment No. 5'
11983	24824		1.52	5.7E-01	BE716051.1	EST_HUMAN	MR3-HIT07036-180700-003-402 HT0736 Homo sapiens cDNA
12659	24968		3.01	5.7E-01	BE969722.2	EST_HUMAN	60165481R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3839763 3'
3357	16117	28772	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3357	16117	28773	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3893	16613	29252	0.97	5.6E-01	AL181601.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	18056	29578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21384	34541	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5'
8702	21384	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5'
9275	22029	35199	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11884	24467		2.57	5.6E-01	BE688260.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11897	24535	37272	1.63	5.6E-01	AA493535.1	EST_HUMAN	6015910.e1 NCL CGAP_P8 Homo sapiens cDNA clone IMAGE:940674 similar to contains element P1R7 repetitive element:
12352	18613	29252	1.69	5.6E-01	AL181501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12378	24776		2.7	5.6E-01	P30505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12773	25027		4.28	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	26606	0.85	5.6E-01	8363612	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2705	15412	28150	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2919	15685	28330	1	5.5E-01	5902085	NT	Homo sapiens superfamily viralidic activity 2 (S. cerevisiae homolog) like (SKIVL), mRNA
3062	18828		1.55	5.5E-01	H46218.1	EST_HUMAN	6017810.e1 Sacchar adult brain N245F1B55Y Homo sapiens cDNA clone IMAGE:176266 3'
3228	15691	28944	4.22	5.5E-01	AF227240.1	NT	Rabbit cal papillomavirus, complete genome
3378	16431	30473	1.7	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.79	5.5E-01	U68097.1	NT	Bos taurus MHC class I beta-chain BoLA-DIB1 gene, partial cds
7187	18873		0.65	5.5E-01	AB015696.1	EST_HUMAN	Cereas auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	AF191768.1	NT	cd2201.v4 NCL CGAP_Homo sapiens cDNA clone IMAGE:1602336 5'
9657	22319		0.7	5.5E-01	U88415.1	NT	Chinese-Congo hemorrhagic fever virus strain SFU 41/665 nucleoprotein gene, complete cds

Page 48 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	22924	36136	0.98	5.5E-01	T05047.1	EST_HUMAN	EST02035 Fetal brain, <i>Stratagene</i> (cat#936208) Homo sapiens cDNA clone HFBC335
11087	23757	37033	1.65	5.5E-01	BF128507.1	EST_HUMAN	BC181107R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12655	25507	4.81	6.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mas2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
140	12955	25598	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mas2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
671	13352	25980	1.16	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds, and unknown genes
571	13352	25981	1.16	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds, and unknown genes
1248	13907	26894	3.41	5.4E-01	AV186087.1	EST_HUMAN	QY44NN0040-070400-100-c04 NN0040 Homo sapiens cDNA
2069	14850	27719	3.43	5.4E-01	AE002247.2	NT	<i>Chlamydomonas reinhardtii</i> AR39, section 74 of 84 of the complete genome
2232	14980	27719	1.91	5.4E-01	AJ276682.1	NT	<i>Drosophila melanogaster</i> mRNA for 15,15' beta ceroleno dioxygenase (beta-diox gene)
5068	17785	30402	0.92	5.4E-01	M74438.1	NT	<i>Rattus rattus</i> UDP-glucuronosyltransferase gene, complete cds
5571	18368	31278	0.74	5.4E-01	AW842327.1	EST_HUMAN	PM2-CH0035-030200-003-c10 CH0035 Homo sapiens cDNA
6068	18876	31845	0.83	5.4E-01	AB075017.1	NT	<i>Rattus norvegicus</i> gene for TIST1, complete cds
6628	19664	32710	0.87	5.4E-01	BE96592.2	EST_HUMAN	607186027R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3606080 3'
7235	19920	32693	0.81	5.4E-01	Z21618.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7235	19920	32694	0.81	5.4E-01	Z21618.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7237	19922	32697	1.48	5.4E-01	Q84428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-CoA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-CoA DEHYDROGENASE]
9890	22540	32697	2.09	5.4E-01	BF572636.1	EST_HUMAN	60207664FT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243990 5'
11016	23697	36948	2.87	5.4E-01	P36658	SWISSPROT	NITRATE REDUCTASE (NADPH) (NR)
11621	24216	37541	3.08	5.4E-01	Q30075	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) [MEROSIN HEAVY CHAIN]
11621	24218	37542	3.08	5.4E-01	Q30075	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) [MEROSIN HEAVY CHAIN]
11944	24499		3.5	5.4E-01	AI858398.1	EST_HUMAN	w57p04.x1 NCL_GCAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb-M13452 LAMIN A (HUMAN);
593	15287	25921	1.54	6.3E-01	AF019413.1	NT	Homo sapiens FLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKIZW), RD, complement factor B (B), and complement component C2 (C2) genes, >
2136	14866	27596	1.01	5.3E-01	AF113018.1	NT	<i>Brassica oleracea</i> var. capitata phospholipase D2 (PLD2) gene, complete cds
2136	14868	27607	1.01	5.3E-01	AF113018.1	NT	<i>Brassica oleracea</i> var. capitata phospholipase D2 (PLD2) gene, complete cds
2786	15491	28230	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO;	Exon SEQ ID NO;	ORF SEQ ID NO;	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	15491	28231	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	AF087959.1	NT	Homo sapiens secreted C-type lectin precursor (SLCCL) gene, complete cds
4187	16628		1.58	5.3E-01	U93937.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30860	1.98	5.3E-01	A1820821.1	EST_HUMAN	z442h12.5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30861	1.98	5.3E-01	A1820821.1	EST_HUMAN	z442h12.5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711 5'
5466	18265	31157	0.84	5.3E-01	AA193872.1	EST_HUMAN	z442g08.7 Soares_NHMP01 S1 Homo sapiens cDNA clone IMAGE:666112 5'
5466	18265	31157	0.84	5.3E-01	AA193872.1	EST_HUMAN	z442g08.7 Soares_NHMP01 S1 Homo sapiens cDNA clone IMAGE:666112 5'
5559	18356	31266	1.82	5.3E-01	BE645620.1	EST_HUMAN	7673c12.1 NCL CGAP P228 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5559	18356	31267	1.82	5.3E-01	BE645620.1	EST_HUMAN	7673c12.1 NCL CGAP P228 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
8802	21494		1.8	5.3E-01	LO1850.2	NT	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); Roridalia gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8854	21645	34692	0.81	5.3E-01	BF433956.1	EST_HUMAN	7671c12.1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
8854	21645	34693	0.81	5.3E-01	BF433956.1	EST_HUMAN	7671c12.1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
10111	22759	35971	0.62	5.3E-01	A054210.1	EST_HUMAN	W94902.1 NCL CGAP_Mel13 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW-COX4, HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11550	24149	37450	7.3	5.3E-01	BE568291.1	EST_HUMAN	601339897.1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11789	24379	37706	1.72	5.3E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
11877	25206		4.03	5.3E-01	AA916053.1	EST_HUMAN	q930w05.1 NCL CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811
797	13589	28228	18.35	5.2E-01	L20770.1	NT	APOLIPROTEIN D PRECURSOR (HUMAN); Oncofetal melanogaster helix-loop-helix mRNA, complete cds
1141	13896	28657	8.29	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1769	13923	28585	1.77	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT6)
1879	14616		2.35	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2142	14872	27605	2.55	5.2E-01	A3018383.2	NT	Homo sapiens chromosome 21 segment HS21 C085
3117	15682	28521	1.23	5.2E-01	U05942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3231	15994		1	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii lsd gene for isocitrate dehydrogenase, complete cds
3400	16158		1.58	5.2E-01	AI16780.1	NT	Acetabacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3437	16183	28843	2.27	5.2E-01	AA984165.1	EST_HUMAN	Bovine chimeric strain T4 cDNA library under conditions of nitrogen deprivation am77g05.1 Siralagene schizos brain S11 Homo sapiens cDNA clone IMAGE:1618504 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16376		0.76	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast middle dehydrogenase precursor (p mch) mRNA, nuclear gene encoding
4568	17903	28630	0.82	5.2E-01	6752647	NT	Chloroplast protein, complete cds
4933	17679		1.02	5.2E-01	7106444	NT	Mus musculus acetylcholine receptor beta (Acbt) mRNA
5567	18364	31272	0.87	5.2E-01	AJ284261.1	EST_HUMAN	Mus musculus vanilloid receptor-like protein 1 (Vrl1) mRNA
9830	25126	35474	0.76	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9830	25126	35476	0.76	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832	22483	35695	0.48	5.2E-01	AA194518.1	EST_HUMAN	zq05b09.r1 Strabagene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
9926	22574	35772	1.35	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12744	25010		7	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
803	13381	28013	1.84	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
633	13412	25047	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
633	13412	29048	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1648	14304		1.09	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2017	14762		1.29	5.1E-01	BF683096.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4057	16802	29433	3.86	5.1E-01	AI894495.1	EST_HUMAN	W83672.x1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2427263 3'
4164	16904	29533	2.81	5.1E-01	P98380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5103	17821	39438	1.01	5.1E-01	U72953.1	NT	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6128	18008	31874	0.87	5.1E-01	BE541068.1	EST_HUMAN	601063605F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6183	18960		0.93	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAUF07 5'
6818	19179	32602	1.69	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Scarae placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34304	0.93	5.1E-01	AW809891.1	EST_HUMAN	QV4-S1T0023-160400-172-401 ST0023 Homo sapiens cDNA
8470	21162	34305	0.93	5.1E-01	AW809891.1	EST_HUMAN	QV4-S1T0023-160400-172-401 ST0023 Homo sapiens cDNA
9583	22238	35420	4.33	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9587	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	66B1 Human retina cDNA Tapp509-cleaved sublibrary Homo sapiens cDNA not directional
10080	22708	35926	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	601658663F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12328	24745		3.55	5.1E-01	BF493982.1	EST_HUMAN	nc65f10.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2130	14651	27590	1.24	5.0E-01	4895552	NT	TAR1 repetitive element 1
2130	14651	27590	1.24	5.0E-01	4895552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2130	14651	27591	1.24	5.0E-01	4895552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA

Page 51 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27601	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE8), and putative chromosome replication protein (gdaA) genes, complete cds; and termination factor Rho (rho) gene>
2140	14870	27602	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE8), and putative chromosome replication protein (gdaA) genes, complete cds; and termination factor Rho (rho) gene>
3811	16863	29196	1.13	5.0E-01	L38483.1	NT	Rattus norvegicus jagrad protein mRNA, complete cds
3854	16864	29241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	19312		0.65	5.0E-01	BF576189.1	EST_HUMAN	602132842F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE-4271939 5'
7562	20232	33334	0.75	5.0E-01	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7562	20232	33335	0.75	5.0E-01	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8428	21121		1.82	5.0E-01	IM92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8569	21261	34399	0.71	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE-4043485 3'
9368	20429	33547	2.74	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE-4136632 5'
9525	22178	35362	1.36	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	35363	1.36	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10290	22533		1.12	5.0E-01	BE369218.1	EST_HUMAN	60145024F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE-3849438 5'
12026	24654		4	5.0E-01	AF029215.1	NT	Mus musculus MRG OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24689		1.86	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12726	24697		4.39	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
772	13544	28205	2.43	4.9E-01	BE571462.1	EST_HUMAN	602076949F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE-4243560 5'
1655	14402	27090	1.54	4.9E-01	AJ243855.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1699	14636	27345	1.16	4.9E-01	U40669.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5321	18124	30783	0.89	4.9E-01	Q61954	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31686	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7552	20033	33111	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mIEF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPENTYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
7605	20271	33378	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPENTYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
8888	21519		1.45	4.8E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE-4102503 5'

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9088	21778	34939	0.99	4.8E-01	AW338905.1	EST_HUMAN	h69022.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907286 3' similar to TR.O96714 O95714 HERC2.
9186	25431		1.96	4.9E-01	10946993	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10216	22884	36076	0.94	4.9E-01	AF033980.1	NT	Mus musculus adenylate cyclase 1 (Adcy1) cDNA, partial cds
10419	23065	36268	0.71	4.9E-01	X80090.1	NT	H.sapiens DNA for BCL2A gene and BCL2A/IGH locus fusion
11625	24486		1.72	4.8E-01	AF176912.1	NT	Homo sapiens neurotrophin-1b-cell stimulating factor-3 gene, complete cds
12709	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	hg22et11.61 NCI_CGAP_C610 Homo sapiens cDNA clone IMAGE:1144652 3'
4288	17037		0.77	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5420	18219	30530	10.79	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for mobile recombination, complete cds
6579	19342	32396	0.79	4.8E-01	U92982.1	NT	Mus musculus slow skeletal muscle troponin T (Tnnit1) gene, complete cds
6589	19352		3.78	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.61 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7218	19801		1.99	4.9E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7665	20235	33339	0.78	4.8E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
7681	20325	33434	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7691	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33621	1.2	4.8E-01	AI820744.1	EST_HUMAN	Y17710.y6 Soares_breast_2NblHbSt Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER8 repetitive element.
8144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	PM1-H1T0350-201299-004-004 HT0350 Homo sapiens cDNA
10059	23322		1.88	4.8E-01	X83502.1	NT	S.cerevisiae ORF's from chromosome X
12717	25165		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
12765	25216		1.98	4.8E-01	AI132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6422	19180	32180	8.41	4.7E-01	BF217173.1	EST_HUMAN	601183389F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4099387 5'
6841	19423	32389	0.94	4.7E-01	AI204374.1	EST_HUMAN	q72099.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:4099387 5'
7764	20460	33984	0.83	4.7E-01	T11414.1	EST_HUMAN	Hbc811 Human pancreatic islet Homo sapiens cDNA clone IMAGE:1755544 3'
7764	20460	33985	0.83	4.7E-01	T11414.1	EST_HUMAN	Hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
8974	21654	34816	0.52	4.7E-01	6981501	NT	Rattus norvegicus Spermatid binding protein (Sbp), mRNA
10751	23436		6.11	4.7E-01	AF102673.1	NT	Influenza A virus isolate H5N1697 hemagglutinin (HA) gene, partial cds
11022	23694	36697	2.2	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
11252	23914	37206	1.61	4.7E-01	BF629588.1	EST_HUMAN	60204398F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
11349	24039	37342	1.7	4.7E-01	AW869448.1	EST_HUMAN	RC9-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12118	24039		1.32	4.7E-01	BE887763.1	EST_HUMAN	601161133F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912483 5'
12237	24689		1.51	4.7E-01	AW341561.1	EST_HUMAN	h611c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'

Page 53 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12873	26055		1.63	4.7E-01	AF000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 148501-173850 nt, position (777)
12871	26300		1.38	4.7E-01	6679502	NT	Mus musculus probasome (prosome, macropin) 26S subunit, ATPase 3 (Psmc3), mRNA
31726	16479	29116	1.57	4.9E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3726	16479	29117	1.57	4.9E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18138	30785	1	4.9E-01	BF313593.1	EST_HUMAN	601590234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4123472 5'
5333	18138	30785	1	4.9E-01	BF313593.1	EST_HUMAN	601590234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4123472 5'
5355	18185	30875	3.11	4.9E-01	Q60843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5355	18185	30875	3.11	4.9E-01	Q60843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5459	18258	31148	1.84	4.9E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3943637 5'
5472	18271	31163	2.17	4.9E-01	A1247678.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5472	18271	31164	2.17	4.9E-01	A1247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5480	18279	31175	1.6	4.9E-01	P20050	SWISSPROT	TR:O16338 O16338 BUTYRPHILIN ;
5500	18557		0.99	4.9E-01	AF212124.1	NT	MEIOSIS SPECIFIC PROTEIN HOP1
5645	18440		0.77	4.9E-01	BE617247.1	EST_HUMAN	Arnold schwartz cyclochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5909	18598	31526	0.59	4.9E-01	D28215.1	NT	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6163	18040	31611	1.21	4.9E-01	AE000894.1	NT	Unidentified soil bacterium 16S rRNA gene encoding 16S ribosomal RNA
6669	19566	32620	3.2	4.9E-01	U62332.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of line complete genome
6669	19566	32621	3.2	4.9E-01	U62332.1	NT	Emmerella nidulans NEUPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	25105	32884	0.57	4.9E-01	L07320.1	NT	Emmerella nidulans NEUPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7629	20295	33403	0.91	4.9E-01	AA493577.1	EST_HUMAN	Murine cytomegalovirus g1 protein gene, complete cds
7658	20322		0.59	4.9E-01	Q60069	SWISSPROT	nm4105.g1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element/contains element L1 repetitive element ;
8219	20913	34049	10.11	4.9E-01	BF697399.1	EST_HUMAN	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 8 KD PROTEIN 2 (8K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NLA) (N)]
9201	21870	35035	1.11	4.9E-01	P55202	SWISSPROT	602130953F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287828 5'
							ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

Page 54 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripr
9201	21870	35036	1.11	4.8E-01	P59202	SWISSPROT	ATRIAL Natriuretic Peptide Receptor B Precursor (ANP-B) (ANPRB) (GC-B) GUANYLATE CYCLASE
9876	22526	35720	1.84	4.8E-01	A1915834.1	EST_HUMAN	wg73a12.x1 Soares_NSF_FB_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
9876	22528	35721	1.64	4.8E-01	A1915834.1	EST_HUMAN	wg73a12.x1 Soares_NSF_FB_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10812	22592		2.3	4.8E-01	P38183	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
10822	23602	36850	10.22	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT10730-100500-075-g05 HT10730 Homo sapiens cDNA
10922	23602	36851	10.22	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT10730-100500-075-g05 HT10730 Homo sapiens cDNA
11450	23217	39449	5.32	4.8E-01	AFO19359.1	NT	Human thiopeptide methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	39450	5.32	4.8E-01	AFO19359.1	NT	Human thiopeptide methyltransferase (TPMT) gene, exon 10 and complete cds
12103	24045		1.77	4.8E-01	D63318.1	EST_HUMAN	HUM103F08B Clontech human fetal brain polyA+ mRNA (H6559) Homo sapiens cDNA clone GEN-105F03 5'
1904	14641	27350	1.43	4.8E-01	AE001931.1	NT	Drosophila melanogaster R1 section 68 of 229 of the complete chromosome 1
1904	14641	27351	1.43	4.8E-01	AE001931.1	NT	Drosophila melanogaster R1 section 68 of 229 of the complete chromosome 1
2873	15940	28284	4.5	4.8E-01	A4877088.1	EST_HUMAN	355d02.x1 Soares_fetal_liver_aplees_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454176 3'
3312	16072	28722	4.68	4.8E-01	Q06763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3372	16131	28787	1.07	4.8E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4007	16753		0.95	4.8E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 2(V) CHAIN
4035	16800	29431	0.88	4.8E-01	A1708908.1	EST_HUMAN	est5609.x1 Berralead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2353480 3'
4155	17897		4.25	4.8E-01	AW187495.1	EST_HUMAN	hcd9g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4680	17817	30236	1.1	4.8E-01	BE95445.2	EST_HUMAN	30167223RT.NH.LMGCG_87 Homo sapiens cDNA clone IMAGE:3866023 3'
5481	18260	31151	1.48	4.8E-01	AW508814.1	EST_HUMAN	QV2P7T0012-140100-031-c09 PT0012 Homo sapiens cDNA
6510	19275		1.45	4.8E-01	Q00656	SWISSPROT	COAT PROTEIN
7312	18665	33073	1.27	4.8E-01	M37038.1	NT	Rat nuclear proteins B23.1 and B23.2
7500	20180	33273	2.54	4.8E-01	A1858846.1	EST_HUMAN	W82902.x1 NC1 CGAP_U11 Homo sapiens cDNA clone IMAGE:2428618 3' similar to TRQ29223 Q92923
7621	20287	33396	0.95	4.8E-01	P50070	SWISSPROT	SW18NF COMPLEX 170 KDA SUBUNIT. ;
8206	20900		0.86	4.8E-01	M32681.1	NT	DNA PRIMASE
8302	20966	34134	3.6	4.8E-01	A1648568.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							5256g1.x1 NC1 CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8457	21149	34292	0.83	4.8E-01	Q52728	SWISSPROT	Homo sapiens hypothetical protein DKFZp447G183 (DKFZp447G183), mRNA
8680	21372		2.34	4.8E-01	114447788	NT	

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8807	21588	34728	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
8840	22491		1.02	4.5E-01	9530318	NT	Bombayx mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#939206) Homo sapiens cDNA clone HFBCY17
10392	23038	36256	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#939206) Homo sapiens cDNA clone HFBCY17
10772	23455	36869	2.15	4.5E-01	AW591271.1	EST_HUMAN	Y01401.x1 NCI CGAP U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT8_MOUSE
11217	23880		1.52	4.5E-01	AV716392.1	EST_HUMAN	Q64262 VIRAL INTEGRATION SITE PROTEIN INT-6, [1].
11895	25394		3.62	4.5E-01	BE871461.1	EST_HUMAN	AV716392 GLC Homo sapiens cDNA clone GLOCED12 5'
12540	24880		1.85	4.5E-01	BF337531.1	EST_HUMAN	901446201.F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3852861 5'
12611	24918		3.37	4.5E-01	11422068	NT	902035275.F1 NCI_CGAP_Bm54 Homo sapiens cDNA clone IMAGE:47183260 5'
2388	15108	27847	3.39	4.4E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3310	15070	28719	1.29	4.4E-01	AF068790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	15070	28720	1.29	4.4E-01	AF068790.1	NT	Rattus norvegicus SynGAP-B mRNA, complete cds
3313	15073	28723	2.92	4.4E-01	BF059726.1	EST_HUMAN	Rattus norvegicus SynGAP-B mRNA, complete cds
4209	19530		1.88	4.4E-01	BE378707.1	EST_HUMAN	797102.Y1 NCI_CGAP_Bm16 Homo sapiens cDNA clone IMAGE:3393795 5'
5334	18137	30797	1.2	4.4E-01	P04029	SWISSPROT	601237739.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603953 5'
5334	18137	30798	1.2	4.4E-01	P04029	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5602	15307	31309	1.59	4.4E-01	365019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5619	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	musclin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 350 nt]
5684	18551	31591	1.46	4.4E-01	A1188413.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
5684	18551	31592	1.46	4.4E-01	A1188413.1	EST_HUMAN	q02h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6146	18923	31804	1.78	4.4E-01	AV080795.1	EST_HUMAN	UNKNOWN PROTEIN ;
6236	19010		1.42	4.4E-01	AA771832.1	EST_HUMAN	q02h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
7297	19980	33056	1.04	4.4E-01	AE000571.1	NT	UNKNOWN PROTEIN ;
7723	25119		0.6	4.4E-01	AE001188.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7740	20436		9.71	4.4E-01	Z11678.1	NT	ae0641.1t Strategene scilicet brain S11 Homo sapiens cDNA clone IMAGE:970955 3' similar to gb:M16038
8651	21353	34500	0.84	4.4E-01	AA059427.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8049	21738	34898	0.7	4.4E-01	AF112840.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
							Tropaeolum pallidum section 4 of 87 of the complete genome
							S. tuberosum mRNA for induced stolon tip protein (partial)
							206a03.8t Strategene cdna (9637204) Homo sapiens cDNA clone IMAGE:509836 3'
							HIV-1 isolate 86107v8 from USA, envelope glycoprotein (env) gene, partial cds

Page 56 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21771	34934	0.57	4.4E-01	AW612578.1	EST_HUMAN	h05d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to
9190	21860	35026	1.24	4.4E-01	O62936	SWISSPROT	SW-MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9862	22512	35709	2.19	4.4E-01	A1269850.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
9863	22513		1.88	4.4E-01	P28922	SWISSPROT	q35f00.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9897	22645	35857	4.31	4.4E-01	P36660	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10273	22921	36132	1.33	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36133	1.33	4.4E-01	S76404.1	NT	beta-HKAH1-K-ATPase beta-subunit [rats, Genomic, 9883 nt, segment 2 of 2]
12148	24636	31095	3.44	4.4E-01	5977674	NT	beta-HKAH1-K-ATPase beta-subunit [rats, Genomic, 9883 nt, segment 2 of 2]
12579	24903	31000	3.35	4.4E-01	5977674	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12683	24971		1.91	4.4E-01	P94726	SWISSPROT	Auagropia californica nucleopolydnavirus, complete genome
12766	25152		1.43	4.4E-01	AW395338.1	EST_HUMAN	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
402	13187	25835	2.17	4.3E-01	AF155218.1	NT	RC2-CT0320-281769-012-07 CT0320 Homo sapiens cDNA
402	13187	25836	2.17	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2875	15642		1.64	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3056	15822	29468	0.75	4.3E-01	AW195269.1	EST_HUMAN	CM2-DT003-310200-377-001 DT003 Homo sapiens cDNA
4131	16873	29501	1.29	4.3E-01	J00306.1	NT	MRD-BN0070-270300-508-604 BN0070 Homo sapiens cDNA
4374	13187	29535	1.18	4.3E-01	AF155218.1	NT	Human somatostatin 1 gene and flanks
4374	13187	29536	1.18	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4902	17629		1.19	4.3E-01	AL161802.2	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5260	18095	30742	0.8	4.3E-01	P48834	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5260	18086	30743	0.8	4.3E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5798	18589	31515	1.69	4.3E-01	BE191955.1	EST_HUMAN	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5917	18508	31534	2.02	4.3E-01	AF178925.1	NT	QV1-HT0039-070500-191-d08 HT0039 Homo sapiens cDNA
6808	19371	32384	4.78	4.3E-01	AJ001678.1	NT	Salimif sclerous olfactory receptor (SSC186) gene, partial cds
6889	19606	32646	0.6	4.3E-01	AF075929.1	NT	Colnirix colnirix japonica lfnG gene
6767	19511		0.91	4.3E-01	O33397	SWISSPROT	Equus caballus microsatellite LEX027
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	DNA GYRASE SUBUNIT B
7496	20168	33260	0.61	4.3E-01	U51002.1	NT	60-223134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158266 5'
8528	21019		2.72	4.3E-01	U97040.1	NT	Mus musculus Dnk-2 gene, complete cds
9154	21885	35053	0.98	4.3E-01	Y14804.1	NT	Methanococcus voltae flagellar-related protein C1 (flaC-fla) genes, complete cds
9626	22278	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	Erwinia amylovora rcsA gene
9626	22278	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCI_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2968554 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	22776	35690	0.84	4.3E-01	AW170589.1	EST_HUMAN	xr36d05.x1 Scores_NHICc_cervical_lumbar Homo sapiens cDNA clone IMAGE:2689400 3' similar to
10409	23055	38272	0.5	4.3E-01	H65202.1	EST_HUMAN	TR-000189 000189 MU-ADP-TIN-RELATED PROTEIN 2 ;
10849	18906	32646	2.45	4.3E-01	AF075628.1	NT	yf45b05.x1 Scores_fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:208209 3'
11166	23033	37113	1.29	4.3E-01	AW93658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11168	23833	37114	1.29	4.3E-01	AW93658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
11745	24336	37662	1.84	4.3E-01	AI074332.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
12770	23029		2.18	4.3E-01	AJ003022.1	NT	1294404.x1 NCI_CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2283351 3'
1337	15566	26761	1.54	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor wlt1 gene
1841	14676		1.23	4.2E-01	AJ761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3598	18349	28990	4.4	4.2E-01	AE003947.1	NT	nc24d09.x1 NCI_CGAP_G051 Homo sapiens cDNA clone IMAGE:1286668 3'
3628	16381	29021	1.41	4.2E-01	AI280338.1	EST_HUMAN	Xylella fastidiosa, section B3 of 229 of the complete genome
3698	17868		0.85	4.2E-01	N61203.1	EST_HUMAN	ql04b01.x1 Scores_NHMPV_S1 Homo sapiens cDNA clone IMAGE:1876945 3'
3964	18713	26352	0.97	4.2E-01	Q04686	SWISSPROT	7881E1 fetal brain cDNA Homo sapiens cDNA clone 7881E1-K similar to R07879_Z40498
4649	17883	30015	4.88	4.2E-01	AA634093.1	EST_HUMAN	SOX-8 PROTEIN
4731	17463	30100	3.46	4.2E-01	R13467.1	EST_HUMAN	h16901.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:987777 similar to gb:M33600 HLA GLASS
5626	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5693	18487	31408	1.53	4.2E-01	AW854162.1	EST_HUMAN	yf77d01.t1 Scores_infant brain TNIB Homo sapiens cDNA clone IMAGE:28278 5'
6112	18889	31858	1.01	4.2E-01	AL163247.2	NT	60187672.F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
6852	18652	32582	10.8	4.2E-01	AI188472.1	EST_HUMAN	RC3-CT0254-060400-028-g04 CT0254 Homo sapiens cDNA
6911	25101	32694	2.15	4.2E-01	AI188472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6953	19686	32734	7	4.2E-01	AL151547.2	NT	AUT86472 PLACC2 Homo sapiens cDNA clone PLACC2000470 3'
6993	20586	33715	2.21	4.2E-01	AW957448.1	EST_HUMAN	AI188472 PLACC2 Homo sapiens cDNA clone PLACC2000470 3'
7691	20586	33716	2.21	4.2E-01	AW957448.1	EST_HUMAN	Brcal1 breast cancer gene [a1a, WF, spleen, Genomic, 419 nt, segment 2 of 2]
8106	20600	33932	0.61	4.2E-01	4758039	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8670	22520		0.94	4.2E-01	AA705007.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
10061	22729	35644	0.45	4.2E-01	AF161854.1	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10353	23039	36256	1.78	4.2E-01	AW93658.1	EST_HUMAN	265601.s1 Scores_fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:462849 3'
10372	23691	36901	2.69	4.2E-01	AB023485.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
11370	23977	37277	2.11	4.2E-01	BE598485.2	EST_HUMAN	MR3-SN0010-280300-103-R07 SN0010 Homo sapiens cDNA
1072	13830	26488	1.83	4.1E-01	AI905481.1	EST_HUMAN	Oryzalis latipes OIGC7 for membrane guanylyl cyclase, complete cds
							001600352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3300585 3'
							RC-BT0091-210799-142 BT0091 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13338	28497	1.1	4.1E-01	AY705243.1	EST_HUMAN	AY705243 ADB Homo sapiens cDNA clone ADBAHF08 8'
1081	13339	28498	1.1	4.1E-01	AY705243.1	EST_HUMAN	AY705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2715	15422	28161	1.1	4.1E-01	U705243	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2841	15708	28355	2.17	4.1E-01	AL181536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2841	15708	28356	2.17	4.1E-01	AL181536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16506	29142	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST1373384 MAGE cDNAs, MAGE Homo sapiens cDNA
3754	16506	29143	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST1373384 MAGE cDNAs, MAGE Homo sapiens cDNA
4241	16882	26607	2.63	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoC, isoH, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ

Page 59 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2868	15734	28393	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2968	15734	28394	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3893	15436	29080	1.96	4.0E-01	AF069033.1	NT	Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3807	15559	29181	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
3807	15559	29102	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
4767	17499	31749	7.97	4.0E-01	Q31849	SWISSPROT	NADH+PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5820	18609	31538	1.23	4.0E-01	AW670610.1	EST_HUMAN	EST382891 IMAGE ressequences, MAGK Homo sapiens cDNA
6345	19115	32104	0.94	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE]
7728	20391	33504	0.86	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7828	20524	33649	0.44	4.0E-01	BF02834.1	EST_HUMAN	MR4-TN0110-180600-202-g02 TN0110 Homo sapiens cDNA
7910	20605	33736	1.04	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8904	21595	34736	1.17	4.0E-01	AA323283.1	EST_HUMAN	EST280681 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030332.1	EST_HUMAN	60156285F1 NH1_MGC_58 Homo sapiens cDNA clone IMAGE:3829082 5'
11721	24316		2.83	4.0E-01	L76980.1	NT	Synechocystis sp. PCC 6813 transposase gene, complete cds
12162	25222		2.28	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12884	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STES INTERGENIC REGION
1356	14104	26780	1.85	3.9E-01	AF206518.1	NT	Gorilla gorilla carboxyl-ester lyase (CEL) gene, complete cds
2948	13558	28101	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2709	15418	28163	4.27	3.8E-01	X62032.1	NT	H. sapiens B-myb gene
2709	15418	28164	4.27	3.8E-01	X62032.1	NT	H. sapiens B-myb gene
3093	15688	29499	4.73	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, tyrB2, cys3 genes and ori3
4932	18604	29435	1.05	3.9E-01	BF562811.1	EST_HUMAN	761401.x1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
4932	17660	30270	1.74	3.9E-01	BE726867.1	EST_HUMAN	60156304F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE:3833669 5'
6843	16831	31568	3.91	3.8E-01	BF206036.1	EST_HUMAN	60188236F1 NH1_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
7854	20549	33674	0.92	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CM3-C710105-107599-204-508 C710105 Homo sapiens cDNA
8769	21461		0.58	3.9E-01	BF346834.1	EST_HUMAN	60201994F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155322 5'
9134	21822	34988	1.28	3.9E-01	AW105888.1	EST_HUMAN	XB6602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701391 3' similar to TR-O94821
9445	22122	35301	1.46	3.9E-01	AB037337.1	EST_HUMAN	094821 KIAA0713 PROTEIN ; wp76e02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467058 3' similar to SW/RX6_HUMAN P48392 BINDING REGULATORY FACTOR.;

Page 60 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22429	35535	3.03	3.8E-01	M19879.1	NT	Human cblbindin 27 gene, exons 10 and 11, and 11 and Alu repeats
9845	22498		0.59	3.8E-01	11495620	NT	Porphyria variegata mitochondrial, complete genome
10068	22714	35932	0.77	3.8E-01	D88722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.8E-01	AV695974.1	EST_HUMAN	AV695974 GGC Homo sapiens cDNA clone GK9CQC11 5'
11753	23434	37674	1.47	3.8E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
11848	24395		3.37	3.8E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12066	24581		2.08	3.8E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.8E-01	11433335	NT	Homo sapiens hypochlorite protein FLJ10593 (FJ10593), mRNA
156	12971		8.33	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1883	14601		1.03	3.8E-01	AE003870.1	NT	Xylaria fastidiosa, section 16 of 229 of the complete genome
2460	15178	27918	1.29	3.8E-01	UA1949.1	NT	Ceanothus thibetica brigitae acetylcholinesterase (ace-1) gene, complete cds
2576	15280	28027	1.62	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2638	15601	28092	3.66	3.8E-01	6578002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	15769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 89SE-MP1213)
3043	15809	28458	1.39	3.8E-01	AF043393.1	NT	Plasmodium falciparum aminopeptidase N (ampN) gene, partial cds
3477	16233	28857	7.68	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38512.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3541	16283		1.22	3.8E-01	AI807219.1	EST_HUMAN	wf38512.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16482	28127	1.15	3.8E-01	BE144060.1	EST_HUMAN	PXG-H103339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16647	29287	0.97	3.8E-01	AF794095	NT	Mus musculus general transcription factor II (Gtfd2), mRNA
4043	16788	29416	0.74	3.8E-01	AJ271361.2	NT	Tekdigr rubripes vnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	18021		0.74	3.8E-01	S46925.1	NT	prien protein (mirk, Genomic, 2448 nt)
6528	19284	32238	5.5	3.8E-01	BE072399.1	EST_HUMAN	QV3-B10337-271295-049-e02 BT0537 Homo sapiens cDNA
6662	19579	32614	4.59	3.8E-01	AI974601.1	EST_HUMAN	tas4f11.x1 Soares, total, fetus, NB2HFB, 9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7416	20093		4.42	3.8E-01	X81597.1	NT	M.musculus gene for kallikrein-binding protein
8195	20890	34028	0.86	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8455	21147	34289	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8523	21216	34358	1.02	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8716	21408	34551	1.28	3.8E-01	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.55	3.8E-01	T95413.1	EST_HUMAN	y43106.r1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element/contains PTRS repetitive element

Page 61 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10695	23366		1.67	3.8E-01	AY755814.1	EST_HUMAN	AY755814.BM Homo sapiens cDNA clone BMFBCE07 5'
11521	24121		3.18	3.8E-01	BE716216.1	EST_HUMAN	RCCHT0041-040800-332-b12 HT0341 Homo sapiens cDNA
11593	24288	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	Y62H1.1.s1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:30289 3'
11593	24288	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	Y62H1.1.s1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:30289 3'
12149	24336		4.76	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (exon 10 of 70) of the complete genome
12270	25316		2.08	3.8E-01	U94769.1	NT	Human p53 (TP53) gene, complete cds
12384	24779		3.39	3.8E-01	BE829236.1	EST_HUMAN	QV3-E170063-190700-271-a05 E170663 Homo sapiens cDNA
12723	24994		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bax-3 (bax-3) gene, exon 3 and complete cds
12771	25291		1.74	3.8E-01	AF291463.1	NT	Mus musculus vomeronasal receptor VIR44 (V1ra4) gene, complete cds
12786	25040	30898	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27944	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3453	16209	28860	9.64	3.7E-01	AF056336.1	NT	Danio rerio bona morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	28572	7.39	3.7E-01	AI218707.1	EST_HUMAN	cd3207.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4386	17025	28651	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-502 OT0007 Homo sapiens cDNA
4397	17095	28730	2.55	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5676	18470	31366	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5690	19547	31688	0.9	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6417	19185	32183	0.66	3.7E-01	M10806.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
8438	19204	32794	0.72	3.7E-01	L10353.1	NT	Mus sadicola heptoglobin mRNA, complete cds
7043	19734	32794	3.23	3.7E-01	11528843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7685	20349	33463	0.6	3.7E-01	T68302.1	EST_HUMAN	Y650407.r3 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66324 5'
7719	20383	33497	0.59	3.7E-01	AW511328.1	EST_HUMAN	Id45405.x1 Scores_NFL_T_GRC_S1 Homo sapiens cDNA clone IMAGE:2912467 3' similar to contains Alu repetitive element contains L1.12 L1 repetitive element;
8227	20921	34059	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8293	20957	34096	0.65	3.7E-01	AA902812.1	EST_HUMAN	cd43311.s1 NCL_OGAP_1a2 Homo sapiens cDNA clone IMAGE:1616701 3'
9101	21769		1.31	3.7E-01	AJ271386.1	NT	Galus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10066	22717		0.6	3.7E-01	K00694.1	NT	mouse Ig gamma1 alpha membrane exons region
10110	22756	35970	4.12	3.7E-01	AJ304911.1	EST_HUMAN	qt46007.x1 Scores_fetal_junc_XBHL19W Homo sapiens cDNA clone IMAGE:1950697 3'
10764	23448	36960	1.66	3.7E-01	X05686.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MH-C)
10957	23633	36882	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.37)
11678	24271	37693	1.43	3.7E-01	D78348.1	EST_HUMAN	HUM230A068 Homo aorta polyA+ (T-fujikawa) Homo sapiens cDNA clone GEN-230A06 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11771	24362		2.87	3.7E-01	8877678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11889	24943		2.11	3.7E-01	J04882.1	NT	Human heart/aortic muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24358		3.09	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12488	24847		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZ762K075.11762 (synonym: hme2) Homo sapiens cDNA clone DKFZ762K075.5
12448	24848	30895	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
234	13062	25701	2.17	3.6E-01	AJ009609.1	NT	Bressica nepus mRNA for MAP4K alpha2 protein
975	13740		8.22	3.6E-01	U69241.1	NT	Human mlbp gene, partial cds
1291	14040	28713	3.83	3.6E-01	T80235.1	EST_HUMAN	Y030403.11 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:24443.5
1291	14040	25714	3.83	3.6E-01	T80255.1	EST_HUMAN	Y030403.11 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:24443.5
1909	14648	27356	6.73	3.6E-01	AW590184.1	EST_HUMAN	Hg33102.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2847419.3
1909	14648	27357	6.73	3.6E-01	AF216207.1	EST_HUMAN	Hg33102.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2847419.3
1944	14679	27393	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2287	14993		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.89	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2478	15197	27638	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27637	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27950	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-q07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2836	15348	28090	1.44	3.6E-01	P24208	SWISSPROT	Discothila melanogaster sugar transporter 3 (cut3) mRNA, complete cds
2900	17884		7.16	3.6E-01	AF169485.1	NT	H. sapiens serotonine transporter gene, exons 9 and 10
3462	18218	28871	2.19	3.6E-01	X76739.1	NT	H. sapiens serotonine transporter gene, exons 9 and 10
3482	18218	28872	2.19	3.6E-01	X76739.1	NT	H. sapiens serotonine transporter gene, exons 9 and 10
4375	17112	29745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC5-HT0845-16080-014-512 HT0845 Homo sapiens cDNA
4948	17676	30285	2.38	3.6E-01	AW339393.1	EST_HUMAN	hcd204.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872666.3
5295	18103	30762	0.82	3.6E-01	AJ008585.1	NT	Homo sapiens lba gene Intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	Human sapiens PHEX gene
6388	19155	32154	1.72	3.6E-01	Y10198.1	NT	X746061.1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:275987.5
7048	19739		3.24	3.6E-01	R6490.1	EST_HUMAN	wf2810.x1 Scores_thymus_NHFT_Homo sapiens cDNA clone IMAGE:2613010.3 similar to TR:O15117
7183	19869	32943	1.9	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN [1];
8123	20817	33953	0.56	3.6E-01	P68187	SWISSPROT	SGO-SPONDIN

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8800	21591	34731	2.74	3.6E-01	45049556	NT	Homo sapiens (yeast)-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	45049556	NT	Homo sapiens (yeast)-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091	21780	34644	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9290	21986	35139	1.04	3.6E-01	X17650.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9299	21986	35140	1.04	3.6E-01	X17650.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9369	21944	35621	0.57	3.6E-01	X62825.1	NT	G. perflingens ple gene for phospholipase C upstream region containing bent DNA fragment
9793	22414	35621	14.87	3.6E-01	Q83164	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y41S
9893	22543	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9893	22643	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10864	23544	36791	3.31	3.6E-01	BE902390.1	EST_HUMAN	801676418FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3958997 5'
11062	23722	36983	4.12	3.6E-01	AB004233.1	NT	Arabidopsis thaliana mRNA for StpB, complete cds
11421	23188	38419	3.4	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11903	25416		1.83	3.6E-01	Y19210.1	NT	Homo sapiens HHb5 gene for hair keratin, exons 1 to 9
11978	24522		1.4	3.6E-01	D60901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271800-402289
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
12135	24624		4	3.6E-01	U68888.1	NT	Mus musculus Emr1 mRNA, complete cds
12493	24850		2.12	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12746	25393		2.23	3.6E-01	AW190228.1	EST_HUMAN	X60e11.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.03	3.5E-01	6578633	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.59	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
708	13482	26132	1.59	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
702	13535	26184	4.25	3.5E-01	BF129786.1	EST_HUMAN	801811060RT NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4033951 3'
1615	14362	27053	1.1	3.5E-01	BF310688.1	EST_HUMAN	601894533FT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4124241 5'
1636	14362	27069	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOXA-1 (HOX-1.4) (MH-3)
2612	15500	28066	1.76	3.5E-01	AA22352.1	EST_HUMAN	zbb08.01 Stragogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'

Page 64 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16337		0.86	3.5E-01	AA642183.1	EST_HUMAN	ind003.at NCL CGAP Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	16972	29596	1.87	3.5E-01	AF071283.1	NT	Danio rerio homeobox protein (hox2b) gene, complete cds
4443	17179	29505	0.94	3.5E-01	BE146585.1	EST_HUMAN	RC5-H10218-181069-071-g02 HT0218 Homo sapiens cDNA
4627	17362	29395	1.02	3.5E-01	Y18477.1	NT	Mus musculus Alx412B gene 5' flanking region
4880	17607	30230	4.58	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CAT) gene, exons 1 through 5
5251	18057	30685	0.76	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30686	0.76	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5402	18201	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6143	18921		0.98	3.5E-01	AW1863916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.6	3.5E-01	AA431833.1	EST_HUMAN	zw7903.r1 Sources: Testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TRG1066935
6359	19129	32124	0.86	3.5E-01	U37150.1	NT	GI068935 F10F2.1:
6595	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	Bot tauus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6595	19438		4.24	3.5E-01	X86505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	S serofa mRNA for QD31 protein (PECAM-1)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7870	20605		2.19	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7973	20668	33780	0.71	3.5E-01	BF398871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8366	21059		0.83	3.5E-01	AF051581.1	EST_HUMAN	RC4-E10024-250600-014-007 E10024 Homo sapiens cDNA
8825	21517	34662	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9536	22288	35481	1.62	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9780	22437	35844	5.64	3.5E-01	Z29825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9887	22517	35713	0.96	3.5E-01	BE174784.1	EST_HUMAN	Xlaevis gene for albumin including HP1 enhancer
10635	23327	36564	2.78	3.5E-01	X67034.1	NT	OV2-H10577-060400-128-c07 HT0577 Homo sapiens cDNA
10946	23625	36876	2.39	3.5E-01	AJ243178.1	NT	C.gribeau hoxd9a3 gene for opsin protein
10946	23625	36876	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24106	37419	1.34	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11595	24184	37459	1.84	3.5E-01	N77587.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
11618	24210		1.71	3.5E-01	M82885.1	NT	X50h12.r1 Sources: multiple, eukaryotic, 2NHLN5P Homo sapiens cDNA clone IMAGE:290375 5'
11684	24279	37801	1.61	3.5E-01	L05145.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11776	24387		1.36	3.5E-01	A084773.1	EST_HUMAN	Human glucokinase (GCK) gene, repeat polymorphism
12063	24578		1.47	3.5E-01	X64565.1	NT	HA0542 Human fetal liver cDNA library Homo sapiens cDNA
12214	24676		2.32	3.5E-01	AE001774.1	NT	B.taurus alpa1 gene for F0(F1) ATP synthase alpha-subunit
							Thermoboga maritima section 86 of 136 of the complete genome

Page 66 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.5E-01	AE010691.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12783	25269	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	y654f1.1 Scores retina N2b-HR Homo sapiens cDNA clone IMAGE:218997 5'
12793	25269	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	y654f1.1 Scores retina N2b-HR Homo sapiens cDNA clone IMAGE:218997 5'
691	13468		1.95	3.4E-01	AJ242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from LC4 cervical carcinoma cell line
955	13720	26386	7.61	3.4E-01	Y06798.2	NT	Pseudomonas fluorescens coR, cds genes, crf22 and partial inaA gene
1300	14052	26725	1.72	3.4E-01	Y06954.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2403	15121	27658	2.92	3.4E-01	D90309.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3146	15910	28555	1.08	3.4E-01	D80509.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28568	6.23	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (ONGC1) mRNA, complete cds
3338	16098	28749	0.9	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28833	3.48	3.4E-01	AF108835.1	NT	Methylovorus sp. strain SST putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.69	3.4E-01	BF449010.1	EST_HUMAN	Tn94d01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4028	16774		2.38	3.4E-01	AA584188.1	EST_HUMAN	ncf1b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4480	17198	29823	0.82	3.4E-01	AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4599	17534	29893	1.54	3.4E-01	BE068912.1	EST_HUMAN	MR4-B10403-230200-202-01 B10403 Homo sapiens cDNA
4898	17626		3.23	3.4E-01	AI240873.1	EST_HUMAN	q95605.x1 NCI_CGAP_K43 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5143	17882		0.98	3.4E-01	U75748.1	NT	Homo sapiens eukaryotic transporter (USERT) gene, promoter region, exons 18 and 2, and partial cds
5599	18394	31304	2.62	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5721	18513		6.09	3.4E-01	AA085313.1	EST_HUMAN	zn12811.t1 Stratiene INT neuron (8637233) Homo sapiens cDNA clone IMAGE:547221 3'
5917	18702		1.99	3.4E-01	L02971.1	NT	Echovirus 21 HAB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6940	18722	31681	0.98	3.4E-01	BE748912.1	EST_HUMAN	601578111.NH_MGC_55 Homo sapiens cDNA clone IMAGE:3838628 3'
8017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	U1-H181-aa-s-12-5-U1.1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:271582 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	DKFZ761A249.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6844	19406		1.56	3.4E-01	N66226.1	EST_HUMAN	zb56e12.at Scores_fetal_lung_Nhlh1gW Homo sapiens cDNA clone IMAGE:307342 3'

Page 66 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	19548	32578	1.02	3.4E-01	AI468082.1	EST_HUMAN	tm6305.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:5374031
6959	19441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7806	20501		0.49	3.4E-01	AE000493.1	NT	602085283FT NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4249395 6'
8135	20829	33984	0.6	3.4E-01	Y14630.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
				3.4E-01	Y14630.1	NT	Homo sapiens TCRVAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF468010.1	EST_HUMAN	7a94601.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UUI5
8386	21079		1.51	3.4E-01	AA337063.1	EST_HUMAN	QBLJH5.DJ16C9.1;
8451	21153	34296	0.72	3.4E-01	U04690.1	NT	EST41765 Eriodiscus cholesteryl 7-alpha-hydroxylase gene, complete cds
8751	21443	34560	1.7	3.4E-01	9633624	NT	Bovine enterovirus strain K25/7, complete genome
9112	21800	34694	4.42	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
9321	21800	34665	4.42	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
9346	20417	33536	0.51	3.4E-01	AB017610.1	NT	Epiphytaria fluvialis mRNA for PLC-gamma5, complete cds
9346	20417	33537	4.87	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9397	22059	35229	0.5	3.4E-01	AF163667.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9595	22248	35433	1.01	3.4E-01	U68763.1	NT	Dicystidium discidium putative CMF receptor CNFR1 mRNA, complete cds
9789	22440	35648	1.85	3.4E-01	AJ225084.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10376	23022		0.82	3.4E-01	AE004066.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
				3.4E-01	AE004066.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10940	23620		4.72	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
10984	23659	36912	2.6	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11032	23703	36971	2.17	3.4E-01	AF045981.1	NT	Radiiia arcalis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11253	23915	37207	1.81	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 35 and 37
11253	23915	37208	1.61	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 35 and 37
11483	24094	37366	1.88	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerinMUC18, complete cds
11513	24113	37423	3.65	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11798	24376	37706	1.72	3.4E-01	BF061948.1	EST_HUMAN	7168812.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
11861	24445	37766	1.68	3.4E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11861	24445		1.85	3.4E-01	U06004.1	NT	Human variegation virus putative replicase gene, partial cds
12197	24668		11.43	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
				3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12224	25182		1.01	3.4E-01	BE218652.1	EST_HUMAN	h42408.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.i3 P TR3 repetitive element;

Page 67 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25292		2.28	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24761	31035	2.2	3.4E-01	AJ287131.1	NT	Mus musculus SLI, MAP_17, GYP_17, SOL & GYP_17 genes
12688	24974		1.82	3.4E-01	AF019413.1	NT	Human sapiens HLA class II region containing tenascin X (tenascin-X) gene, partial cds, cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5LJ nccX gene
103	12840	26453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5LJ nccX gene
435	13221	25987	0.9	3.3E-01	AL101545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
618	13397	25032	2.01	3.3E-01	7682485	NT	Human sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26597	2.85	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	28705	3.76	3.3E-01	BF56880.1	EST_HUMAN	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1336	14085	26760	1.2	3.3E-01	U43626.1	NT	Mus musculus disintegrin 5 (Dgn5), mRNA
1601	14347	27035	1.47	3.3E-01	6755685	NT	EST36722 Embryo, 8 week (Homo sapiens cDNA 5' end
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylobacterium capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2404	15125		4.62	3.3E-01	4507834	NT	Human sapiens uridine monophosphate synthetase (uracil phosphate synthetase and oridine-5'-decarboxylase) (UMPS) mRNA
2949	15715	25358	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3051	15817	25462	1.48	3.3E-01	AJ007832.2	NT	Streptomyces aguilaeus mitramycin biosynthetic genes
3466	16243	28699	1.07	3.3E-01	AB012522.1	NT	Human sapiens MTA1-L1 gene, complete cds
3789	16541	29176	2.1	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3795	16551	29183	0.97	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3932	16682	29323	1.03	3.3E-01	4757739	NT	Human sapiens A kinase (PKA) anchor protein 5 (AKAP5), mRNA
3947	16697	29336	1.47	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3983	16731	29365	1.76	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4334	17073		1.6	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regulation, partial cds
4641	17376		1.23	3.3E-01	AIS39114.1	EST_HUMAN	PEPTIDE TRANSPORTER 1 (HUMAN);
4786	17517	30139	1.22	3.3E-01	D64003.1	NT	Synchytrium sp. POC6803 complete genome, 22/27, 27/55/03-2668766
5148	17855		0.96	3.3E-01	AW097982.1	EST_HUMAN	QV0-DT10047-170200-123-H08 DT10047 Homo sapiens cDNA
5241	18047	30675	2.61	3.3E-01	X89519.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5241	18047	30676	2.61	3.3E-01	X89519.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein

Page 68 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5700	18494	31417	0.74	3.3E-01	BF215873.1	EST_HUMAN	601846900.F1.NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4078623.5'
5856	18543	31882	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768.T1.NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3875763.3'
5856	18543	31883	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768.T1.NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3875763.3'
5947	18729	31689	1.18	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
5947	18729	32851	0.71	3.3E-01	AB034233.1	NT	Flexibacter lilacalis gylB gene for DNA gyrase B subunit, partial cds
6695	19512	32852	0.71	3.3E-01	AB034233.1	NT	Flexibacter lilacalis gylB gene for DNA gyrase B subunit, partial cds
6789	19533	32550	4.82	3.3E-01	AI628131.1	EST_HUMAN	Y64H01.X1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2289809.3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6789	19533	32551	4.82	3.3E-01	AI628131.1	EST_HUMAN	Y64H01.X1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2289809.3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7682	20346	33458	1.88	3.3E-01	N85148.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498.5' similar to TEGT
8460	21132	34295	18.82	3.3E-01	BF683654.1	EST_HUMAN	601240372.F1.NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800.5'
8659	21351	34497	0.48	3.3E-01	AU128115.1	EST_HUMAN	AU128115.NT2RP1 Homo sapiens cDNA clone NT2RP1000130.5'
8659	21351	34498	0.48	3.3E-01	AU128115.1	EST_HUMAN	AU128115.NT2RP1 Homo sapiens cDNA clone NT2RP1000130.5'
9012	21702	34852	0.81	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9278	22032	35203	0.81	3.3E-01	BE828461.1	EST_HUMAN	CN3-E1T0041-190500-187-d10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828461.1	EST_HUMAN	CN3-E1T0041-190500-187-d10 ET0041 Homo sapiens cDNA
8411	22073	35244	2.62	3.3E-01	N69866.1	EST_HUMAN	z647901.g1 Soares, fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:287649.3'
8452	22002	35174	2.77	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250600-011-g04 TN0077 Homo sapiens cDNA
8891	22541		2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGC) gene, exons 1-3, complete cds
10822	23315	36554	3.13	3.3E-01	X63953.1	NT	D. mauritiana Ach gene
10822	23315	36555	3.13	3.3E-01	X63953.1	NT	D. mauritiana Ach gene
10851	23628		1.7	3.3E-01	BF528469.1	EST_HUMAN	602070802.F1.NCI CGAP Brf64 Homo sapiens cDNA clone IMAGE:4213585.5'
11198	23861	37147	11.81	3.3E-01	BE216351.1	EST_HUMAN	h51g02.x1 NCI CGAP L224 Homo sapiens cDNA clone IMAGE:3176978.3'
11317	24008	37313	3.23	3.3E-01	P47963	SWISSPROT	L-220 (CBP30)
11719	24815		3.06	3.3E-01	AA606821.1	EST_HUMAN	cb17a02.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1338850.3'
11741	24840	25453	1.87	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRLJ1 nodX gene
11877	24521	37266	1.71	3.3E-01	6598319	NT	Homo sapiens aldolhyde oxidase 1 (ADOX1), mRNA
12676	24987		3.34	3.3E-01	AF000002.1	NT	Proccoccus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

Page 69 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
701	13476		1.43	3.2E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13894	26555	27.93	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26977	1.38	3.2E-01	Z60202.1	NT	P. vulgaris wcs-1 gene
1369	14117	28792	5.42	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1777	14509	27210	1.25	3.2E-01	Z38041.1	NT	S cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27222	4.7	3.2E-01	AW057164.1	EST_HUMAN	EST T36928 MAGC resequences, MAGD Homo sapiens cDNA
1777	14519	27223	4.7	3.2E-01	AW057164.1	EST_HUMAN	EST T36928 MAGC resequences, MAGD Homo sapiens cDNA
1835	14574	27285	1.23	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2157	14887	27621	2.82	3.2E-01	BF203817.1	EST_HUMAN	601868804.F1.NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512.5'
2543	15257		2.01	3.2E-01	7710079	NT	Mus musculus Pbx/knotted1 homeobox (Pbxox1), mRNA
2713	15420	28159	1.08	3.2E-01	AF060598.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3694	18347		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4305	17044	29669	0.91	3.2E-01	4759195	NT	Homo sapiens synaptobin (SYM) mRNA
4383	17101	29738	1.52	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4464	17200	29828	1.21	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 817 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4688	17422		6.7	3.2E-01	BF663817.1	EST_HUMAN	602081972.F1.NIH_MGC_81 Homo sapiens cDNA clone IMAGE:424693.5'
4826	17557	30179	1.17	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
4965	17680	30299	0.74	3.2E-01	BE782748.1	EST_HUMAN	601465591.F1.NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3663799.5'
5190	17898	30621	3.26	3.2E-01	BE173954.1	EST_HUMAN	GM-H10569-Q08300-299-110 H10569 Homo sapiens cDNA
6888	18555	31568	1.07	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6211	18988	31663	0.9	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P53), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c2
6501	19288	32268	0.84	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHITA Homo sapiens cDNA clone FHITAAB101.5'
6634	19398		1.09	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
7755	20451	33575	0.51	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMOT gene for LIM domain only 1 protein, exon 1
8072	20768	33995	1.48	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8164	20858	33990	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wx1
8285	20952	34098	14.41	3.2E-01	X02508.1	NT	H-sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8286	20956	34103	13.76	3.2E-01	BF311635.1	EST_HUMAN	6016897107.F1.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:412663.5'
8361	21034		1.38	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

Page 70 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8368	21091	34228	1.24	3.2E-01	BF246771.1	EST_HUMAN	60185580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	60185580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8471	21163	34306	2.66	3.2E-01	AE002015.1	NT	Dermococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
8571	21263	34401	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, Y-region (VH6-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, Y-region (VH6-a2) gene, partial cds
8655	21598	34607	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21G004
8876	21698		2.18	3.2E-01	M88511.1	NT	Human monocytic antigen CD14 (CD14) mRNA, complete cds
9048	21737	34894	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
8894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, rrpC and rrpD genes, complete cds, and unknown genes
10099	22747	35862	0.45	3.2E-01	BE526230.1	EST_HUMAN	hV6805.X1 NCI_CGAP_LUG2 Homo sapiens cDNA clone IMAGE:3181669 3'
10210	22858		3.41	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10586	23261	36498	3.94	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HF80221
12010	25317		3.91	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	25374		1.44	3.2E-01	BE868948.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 6'
12524	24871		4.21	3.2E-01	Q83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxydylate deaminase gene, complete cds
12712	25344	30606	1.76	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2677	15388	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	y60h08.1 Soares fetal liver spleen 1NF1.3 Homo sapiens cDNA clone IMAGE:125051 5' similar to gbM64241 QM PROTEIN (HUMAN);
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	19530		1.29	3.1E-01	AW529036.1	EST_HUMAN	h446h08.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3170	15933		3.95	3.1E-01	AE020089.1	NT	Mus musculus gene for Ser/Thr kinase KIAA18RE, exon 6
3887	16637	26278	0.86	3.1E-01	AJ257168.1	NT	Deinacard carboxylate mRNA for transcription factor E2F (E2F gene)
4908	17659	30250	0.73	3.1E-01	AE003984.1	NT	Xyella fastidiosa, section 130 of 229 of the complete genome
6300	18190	30882	9.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
6513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HIT238
5514	18312	31213	0.67	3.1E-01	Z74893.1	NT	S.cerevisiae chromosome XI reading frame ORF YOL141W
5524	18322		0.86	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polyovitin
6695	19478	31398	2.11	3.1E-01	AF184122.1	NT	Homo sapiens laminin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R94322.1	EST_HUMAN	y41104.1 Soares fetal liver spleen 1NF1.3 Homo sapiens cDNA clone IMAGE:188397 5'

Page 71 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8374	19143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-304 HN0001 Homo sapiens cDNA
8439	19207	32203	1.01	3.1E-01	AI294488.1	EST_HUMAN	q339d01.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1874889 3'
8593	19346	32360	3.91	3.1E-01	X71897.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6873	25081	30545	2.41	3.1E-01	BE737392.1	EST_HUMAN	607306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3940420 5'
7579	20248	33354	0.77	3.1E-01	4885330	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	R46318.1	EST_HUMAN	y94801.s1 Scores triant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8802	22463	35655	0.64	3.1E-01	6879322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (PIP5K1c), mRNA
8987	22915	35818	1.05	3.1E-01	BF696939.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
8987	22815	35819	1.05	3.1E-01	BF696939.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10029	22877	35893	1.74	3.1E-01	AI244001.1	EST_HUMAN	q51611.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb-S65700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10201	22849		0.63	3.1E-01	T55325.1	EST_HUMAN	y447008.at Stralagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:IM91036_maz2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10741	23428	35672	1.26	3.1E-01	BF218117.1	EST_HUMAN	607183592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095514 5'
11524	24124	37430	2.66	3.1E-01	7682231	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	24623		1.48	3.1E-01	AF284308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12165	24847		3.03	3.1E-01	AF304182.1	NT	Silvestrodon vitreum 40S ribosomal protein S11 mRNA, partial cds
12304	24729		2.82	3.1E-01	AF165953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12680	24980		3.46	3.1E-01	AF168778.1	NT	Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synsphiophysin genes, complete cds; and L-type calcium channel a-
12699	25347		1.35	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Poly(p)-pending), mRNA
70	15512	25533	2.01	3.0E-01	6755963	NT	Mus musculus protein kinase G, epsilon (Pkcε), mRNA
247	13058	25698	14.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1202	13954	26818	2.51	3.0E-01	AW300400.1	EST_HUMAN	x63508.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	14244	26930	5.97	3.0E-01	AJ009755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2132	14662	27592	1.2	3.0E-01	AF237778.1	NT	Rattus norvegicus Cas2/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3206	15608		1.18	3.0E-01	AF030481.1	NT	Corynebacterium sp. ALY-1 alP/G gene for polyphosphate kinase, complete cds
3846	16597	29234	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281169-001-g01 ST0262 Homo sapiens cDNA
4477	17212	29837	1.95	3.0E-01	AJ009755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5287	16073	30702	7.22	3.0E-01	BE741628.1	EST_HUMAN	6071594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5349	18162	30833	0.77	3.0E-01	AF229247.1	NT	Canis lupus orthopoxvirus hemagglutinin gene, complete cds

Page 72 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5417	18216	30924	3.94	3.0E-01	BE683576.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5417	18216	30925	3.84	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 1291ev Clara cell 10 kd protein (MCC10) gene, complete cds
6732	18566	32598	3.08	3.0E-01	D16313.1	NT	Mus musculus 15 gene, complete cds
6732	17331	30557	0.81	3.0E-01	U02359.1	NT	Strongylocentrotus purpuratus 3457 kDa lentilin-binding protein mRNA, partial cds
8827	19488	32510	0.85	3.0E-01	AF229247.1	NT	Canilago orthopoxvirus hemagglutinin gene, complete cds
7021	19173	32770	0.71	3.0E-01	AL162206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7237	19912	32985	2.77	3.0E-01	10947007	NT	Mus musculus midbrain (Midn-pand) mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PapA (pspA) gene, partial cds
7827	20522	33948	1.3	3.0E-01	AE001785.1	NT	Thermoloba maritima section 67 of 138 of the complete genome
8271	20665		2.97	3.0E-01	6910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
8374	21067	34207	1.32	3.0E-01	BE569063.1	EST_HUMAN	601339078F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594.5'
8728	21420	34554	0.51	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (psbC) gene, partial cds
8770	21462		0.8	3.0E-01	7681686	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9116	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative
9856	22506		43.84	3.0E-01	BE001129.1	EST_HUMAN	enhanceable phosphoribosyltransferase gene, partial cds; and unknown gene
9858	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	60213327F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:288336.5'
10042	22690	35908	0.49	3.0E-01	AF162588.3	NT	Actinobacillus actinomycetomycellans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10042	22690	35909	0.49	3.0E-01	AF152588.3	NT	Actinobacillus actinomycetomycellans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10294	22941	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:2606035.3'
10296	22943	36157	1.88	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
10316	22963	36179	0.73	3.0E-01	BF68841.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097.5'
10316	22963	36180	0.73	3.0E-01	BF68841.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097.5'
11172	24363	37694	1.65	3.0E-01	H51029.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:194107.5'
11772	24363	37695	1.65	3.0E-01	H51029.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:194107.5'
12416	25302		2.82	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gadh-2) gene
12683	25345		5.51	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
2018	14753	27410	1.43	2.8E-01	AE000736.1	NT	Aquifex aeolicus section 88 of 109 of the complete genome
2245	14873	27711	1.16	2.9E-01	AF222718.1	NT	Chrysodidymus synuroideus mitochondrion, complete genome
3246	16008	28658	2.73	2.8E-01	AW754236.1	EST_HUMAN	PM1-CT0326-171260-001412 CT0326 Homo sapiens cDNA

Page 73 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
3246	16008	28059	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT10326-11298-001-412 CT10326 Homo sapiens cDNA
3877	16627	29265	0.72	2.9E-01	AA108398.1	EST_HUMAN	h221a1.1X1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gbD16050 N1L-2-A
4052	16787	29427	0.73	2.9E-01	AB016425.1	NT	ZINC FINGER PROTEIN HUMAN; contains element L1 repetitive element;
4064	16809		0.77	2.9E-01	AA002802.1	EST_HUMAN	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4462	17188	29813	1.1	2.9E-01	AA284488.1	EST_HUMAN	z62f10.1X1 NCL CGAP_GCB8 Homo sapiens cDNA clone IMAGE:2480395 3'
5177	17988		1.86	2.9E-01	B37485.1	EST_HUMAN	z57f12.1X1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu
5310	18507	32532	0.79	2.9E-01	AF321001.1	NT	repetitive element;
5677	18471	31387	5.19	2.9E-01	X59098.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5677	18471	31388	5.19	2.9E-01	X56098.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5689	18482	31401	6.4	2.9E-01	6679692	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5955	18747	31708	1.47	2.9E-01	AA418145.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6187	18944	31637	1.08	2.9E-01	AI797128.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6233	19007	31884	2.4	2.9E-01	U03420.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6395	19135	32130	0.86	2.9E-01	R69194.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6395	19135	32131	0.88	2.9E-01	R69194.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6621	19393		0.85	2.9E-01	Z59155.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6650	17698	30523	1.52	2.9E-01	AF142328.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
6906	16658	32737	2.56	2.9E-01	Q04399	SWISSPROT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
7059	19750	32813	2.06	2.9E-01	AF100956.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
7820	20516	33640	1.07	2.9E-01	BE640422.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
7820	20515	33641	1.07	2.9E-01	BE640422.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
8049	20743	33875	0.48	2.9E-01	AJ237637.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
8049	20743	33876	0.48	2.9E-01	AJ237637.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
8062	20769		0.94	2.9E-01	BF217743.1	EST_HUMAN	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
8237	20931		0.46	2.9E-01	AF197495.1	NT	Y77612.1X1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'

Page 74 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8463	21185	34328	0.84	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901.3'
8823	21515	34960	1.02	2.9E-01	AF229008.1	NT	Arabidopsis thaliana sulfonylesterase receptor-like protein mRNA, complete cds
9331	21622	34765	0.85	2.9E-01	M22452.1	NT	Saboon lymphocyte homing/adhesion receptor mRNA, complete cds
9146	21876	35040	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9145	21876	35041	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10810	23493	36728	1.93	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37059	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37060	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.50	2.9E-01	AA035373.1	EST_HUMAN	hV59H02.st NCI CGAP_P112 Homo sapiens cDNA clone IMAGE1273779 similar to contains LTR8.12 LTR8 repetitive element;
11579	24178	37493	3.95	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
11600	24199	37519	1.82	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24199	37520	1.82	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12432	24821	31024	4.05	2.9E-01	AF092453.1	NT	Homo sapiens TNF-alpha-inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.86	2.9E-01	V08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	V08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP180 mRNA, complete cds
560	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1061	13819	26481	3.89	2.8E-01	AF168050.1	NT	Gutta guira oocyte maturation factor Mos (c-mos) gene, partial cds
1264	14003	26871	1.62	2.8E-01	BE313442.1	EST_HUMAN	801148733FF NIH_MGC_19 Homo sapiens cDNA clone IMAGE3163688.6'
1264	14003	26872	1.62	2.8E-01	BE313442.1	EST_HUMAN	801148733FF NIH_MGC_19 Homo sapiens cDNA clone IMAGE3163688.5'
1268	14017	26884	1.34	2.8E-01	D66650.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 80 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW590020.1	EST_HUMAN	QV1-CT0394-120200-005-505 CT0394 Homo sapiens cDNA
2008	1742	27467	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKF7568J2321 J1 595 (synonym: huler1) Homo sapiens cDNA clone DKF7568J2321
2127	14858	27588	1.41	2.8E-01	AW511185.1	EST_HUMAN	h444603.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2912333.3'
2475	15193	27933	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15193	27934	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2549	15294		1.89	2.8E-01	AL161656.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2670	15300	28118	0.97	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoxygenase, complete cds
2970	17398		1.29	2.8E-01	AF179490.1	NT	Toxoplasma gondii 60kDa heat-shock protein (HSP90) mRNA, partial cds
2971	17397	28386	2.04	2.8E-01	AF174037.1	NT	B laurus microsatellite (ETH121)
2971	17397	28387	2.04	2.8E-01	Z14037.1	NT	B laurus microsatellite (ETH121)
3373	18132	28788	1.13	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genome DNA, 777001-994000 nt, position (4/7)

Page 75 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3978	18728	29360	1.56	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4174	18914		1.95	2.8E-01	AA090868.1	EST_HUMAN	ov44p10.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
4422	17158	29769	0.89	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contig; putative Magea5 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29763	2.31	2.8E-01	F13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30128	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE112) polyprotein precursor, gene, partial cds
4777	17509	30131	2.87	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	BF528188.1	EST_HUMAN	Q02042601.F1 NC1 CGAP_Bm57 Homo sapiens cDNA clone IMAGE:4180129 5'
4829	17560	30182	1.91	2.8E-01	AI072669.1	EST_HUMAN	q156c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:4180129 5'
5228	20084	30660	24.66	2.8E-01	AA346997.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' end
5519	18317	31218	3.07	2.8E-01	AB016925.1	NT	Homo sapiens OCTN2 gene, complete cds
6727	18519		0.95	2.8E-01	AW592583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
5848	18635		0.83	2.8E-01	AA404576.1	EST_HUMAN	244161.r1 Soares every tumor NkxHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6083	28418		0.66	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6532	19384	32409	8.34	2.8E-01	BF611215.1	EST_HUMAN	UJH-B14-eef-04-0-J1.1et1 NC1 CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7341	20022		1.17	2.8E-01	U09693.1	NT	Marsilea quadrifida ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7382	20062	33140	0.68	2.8E-01	X69080.1	NT	L-asculinum ypd2 mRNA for GTP-binding protein
7991	20686	33811	1.28	2.8E-01	AI346128.1	EST_HUMAN	q148f01.x1 NC1 CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06333_cds1
7991	20686	33812	1.28	2.8E-01	AI346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U17698.1	NT	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8412	21405	34244	0.61	2.8E-01	AA611629.1	EST_HUMAN	q102h05.s1 NC1 CGAP_Co12 Homo sapiens cDNA clone IMAGE:1416693 3' similar to gb:M87789 IG
8468	21100		7.34	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
8366	21941	35115	0.92	2.8E-01	U17251.1	NT	032022807.F1 NC1 CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158525 5'
9611	22284		0.88	2.8E-01	L13654.1	NT	Neurospora crassa negative regulator aulicor controller-2 (econ-2) gene, complete cds
9788	22439	35640	0.66	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
							Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds

Page 76 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35847	0.66	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.62	2.8E-01	AF204393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9880	22608	35813	3.35	2.8E-01	7709163	NT	Homo sapiens hypochlorite protein (LOC5319), mRNA
10211	22859		1.47	2.8E-01	8628154	NT	Fujimori sarcoma virus, complete genomes
10251	22869	39109	0.8	2.8E-01	BE969727.2	EST_HUMAN	601674822RT NIH_MGC_S7 Homo sapiens cDNA clone IMAGE:3839786 3'
10644	23335	39573	2.42	2.8E-01	BF241062.1	EST_HUMAN	60180794FT NIH_MGC_S5 Homo sapiens cDNA clone IMAGE:4109350 5'
10644	23335	39574	2.42	2.8E-01	BF241092.1	EST_HUMAN	60180794FT NIH_MGC_S5 Homo sapiens cDNA clone IMAGE:4109350 5'
10671	23362	39603	3.83	2.8E-01	BF685970.1	EST_HUMAN	60185214FT NIH_MGC_S8 Homo sapiens cDNA clone IMAGE:4076028 5'
10784	23477	39719	1.33	2.8E-01	AF051662.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 3' flanking region, exons 1 through 7 and complete cds
11247	23809		4.51	2.8E-01	BF674023.1	EST_HUMAN	602137418FT NIH_MGC_S3 Homo sapiens cDNA clone IMAGE:4273853 5'
11563	24192	37510	17.65	2.8E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/8
12408	24789		15.41	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12509	24881	31013	4.22	2.8E-01	BE176599.1	EST_HUMAN	PM44-H10606-030400-001-a07 HT0608 Homo sapiens cDNA
12632	24877	31019	1.77	2.8E-01	BE900116.1	EST_HUMAN	601873020FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955586 5'
12685	25308		2.92	2.8E-01	11433628	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
12806	25401		1.49	2.8E-01	AW025400.1	EST_HUMAN	wu5605.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2827928 3'
464	13249	25880	3.97	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
599	13377	28007	3.25	2.7E-01	AA450081.1	EST_HUMAN	z03510.s1 Soares_total_taus_Nb2HF9_8w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1238	13987	28654	2.13	2.7E-01	AB004505.1	NT	Ipomoea purpurea transposable element T1p100 gene for transposase, complete cds
1617	14394		1.58	2.7E-01	X70815.1	NT	G.lambia SR2 gene
1722	14465	27164	3.5	2.7E-01	W58067.1	EST_HUMAN	z022101r1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1769	14511	27212	2.69	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2131	15566		2.25	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular stomatitis virus type 2, promoter region and exon 1
2367	15069	27629	10.01	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITT0089PU (M89), partial
2457	15175	27914	4.07	2.7E-01	AJ310858.1	EST_HUMAN	z04311.x2 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
2899	16668	28314	1.2	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spt14) mRNA, complete cds
2983	15749		2.53	2.7E-01	BF086284.1	EST_HUMAN	GM1-HT10875-060800-385-a05 HT0875 Homo sapiens cDNA
3263	15044	28993	0.68	2.7E-01	8393620	NT	Rattus norvegicus insulin receptor (Insr), mRNA
3392	16740	29374	1.97	2.7E-01	AJ828015.1	EST_HUMAN	w02201.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'

Page 77 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4002	16749	28380	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	16749	28381	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4008	16754	28384	2.12	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4690	17703		2.85	2.7E-01	AW866131.1	EST_HUMAN	RC1-OT10286-200200-016-c03 CT10286 Homo sapiens cDNA
5011	17733	30339	2.63	2.7E-01	AA100698.1	EST_HUMAN	Z99001.r1 Stratiene cdon (8937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gp-X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.63	2.7E-01	AA100696.1	EST_HUMAN	Z99001.r1 Stratiene cdon (8937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gp-X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5195	17983	30309	2.39	2.7E-01	P12727	SWISSPROT	HOMEDBOX PROTEIN HOXA4 (CHOX-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	Aetropora myophilthama mitochondrial cyto gene for cytochrome b, partial cds
6249	19023	31995	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31998	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6516	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6591	19598	32637	2.23	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32699	0.69	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	AI540070.1	EST_HUMAN	ts08h08.x1 NC1 CGAP_CULT1 Homo sapiens cDNA clone IMAGE:2075103 3'
7256	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B05633.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7688	20266	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7688	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7688	20303	33411	0.84	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7688	20303	33412	0.84	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7694	20358	33472	0.71	2.7E-01	U01081.1	NT	Oryzotagus curvicauda UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7793	20459	33583	0.68	2.7E-01	AA013147.1	EST_HUMAN	z635511.a1 Soares, retina N264R Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

Page 78 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7625	20920		0.53	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39287.1	EST_HUMAN	YctH08.01 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:23511.3'
8160	20884	34022	0.8	2.7E-01	AL161652.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.58	2.7E-01	Q14764	SWISSPROT	MAJOR VAILT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21816	34760	0.48	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon, Tn554
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21814		2	2.7E-01	P37628	SWISSPROT	FIMBRIN W PROTEIN
9700	22351	35546	0.61	2.7E-01	D86650.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9981	22629	35638	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22666	35882	3.09	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
10149	22797	36012	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22797	36013	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05.5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05.5'
10724	23412	36653	3.13	2.7E-01	AJ133289.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.5	2.7E-01	Q14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F-B.05C
12482	25190		1.49	2.7E-01	A5008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24893		2.83	2.7E-01	AF27481.1	NT	Homo sapiens fragile 100 oxidoreductase (FOR) gene, exon 6
12811	25064	30929	1.96	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02.5'
457	15542	25883	2.03	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	26785	1.65	2.6E-01	BE850387.1	EST_HUMAN	60151038F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345.5'
1417	14165	26848	1.14	2.6E-01	AB013290.1	NT	Glycine max pseudogenes for Bd 30K
1899	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1899	14626	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							b604010X1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451.3' similar to dbM3607.2 50S RIBOSOMAL PROTEIN L7A (HUMAN); gbM14688_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE)
2086	14818		10.49	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2148	14878	27613	3.7	2.6E-01	MT15644.1	NT	B. maritimus tbcL gene
2476	15194		1.82	2.6E-01	Y12698.1	NT	

Page 79 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	16283		8.87	2.6E-01	BE272440.1	EST_HUMAN	601126016FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3588	16323	28971	8.99	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4079	16923	29449	0.95	2.6E-01	AW59510.1	EST_HUMAN	ESTT371580 IMAGE resources, IMAGE Homo sapiens cDNA
4134	18878	29508	16.7	2.6E-01	BE080598.1	EST_HUMAN	QV1310630-JQ40400-132-603 BT10330 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 verD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17248	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	ad8300.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4601	17336	29965	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3-1) mRNA, complete cds
4687	17401	30035	1.18	2.6E-01	AF142703.1	NT	Ophiostoma matricaria matricaria-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloproteinase disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.8	2.6E-01	H04898.1	EST_HUMAN	351485.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:152288 5'
5267	18063		1.06	2.6E-01	AB035972.1	NT	Paramedius caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	AB82398.1	EST_HUMAN	941803.x1 NCL CGAP_C016 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element
5688	19481	31400	0.73	2.6E-01	AF207650.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pin-2 protooncogene homolog pin-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IG-HM enhancer 3 genes, partial cds; and unknown g*
5690	25417		2.35	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6108	18885	31854	2.26	2.6E-01	AB82557.1	EST_HUMAN	ts02612.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element;
6108	18885	31855	2.26	2.6E-01	AB82557.1	EST_HUMAN	ts02612.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element;
6328	19098	32098	0.91	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 6/7
6570	19334	32344	0.73	2.6E-01	BE762062.1	EST_HUMAN	601581754FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936168 5'
6570	19334	32345	0.73	2.6E-01	BE762062.1	EST_HUMAN	601581754FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936168 5'
6938	19673	32719	0.9	2.6E-01	AB14380.1	EST_HUMAN	wd4804.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:U37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

Page 80 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7289	19972	33050	0.62	2.6E-01	BE146061.1	EST_HUMAN	CMO-HT0245-031169-085-04 HT0245 Homo sapiens cDNA
7329	25110	33465	0.79	2.6E-01	AA139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
7353	20044	33666	0.90	2.6E-01	AA198149.1	EST_HUMAN	zp26261.1 Stragene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627672.5'
7659	20304	33413	1.9	2.6E-01	R10365.1	EST_HUMAN	X37403.1 Sources fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:126004.3' similar to
7697	20351	33465	0.66	2.6E-01	Q08855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C2363.01 IN CHROMOSOME I
7748	20444	33666	1.3	2.6E-01	R02411.1	EST_HUMAN	Y62207.1 Sources fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124212.5'
7804	20499	33920	1.15	2.6E-01	BE144331.1	EST_HUMAN	MFO-HT0165-181199-003-012 HT0166 Homo sapiens cDNA
8040	20735	33987	0.84	2.6E-01	X82841.1	NT	D melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8040	20735	33668	0.84	2.6E-01	X82841.1	NT	D melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8232	20928	34054	3.05	2.6E-01	BF343588.1	EST_HUMAN	602074422F1 NCL CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4150396.5'
8309	21003	34140	2.13	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 73.2 KD PROTEIN C11G1.02 IN CHROMOSOME II
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8594	21286	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35118	0.95	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9639	22291			2.6E-01	AF057121.1	NT	Lorita candidensis cytochrome b (cyt) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9763	22419	35626	1.19	2.6E-01	P87395	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9768	22419	35627	1.10	2.6E-01	P87395	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9830	22578		0.48	2.6E-01	U87581.1	NT	Methanococcus jannaschii section 123 of 160 of the complete genome
10060	22738		0.74	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10406	23052		0.9	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10497	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens NRAMP2 gene for natural resistance-associated macrophage protein 2, complete cds
11400	24008	37310	1.78	2.6E-01	P46280	SWISSPROT	CELL DIVISION PROTEIN FT5W HOMOLOG
11511	24111		66.41	2.6E-01	X51785.1	NT	Human lambda3-immunoglobulin constant region complex (germline)
11896	24534		1.71	2.6E-01	10180655	NT	Mus musculus jerky (JRK), mRNA
12177	25309		3.1	2.6E-01	BE983491.1	EST_HUMAN	601571052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3972612.5'
12242	24693	31077	2.81	2.6E-01	AF316898.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced
12555	24895		1.59	2.6E-01	D38425.1	NT	CaV1.2 cDNA for serine/threonine kinase, complete cds
12725	24996		2.16	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
234	13045	25684	2.95	2.6E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
235	13045	28684	2.39	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
248	13037		3.32	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
813	13594	26250	1.35	2.5E-01	U05984.1	NT	Mus musculus (CF/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1038	13788		1.2	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1089	13857	26517	6.42	2.5E-01	T89837.1	EST_HUMAN	yet11007.r1 Stragelene Lung (M937210) Homo sapiens cDNA clone IMAGE:117466 5'
1509	14255	26941	0.9	2.5E-01	AL116024.1	EST	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1721	14484		4.79	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1876	15581	27323	1.58	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
1876	15581	27324	1.68	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
2407	15128		16	2.5E-01	AE000676.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2500	15217		1.09	2.5E-01	AA251887.1	EST_HUMAN	2511412.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16129		0.84	2.5E-01	BF698103.1	EST_HUMAN	502125525FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4282270 5'
3407	16165		3.04	2.5E-01	AW973471.1	EST_HUMAN	EST1385464 IMAGE sequences, MAGM Homo sapiens cDNA
3524	16280	28835	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
3828	18579	29211	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	18579	29212	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	IQ0314	SWISSPROT	RHB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOL-INHIBITING HORMONE PRECURSOR (MIF)
4706	17438	30070	3.99	2.5E-01	AF007788.1	NT	Chroicoeura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4732	17464	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ201113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE696785.1	EST_HUMAN	907437488FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
4987	17710	30315	0.71	2.5E-01	AW873688.1	EST_HUMAN	hob2f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71FBA_294.D OE22858;
5243	18049	30878	13.48	2.5E-01	863390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
5870	18657	31568	0.73	2.5E-01	AJ005345.1	NT	Homo sapiens KVLQ11 gene
5871	18658		0.98	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6528	19295	32289	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6946	19427	32442	0.76	2.5E-01	8394138	NT	Rattus norvegicus reb1n 3 (RAB1N3), mRNA

Page 82 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7252	19936	33011	0.86	2.5E-01	U13892.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19952		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33259	0.83	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7538	20206	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33564	2.47	2.5E-01	BF100040.1	EST_HUMAN	7574603.xt Soares_NSF_pg_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7754	20450	33574	0.8	2.5E-01	BE960712.1	EST_HUMAN	8071663391R2.NIH.MGC.59 Homo sapiens cDNA clone IMAGE:3526198 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	8071459238F1.NIH.MGC.66 Homo sapiens cDNA clone IMAGE:3862809 5'
8298	20960	34128	0.7	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8634	21228	34968	3.87	2.5E-01	H53298.1	EST_HUMAN	Y640707.1 Soares fetal liver spleen 1NHS1 Homo sapiens cDNA clone IMAGE:202601 5'
8774	21468	34613	0.79	2.5E-01	M89626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35265	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9476	22094	35268	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35253	2.06	2.5E-01	AF085184.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35254	2.08	2.5E-01	AF085184.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
9698	22848	35958	1.39	2.6E-01	AW681097.1	EST_HUMAN	RC3-ST0186-130100-018-407 ST0186 Homo sapiens cDNA
10441	23087	36315	2.13	2.5E-01	AW192246.1	EST_HUMAN	cg40c10.xt NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
10444	23050	36319	1.21	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
11013	23685	36845	3.43	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11847	24244		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
11803	24393	37727	1.29	2.5E-01	U46315.1	NT	Limonoides sigmodontis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds
11862	24490	37808	5.12	2.5E-01	AF200528.1	NT	Zea mays cellulase synthase-4 (Cesa-4) mRNA, complete cds
11960	25388		8.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12366	24768		1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 844001-777000 nt, position (37)
12412	25233	30921	1.37	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNLC mRNA, complete cds
540	13323	25955	1.69	2.4E-01	AA936316.1	EST_HUMAN	on7004.4.t Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
826	13558	26269	3.34	2.4E-01	BF576124.1	EST_HUMAN	802132442F1.NIH.MGC.81 Homo sapiens cDNA clone IMAGE:4271678 5'
1281	14031	26700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1281	14031	26700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1843	14581		32.88	2.4E-01	AF207753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1883	14630	27340	1.33	2.4E-01	AF251708.1	NT	Zucosyl dihydrazide fructose-1,6-bisphosphatase mRNA, complete cds

Page 83 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14864	27664	1.1	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
2165	14894		1.44	2.4E-01	PA5384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAP1 PROTEASE)
2258	14955	27725	2.28	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2382	15104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NC1 CGAP_Cot18 Homo sapiens cDNA clone IMAGE:3318607 3' similar to SW:PRSB_XENLA
2539	15254	27694	2.46	2.4E-01	Z39534.1	NT	O42586.28S PROTEASE REGULATORY SUBUNIT 6A.
2765	15470	28213	2.16	2.4E-01	X71783.1	NT	D.discoidellum (A33-K) ponk gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3129	15894		2.94	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3145	15909	28554	1.46	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retroflit (gag/pol) genes, complete cds
3743	19496	28131	0.73	2.4E-01	AE000312.1	NT	H.sapiens AGT gene, PstI fragment of Intron 4
4010	19756		0.74	2.4E-01	D26980.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4683	17610		1.09	2.4E-01	AL161589.2	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4888	17712	30317	0.93	2.4E-01	DC0944.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
5375	18175	30865	0.98	2.4E-01	AI923707.1	EST_HUMAN	Hepatitis C virus genomic RNA for polyprotein, complete cds
5376	18176	30866	0.98	2.4E-01	AI923707.1	EST_HUMAN	wo33d05.x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	wo33d05.x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5569	18366	31275	8.16	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18366	31276	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5799	25076		0.77	2.4E-01	M83377.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
			0.99	2.4E-01	AJ133836.2	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
							Branchiostoma floridae mRNA for calmodulin 2 (cam2) gene
5805	18595	31520		2.4E-01	BF592336.1	EST_HUMAN	754d404.x1 NC1 CGAP_Br18 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFRA4_HUMAN
5895	18690	31627	3	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4, contains element TAR1 TAR1 repetitive element
5998	18760	31741	2.53	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6050	18830	31793	0.87	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
							AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6441	19209	32206	2.23	2.4E-01	AI698998.1	EST_HUMAN	wo82d11.x1 NC1 CGAP_Part1 Homo sapiens cDNA clone IMAGE:23232220 3' similar to gb:U03464
7243	19928	33004	9.5	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7404	20091		0.65	2.4E-01	N48732.1	EST_HUMAN	Bos taurus guanylyl cyclase-activating protein 2 (gucas2) mRNA, complete cds
7625	20291	33400	0.91	2.4E-01	AF228644.1	NT	yf55c11.r1 Saurea, multiple sclerosis_2NHMSP Homo sapiens cDNA clone IMAGE:277460 5'
8247	20941	34078	1.61	2.4E-01	AJ012585.1	NT	Mus musculus OXlm48e protein (OXlm48e) mRNA, complete cds
							Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

Page 84 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8497	21189	34332	1.02	2.4E-01	BF242784.1	EST_HUMAN	601877679FT NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4106298 5'
8552	21244		0.47	2.4E-01	BF078275.1	EST_HUMAN	602087188FT NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4280372 5'
9030	21720	34874	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NGCTC11188 complete genome; segment 4/6
9030	21720	34875	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NGCTC11188 complete genome; segment 4/6
9463	22013	35181	7.01	2.4E-01	AF03515.1	EST_HUMAN	wd43402.x1 Soares_NFL_T1 GRC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains
9603	22256	35441	0.88	2.4E-01	AF220067.1	NT	NER22.b1 TAR1 repetitive element;
9603	22256	35442	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22984	36202	1.68	2.4E-01	Q03892	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10697	23368	36508	4.6	2.4E-01	AL161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10736	23420	36871	1.39	2.4E-01	AF030189.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11158	23825		2.09	2.4E-01	Z271647.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11840	24424	37765	1.32	2.4E-01	BE617538.1	EST_HUMAN	P. asiatica mosaic virus genomic RNA
11891	24481	37801	1.75	2.4E-01	AF217491.1	NT	60174192T1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3845836 3'
12016	25180		2.34	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana chylene-insensitiv3-like1 (EL1) mRNA, complete cds
12287	25182		1.97	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative me7 protein (me7 gene)
12720	24992		3.69	2.4E-01	BF184542.1	EST_HUMAN	Gallus gallus gene coding for a-actin
380	13187	25810	1.08	2.3E-01	S75898.1	NT	601842848FT NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4083739 5'
822	13401	28069	33.31	2.3E-01	U39713.1	NT	Homo sapiens chromosome 21 segment HS21Q81
852	13430	28069	33.31	2.3E-01	U67696.1	NT	acornase [Pocipha guttata=zebra finches; ovary, mRNA, 3188 nt]
913	13660	28341	4.18	2.3E-01	BE311893.1	EST_HUMAN	Mycoplasma genitalium section 35 of 51 of the complete genome
1558	14305		1.12	2.3E-01	U22837.2	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
1599	14345	27035	1.23	2.3E-01	AJ245480.1	NT	601142073FT NIH_MGC 14 Homo sapiens cDNA clone IMAGE:3505518 5'
1628	14374	27063	2.74	2.3E-01	Y10687.2	NT	Yersinia pestis HmeH (hmsH), HmeF (hmsF), and HmsS (hmsS) genes, complete cds
2038	14772		1.51	2.3E-01	AJ23533.1	NT	Breazea nipus sig gene for S-locus glycoprotein, cultivar T2
2447	15166	27603	2.66	2.3E-01	BE297718.1	EST_HUMAN	Mus musculus cdt5 gene, exon 1, partial
2657	15397	28105	1.58	2.3E-01	M11319.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FL gene
2827	14114	28789	3.38	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
2963	15729	28379	1.36	2.3E-01	AA601379.1	EST_HUMAN	Human erythropoietin gene, complete cds
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	Methanobrevibacterium glyb gene for DNA gyrase subunit B, partial cds, strainIFO 14957
							not16008 at NCI_OGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
							repetitive element; contains element TH-R repetitive element;
							not16007 at Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

Page 65 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3363	18122	28780	1.14	2.3E-01	H86698.1	EST_HUMAN	y97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3821	19573	29205	1.01	2.3E-01	S92821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, Intron 1) [Ira], Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3
3914	16664		5.22	2.3E-01	7862133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4316	17055	29880	1.1	2.3E-01	R82252.1	EST_HUMAN	y1761.r1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:149017 5'
4388	17108		1.88	2.3E-01	L78789.1	NT	Mus musculus reelin (Rtn-1c) gene, promoter region
4417	17163	29784	1.03	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4454	17190	29816	2.51	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4517	17252	29887	6.19	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4988	17711	30318	0.84	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5221	18028	30654	2.93	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.06	2.3E-01	BF059381.1	EST_HUMAN	7430808.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SNSAV
5443	18242	31130	4.58	2.3E-01	X95687.1	NT	P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5563	18360		0.94	2.3E-01	L38112.1	NT	C. familiaris rom1 gene
5685	18460	31374	0.76	2.3E-01	S90371.1	NT	Vitellina cornutum small subunit ribosomal RNA gene
5851	18638	31575	1.59	2.3E-01	A1708940.1	EST_HUMAN	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
5851	18638	31575	1.59	2.3E-01	A1708940.1	EST_HUMAN	CYTROCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5851	18638	31575	1.59	2.3E-01	A1708940.1	EST_HUMAN	CYTROCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6556	19323	32330	0.63	2.3E-01	AF168089.1	NT	Cytodolus cuniculus cytochrome oxidase subunit VIa (cox1a2) mRNA, complete cds, nuclear gene for mitochondrial product
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	as4212.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318987 3' similar to contains Alu repetitive element
7011	19703	32769	1.08	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7188	19874	32947	0.9	2.3E-01	AF000227.1	NT	Secale cereale omega seedin gene, complete cds
7315	19958	33077	3.14	2.3E-01	AF175399.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7318	20001	33079	0.64	2.3E-01	AV176981.1	EST_HUMAN	AV176981 GLC Homo sapiens cDNA clone GLC0G808 5'
7318	20001	33080	0.64	2.3E-01	AV176981.1	EST_HUMAN	AV176981 GLC Homo sapiens cDNA clone GLC0G808 5'
7508	20178		2.94	2.3E-01	6754778	NT	Mus musculus myosin XY (Myo15), mRNA
7513	20316	33278	1.38	2.3E-01	BE688071.1	EST_HUMAN	601511979F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7652	20146		2.73	2.3E-01	N90893.1	EST_HUMAN	zat12a08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
7760	20446	33569	0.71	2.3E-01	AL181558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7692	20587	33717	2.16	2.3E-01	M85931.1	NT	Oxyfichta nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57696.1	NT	Mus musculus proscapsin (papsSGP-1) gene, complete cds
8671	21363	34610	0.56	2.3E-01	AW090541.1	EST_HUMAN	xb00406.x1 NCI CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2591534.3'
8766	21478	34627	0.45	2.3E-01	AW984460.1	EST_HUMAN	EST1376533 IMAGE resequences, MAGH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST194081 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9039	21729	34884	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST194081 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9430	22133	35313	0.62	2.3E-01	6679316	NT	Mus musculus phosphatidylcholine 3-kinase catalytic subunit delta (Pik3cd) mRNA
9609	22292	35448	0.62	2.3E-01	U77074.1	NT	Tribolium castaneum transcription factor homolog (Tc-eve) gene, complete cds
9628	22281	35471	0.5	2.3E-01	BE277650.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988739.5'
9682	22334	35529	0.59	2.3E-01	AW864460.1	EST_HUMAN	EST1376533 IMAGE resequences, MAGH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.41))
9787	22418	35625	0.56	2.3E-01	AW364633.1	EST_HUMAN	PM2-D70038-261.239-001-404 D70038 Homo sapiens cDNA
9834	22485	35686	2.43	2.3E-01	BE173060.1	EST_HUMAN	MRO-H70055-240400-014-g11 H70055 Homo sapiens cDNA
9892	22542	35734	2.76	2.3E-01	AJ259281.1	NT	Rhizobium leguminosarum partial glutamine DNA for exopolysaccharide biosynthesis genes
10340	22987	36205	0.84	2.3E-01	AF201928.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22988	36267	5.11	2.3E-01	BF133577.1	EST_HUMAN	601849156R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092.3'
10937	23617	36867	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23617	36868	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	AE002197.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
11615	24403		1.76	2.3E-01	AV709736.1	EST_HUMAN	AV709736 AOC Homo sapiens cDNA clone ADGAGH91.5'
11655	24439		1.33	2.3E-01	6006010	NT	Homo sapiens integrin, alpha 3 (antigen CD49c, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-4 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12088	24593		4.88	2.3E-01	U72731.1	EST_HUMAN	HCOE5T44 HT29/16 Homo sapiens cDNA clone HCOE44.5'
12120	24612		1.62	2.3E-01	AW853940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
12173	25316	30711	2.88	2.3E-01	AW303823.1	EST_HUMAN	xb21d07.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2813773.3' similar to TR:Q8Z175
12205	25395	30813	8.63	2.3E-01	BE892484.1	EST_HUMAN	Q8Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repulsive element;
12255	24701		2.51	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:390689.5'
						EST_HUMAN	602144459F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4297719.5'

Page 87 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12303	24728		2.35	2.3E-01	AJ008519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12398	24784		1.76	2.3E-01	U49845.1	NT	Pleuroctenella walli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ008519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12947	24952		2	2.3E-01	BF475811.1	EST_HUMAN	ncs3912.x1 Lupaal, scallie, nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element.
88	12914	25552	1.63	2.2E-01	A052190.1	EST_HUMAN	oz14610.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
1557	13304	26993	1.94	2.2E-01	AF187850.1	NT	TRQ13040 C13040 ATP-BINDING CASSETTE PROTEIN ;
2092	14874	27547	2.52	2.2E-01	N34840.1	NT	Fresh-water sponge Emr1 alpha collagen (COLF1) gene
2402	15123	27860	6.3	2.2E-01	BE677538.1	EST_HUMAN	60205603FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249560 5'
2594	15308	28044	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462028FT NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868190 3'
2594	15308	28045	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462028FT NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868190 5'
2884	15551	28264	4.36	2.2E-01	BE155025.1	EST_HUMAN	PM2-HT0353-281269-003-rt12 HT0353 Homo sapiens cDNA
2884	15551	28295	4.36	2.2E-01	BE155025.1	EST_HUMAN	PM2-HT0353-281269-003-rt12 HT0353 Homo sapiens cDNA
2821	15597		1.57	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3397	18148		1.97	2.2E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3784	18546		1.12	2.2E-01	AF155728.1	NT	Xaphophonis maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4105	18848		0.72	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4194	18935	29562	6.45	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlxk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4232	19973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4232	19973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4323	17052	29889	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4323	17052	29890	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4373	17507		1.36	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211216.1	EST_HUMAN	z487055.r1 Stralagene HNT neuron (8637233) Homo sapiens cDNA clone IMAGE:648968 5'
4982	17705		1.1	2.2E-01	L13292.1	NT	Mus musculus Vinculin gene, exon 3
5082	17781		0.83	2.2E-01	S57565.1	NT	hIatamine 12-receptor [rats, Genomic, 1928 nt]
5140	17858	30474	2.04	2.2E-01	5835974	NT	Yidua chab/besala mitochondrion, complete genome
5659	18454	31368	2.07	2.2E-01	5903002	NT	Homo sapiens diaphanous (Draocophila, homolog) 2 (DIAPH2), transcript variant 196, mRNA
5699	18464		4.5	2.2E-01	D64000.1	NT	Synochyotaxis ap. PCO8803 complete genome, 19,27, 2392729-2539899
5910	18584	31645	0.95	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Text) mRNA, complete cds
5910	18594	31647	0.95	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Text) mRNA, complete cds

Page 88 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8606	18389	32381	0.73	2.2E-01	AB038460.1	NT	Homo sapiens gene for fukutin, complete cds
8626	18602	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7028	18721	32777	1.28	2.2E-01	AF082733.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (tbpA) genes, complete cds, and unknown genes
7029	18721	32778	1.28	2.2E-01	AF082733.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (tbpA) genes, complete cds, and unknown genes
7191	18877	32950	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7388	20068	33144	0.63	2.2E-01	AE000035.2	NT	Human glycophorin B gene, exon 4
7628	20284	33402	0.88	2.2E-01	AB024553.1	NT	Mycoplasma pneumoniae M139 section 45 of 63 of the complete genome
7818	20814	33808	2.04	2.2E-01	AF168143.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8440	21466	34279	1.07	2.2E-01	Z49933.1	NT	Mus musculus rrm23-MT gene, promoter region
8784	21611	34632	3.63	2.2E-01	AE001713.1	NT	E. coli sepA and sepB genes
8820	21611	34632	4.35	2.2E-01	AE001713.1	NT	Par. troglodytes MeCP2 gene 3'UTR
9013	21703	34653	1.46	2.2E-01	AW655039.1	EST_HUMAN	Thermolobus maritima section 25 of 139 of the complete genome
9098	21786	34852	1.04	2.2E-01	BF376354.1	EST_HUMAN	PM3-CT0283-241289-009-b07 CT0283 Homo sapiens cDNA
9189	21839	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9207	22088	35259	13.43	2.2E-01	P48634	SWISSPROT	MR1-TN0045-1T0800-006-c02 TN0045 Homo sapiens cDNA
9252	21931	35104	0.69	2.2E-01	AJ009539.1	NT	Z60408.1 Sources melanocyte 2NHIM Homo sapiens cDNA clone IMAGE:291581 5'
9263	22017	35185	0.81	2.2E-01	7657428	NT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9276	22030	35200	3.95	2.2E-01	M89643.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (klp3)
9521	22174	35356	0.88	2.2E-01	O90580	SWISSPROT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9715	22368	35564	3.4	2.2E-01	AF187941.1	NT	Brachydanio rerio apendymin beta and gamma chains (Epd) gene, complete cds
9853	22503	35703	1.85	2.2E-01	BF206507.1	EST_HUMAN	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10076	22724	35941	0.95	2.2E-01	9625671	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-hSP21) mRNA, complete cds; nuclear gene for chloroplast product
10232	22880	36092	0.6	2.2E-01	T59472.1	EST_HUMAN	601609724F NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10232	22880	36093	0.5	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 6, complete genome
10295	22816	36128	0.58	2.2E-01	AF069294.1	NT	X453403.11 Stragene overlay (#637217) Homo sapiens cDNA clone IMAGE:75555 5'
10341	22888		0.81	2.2E-01	AF071001.1	NT	X453403.11 Stragene overlay (#637217) Homo sapiens cDNA clone IMAGE:75555 5'
							Pseudomonas aeruginosa quorum protein ethanol dehydrogenase (xoaA) gene, partial cds; cytochrome c550 precursor (xoaB), NAD+ dependent acetaldehyde dehydrogenase (xoaC), and pyrroloquinone synthase A (pqoA) genes, complete cds, and pyrroloquinone synthase A (pqoA) genes, partial cds

Page 89 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10387	23033	36247	0.8	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.8	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23166	36594	0.48	2.2E-01	AF046720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.50	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.48	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11369	24005	37509	4.83	2.2E-01	X01918.1	NT	Drosophila 88C glue gene cluster
11438	23205	36437	5.22	2.2E-01	7708215	NT	Homo sapiens H-2k binding factor-2 (LOC51560), mRNA
11935	24483		1.00	2.2E-01	BE870659.1	EST_HUMAN	807446957 F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850670 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12040	25380		2.21	2.2E-01	U82871.2	NT	Yitis Whifera cultivar Phoi Noli plasma membrane aquaporin (PIP1a) mRNA, complete cds
12123	24815		2.19	2.2E-01	AF188843.1	NT	RC1-CT0249-141199-021-g04 C10249 Homo sapiens cDNA
12225	17504	30591	3.87	2.2E-01	AW381088.1	EST_HUMAN	h17692.x1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872523 3'
12228	24681		1.6	2.2E-01	AW661922.1	EST_HUMAN	AV594801 GKG Homo sapiens cDNA clone GKCAH802 5'
12731	25371		2.58	2.2E-01	AV694801.1	EST_HUMAN	nm3161.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
950	13716	26382	2.12	2.1E-01	AA569289.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
953	13718	26384	0.77	2.1E-01	AL161504.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1102	13859		2.76	2.1E-01	AE002314.2	NT	Mus musculus interferon (alpha and beta) receptor 2 (finar2), mRNA
1178	13929	28593	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (finar2), mRNA
1176	13929	28594	1.15	2.1E-01	6754299	NT	6k7362.s1 NCI CGAP_GCA Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765
1908	14643	27853	2.07	2.1E-01	AA908824.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2152	14882	27616	4.2	2.1E-01	BF695073.1	EST_HUMAN	60208312BF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247803 5'
2485	15596	27842	1	2.1E-01	H73988.1	EST_HUMAN	XU4107.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2485	15598	27843	1	2.1E-01	H73988.1	EST_HUMAN	XU4107.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2656	15270	28005	0.91	2.1E-01	AF022814.1	NT	Fugu rubripes transcription factor (SUF-1) and heme-oxygenase genes, complete cds
2625	15991	28335	2.3	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3786	16538		6.08	2.1E-01	9833831	NT	Beta vulgaris mitochondrion, complete genome
4032	16777	29408	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082		1.77	2.1E-01	AB03041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4537	17272	28904	1.23	2.1E-01	AB010273.1	NT	Homo sapiens pahsp47 gene, complete cds
5013	17734	30341	1.4	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

Page 90 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	17609	30425	1.09	2.1E-01	AE001528.1	NT	Helicobacter pylori, strain 569, section 87 of 132 of the complete genome
5278	18028	30950	6.24	2.1E-01	BF872695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:2393001 5'
6787	19351	32559	1.4	2.1E-01	AJ223392.1	NT	Dodo fragilis mitochondrial 16S rRNA gene, partial
6798	19459	32481	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7306	18989	33065	0.85	2.1E-01	Q01656	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7306	18989	33066	0.85	2.1E-01	Q01656	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000	238	2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7606	20272	33380	1.84	2.1E-01	AF000949.1	NT	Cenlis familiaris keratin (KRT19) gene, complete cds
7651	20315	33425	1.22	2.1E-01	AF068837.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7651	20316	33426	1.22	2.1E-01	AF068837.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7971	20669		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
							Haemophilus influenzae tmdC, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcD) genes, complete cds
8400	21093	34229	4.44	2.1E-01	U68999.1	NT	DKFZp434H0614.11 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434H0614 5'
8698	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.11 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434H0614 5'
8996	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.11 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434H0614 5'
8957	21648		0.45	2.1E-01	AB022624.1	NT	Homo sapiens APCCL gene, exon 9
8935	21628	34768	5.68	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9404	22066	35237	0.57	2.1E-01	N42536.1	EST_HUMAN	Y171e10.1 Soares melanocyte 2NH-HM Homo sapiens cDNA clone IMAGE:270954 5'
9404	22066	35238	0.57	2.1E-01	N42536.1	EST_HUMAN	Y171e10.1 Soares melanocyte 2NH-HM Homo sapiens cDNA clone IMAGE:270954 5'
9413	22091	35262	2.31	2.1E-01	X97378.1	NT	A.thaliana mRNA for AtRANBP1b protein
9518	22171	35354	1.13	2.1E-01	AB038529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22875	36088	1.47	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10288	22906	36116	2.5	2.1E-01	P2624	SWISSPROT	DIACYLGLYCEROL KINASE DELTA (DGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10284	22912	36122	0.97	2.1E-01	BF574264.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11554	24153	36122	2.19	2.1E-01	11038647	NT	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:270831 5'
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11870	24944		1.38	2.1E-01	X57624.1	NT	RC3-H10622-040500-013-b1 1 HT10622 Homo sapiens cDNA
12377	24775		2.07	2.1E-01	AF217490.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12578	25287		1.47	2.1E-01	L32568.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12635	24935		1.42	2.1E-01	BE622149.1	EST_HUMAN	Human granulins gene
							601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916975 5'

Page 91 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12768	25018	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a59a2a2.x1 NCL_GCAP_G03 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	26950	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGL-18 protein (LOC51038), mRNA
683	13458	26103	1.24	2.0E-01	M77085.1	NT	O cuniculus germline IgH heavy chain V-H pseudogene, allele type VH42
792	13594	20225	2.19	2.0E-01	AF027865.1	NT	Myo myosin heavy chain H100 pseudogene, complete cds
991	13753	28414	1.09	2.0E-01	D90605.1	NT	Synuclein alpha Locus class II region
1103	13980	26519	2.47	2.0E-01	AL163213.2	NT	Yersinia enterocolitica sp. PC08803 complete genome, 7127, 781448-920915
1232	13981	26951	1.77	2.0E-01	AJ132695.5	NT	Homo sapiens chromosome 21 segment HS21C013
1285	14035	26706	1.63	2.0E-01	AW384037.1	EST_HUMAN	Homo sapiens rac1 gene
1443	14190		1.52	2.0E-01	AJ243957.1	NT	PV1-H70422-261264-002-c08 H70422 Homo sapiens cDNA
1470	14217	26904	14.63	2.0E-01	A503408	NT	Plum pox virus strain M, complete genome, isolate PS
1544	14290	26977	1.97	2.0E-01	AB007974.1	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1550	14298	26983	1.01	2.0E-01	AF26700.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0605
1692	14438	27132	1.4	2.0E-01	U22346.1	NT	Homo sapiens sodium iodide symporter mRNA, partial cds
1712	14455		1.87	2.0E-01	AF111170.3	NT	Human bryotin B1 receptor (brady1) gene, complete cds
1752	14494		4.33	2.0E-01	U67625.1	NT	Homo sapiens 14q32 Jcggad2 gene, complete cds, and unknown gene
1883	14620	27329	1.12	2.0E-01	BE871330.1	EST_HUMAN	Methanococcus jannaschii section 67 of 150 of the complete genome
1883	14620	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441.F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	X82877.1	NT	H. sapiens Na ⁺ -D-glucose cotransport regulator gene
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	xp15002.x1 NCL_GCAP_FH9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element
3693	16447		0.89	2.0E-01	P34641	SWISSPROT	CEB-11 PROTEIN
3822	16574	26206	1.12	2.0E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3936	16668	26327	0.76	2.0E-01	Z46806.1	NT	Sus scrofa
4528	17263		8.49	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN00032-150500-223-603 EN00032 Homo sapiens cDNA
4979	17702	30309	5.26	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5009	19237	29893	0.8	2.0E-01	P46907	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATB-10) (HD-ZIP PROTEIN ATB-10)
5359	19161	30845	2.63	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5655	19450	31363	1.94	2.0E-01	11432640	NT	Homo sapiens dual oxidase-like domain 2 (DUOX2), mRNA
5780	19542	31464	0.76	2.0E-01	X91869.1	NT	F. rubripes DNA encoding for valyl-uracil synthetase
5969	19751	31712	0.73	2.0E-01	U16300.1	NT	Saccharomyces cerevisiae Hsp150 (Hsp150), complete cds
6081	19860		0.93	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6192	19968	31643	0.79	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

Page 92 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6336	19105	32094	3.2	2.0E-01	X61033.1	NT	M.auritus mt clss glutathione transferase gene
6436	19203	32200	4.02	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g08 CT0247 Homo sapiens cDNA
7194	19890	32954	1.28	2.0E-01	AF250371.1	NT	Mus musculus phosphoribosyltransferase-1 C isozyme (Pbc) gene, exons 3 through 7
7346	20026	33102	0.69	2.0E-01	P64422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
7679	20359	33452	0.84	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7853	20548		5.8	2.0E-01	AF028026.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33925	2.95	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8624	21310		0.99	2.0E-01	BE692247.1	EST_HUMAN	801344948FT NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677794 5'
9251	21930	35103	0.82	2.0E-01	U82511.1	NT	Dichostellum discolorum random slug cDNA19 protein (rec19) mRNA, partial cds
9290	21957	35129	0.98	2.0E-01	U71122.1	NT	Arabidopsis thaliana trichomonas section 5 of 87 of the complete genome
9456	22006		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9846	22398	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146822.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22589	35792	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22589	35793	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10087	22715	35933	0.68	2.0E-01	AF167814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10087	22715	35934	0.68	2.0E-01	AF167814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22762		0.69	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10305	22932	36167	2.78	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
10744	23431	36874	1.56	2.0E-01	D89088.1	NT	Salvadora pluvius mRNA for transferrin, complete cds
10744	23431	36876	1.66	2.0E-01	D89088.1	NT	Salvadora pluvius mRNA for transferrin, complete cds
11609	24207	37350	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37351	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.51	2.0E-01	AF0206837.2	NT	Pinus taeda promealase liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12546	25210		1.39	2.0E-01	AF302773.1	NT	Homo sapiens nitrin-Ln isoform (nitrin) mRNA, complete cds
12556	25139	30894	1.36	2.0E-01	AW675297.1	EST_HUMAN	EST1387405 MAGS resequences, MAGN Homo sapiens cDNA
12594	24950	30885	3.58	2.0E-01	A023502.1	EST_HUMAN	060410.1 at Soares, basis, NHT Homo sapiens cDNA clone IMAGE:1643810 3'
12618	24924		2.68	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30978	1.87	2.0E-01	11528495	NT	Mus musculus fructosebimase 3 kinase (F3K3) mRNA
108	12928		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor translocator 1 (Arlt1), mRNA
342	13433	26058	6.86	1.8E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	26058	1.43	1.6E-01	U32581.2	NT	Homo sapiens lambsalivata protein kinase C-interacting protein mRNA, complete cds
641	13420	26059	1.43	1.5E-01	U32581.2	NT	Homo sapiens lambsalivata protein kinase C-interacting protein mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	28066	5.97	1.8E-01	BE070801.1	EST_HUMAN	RC3-B1/0502-251199-011-d01 BT0502 Homo sapiens cDNA
649	13427	28066	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-B1/0502-251199-011-d01 BT0502 Homo sapiens cDNA
665	13730		1.73	1.6E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1082	13840	28499	13.43	1.8E-01	A4358813.1	EST_HUMAN	ES167784 Fetal lung II Homo sapiens cDNA 5' end
1349	14097	28772	1.76	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium wuxu reticulocyte binding protein-2 (rbp-2) gene, complete cds
2380	15102	27841	3.61	1.8E-01	8922633	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2523	15699	28333	3.43	1.8E-01	U60065.1	NT	Signatum hispidus p53 gene, partial cds
2539	15704		5.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3002	15768	28417	0.95	1.9E-01	U25146.1	NT	Rattus norvegicus brush border myosin-1 (BBM1) mRNA, partial cds
3390	16149	28803	4.26	1.9E-01	D13197.1	NT	Mouse gene for Immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	R16467.1	EST_HUMAN	Y42740.11 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:129547 5'
3516	16568	29199	1.33	1.6E-01	P39708	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3573	16722	28356	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4053	18608	28438	1.28	1.9E-01	AW754106.1	EST_HUMAN	CH3-C10315-271189-045-b11 CT0315 Homo sapiens cDNA
4208	18647	28573	1.09	1.9E-01	BE834643.1	EST_HUMAN	MR1-FR0010-240700-007-d04 FN0010 Homo sapiens cDNA
4950	17677		1.05	1.8E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	XZ8407.XT NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:261844 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALP-HA-1 (HUMAN);
5558	18355	31295	7.87	1.9E-01	AF127637.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5749	18541	31463	0.7	1.8E-01	AF081216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5795	18586		2.56	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP24 Homo sapiens cDNA clone NT2RP-4001328 5'
6235	19009	31695	0.75	1.9E-01	A1762391.1	EST_HUMAN	wf4402.x1 NCI CGAP_Oat16 Homo sapiens cDNA clone IMAGE:2394099 3'
6294	19067	32080	1.03	1.9E-01	AW1148452.1	EST_HUMAN	wf4408.x1 NCI CGAP_Kid6 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03459 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL, PRECURSOR (HUMAN);
6876	17952	30546	1.69	1.9E-01	R43212.1	EST_HUMAN	Y00847.2x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31653 3' similar to contains MER13 repetitive element ;
6900	19538	32862	0.69	1.9E-01	AF034620.1	NT	Homo sapiens bubby like protein 1 (TULP1) gene, exons 9-11
6900	19638	32863	0.69	1.9E-01	AF034620.1	NT	Homo sapiens bubby like protein 1 (TULP1) gene, exons 9-11
7160	19847	32917	0.62	1.9E-01	U73645.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7391	20070	33149	1.38	1.9E-01	U580625.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB) gene, complete cds
7438	20113	33201	3.11	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7885	20580	33709	1.40	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8586	21278	34417	10.77	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds

Page 94 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21536	34681	1.24	1.8E-01	M14568.1	NT	Mouse cat beta-globin gene mRNA, partial cds
8844	21536	34682	1.24	1.8E-01	M14568.1	NT	Mouse cat beta-globin gene mRNA, partial cds
9775	22426	36632	0.61	1.9E-01	AA912486.1	EST_HUMAN	086910.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10142	22760	39005	0.85	1.8E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
10142	22760	38006	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
10540	23237	39470	2.48	1.8E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10540	23237	39471	2.48	1.8E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	39583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
10986	23681	38915	1.34	1.8E-01	AA912480.1	EST_HUMAN	086902.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gbL21696_cds1 PROTHYMOSIN ALPHA (HUMAN) contains element ORF repetitive element :
10986	23681	38916	1.34	1.8E-01	AA912480.1	EST_HUMAN	086902.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gbL21696_cds1 PROTHYMOSIN ALPHA (HUMAN) contains element ORF repetitive element :
11487	24088	37399	1.53	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11726	24320	37645	2.77	1.8E-01	AJ243219.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37873	1.8	1.9E-01	AJ24344.1	NT	Influenza A/Guangdong/24372 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12399	24785		1.67	1.9E-01	AF055600.1	NT	Drosophila melanogaster diaphanin light chain mRNA, complete cds
30	12658	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p116lpa mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022690.1	NT	Mus musculus Cag gene for chaperonin containing TOP-1 gamma subunit, partial cds
361	13159	28502	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	28158	1.04	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13726	26390	0.94	1.8E-01	AJ012212.1	EST_HUMAN	w47102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1089	13826	25485	1.83	1.8E-01	AF000580.1	NT	Drosophila discoidium plasmid Ddp5, complete genome
1266	14016	26583	6.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26925	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26928	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1639	14577		1.2	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14597		1.58	1.8E-01	AJ733708.1	EST_HUMAN	gb22610.s5 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE :

Page 95 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14645	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Soyab, Soyab, Soyab 0-pps, Soyab5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Soyab16 pseudogene, small inducible cytokine A5 precursor, complete cds
2697	15409		2.35	1.8E-01	AW693728.1	EST_HUMAN	QV3-DT0018-031202-036-q04 DT0018 Homo sapiens cDNA
2698	15685		1.89	1.8E-01	AF184589.1	NT	Junosidum scutell LEAFY protein (LEAFY2) gene, partial cds
2904	19670	28319	1.29	1.8E-01	AW18200.1	EST_HUMAN	47483337 Soares_NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:2659756 3'
3121	15886	28528	1.76	1.8E-01	AW695178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3910	16363	29005	0.88	1.8E-01	H03359.1	EST_HUMAN	yf45d1.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
3910	16363	29006	0.88	1.8E-01	H03359.1	EST_HUMAN	yf45d1.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
4299	17038		1.43	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4519	17254	29888	5.94	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4721	17453	30087	2.9	1.8E-01	AB051897.1	NT	Mus musculus Soyab, Soyab, Soyab 0-pps, Soyab5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Soyab16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17486	30114	0.94	1.8E-01	X62179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
4984	17707	30311	2.03	1.8E-01	AW614270.1	EST_HUMAN	MR3-ST0203-151298-112-q05 ST0203 Homo sapiens cDNA
4990	17723	30325	1.06	1.8E-01	AT62382.1	EST_HUMAN	an28p07.y6 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5035	17754	30337	4.68	1.8E-01	AF181258.1	NT	Mesocricetus auratus Ne-taurocholate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5835	18624	31558	0.69	1.8E-01	N28929.1	EST_HUMAN	y938n08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264063 5'
6037	18817	31777	1.19	1.8E-01	5978428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6) mRNA
6037	18817	31778	1.18	1.8E-01	5978428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6) mRNA
6419	19187	32185	1.15	1.8E-01	Q00Y14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6463	19230		2.06	1.8E-01	N94853.1	EST_HUMAN	y926n02.r1 Soares_multispl. sclerost. 2NBHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6806	19644	32689	1.18	1.8E-01	AB018591.1	NT	Citruslus latens mRNA for wus, complete cds
6909	19844	32690	1.18	1.8E-01	AB018591.1	NT	Citruslus latens mRNA for wus, complete cds
7346	20027	33103	0.7	1.8E-01	AF001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
9242	21921	35091	1.23	1.8E-01	MT7356.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9274	22028	35198	1.22	1.8E-01	9626232	NT	Bacteriophage lambda, complete genome
9391	22053		0.5	1.8E-01	AA493781.1	EST_HUMAN	nh02a05.s1 NO_CGAP_Thyl1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1 13 L1 repetitive element;
9473	22126	35305	0.94	1.8E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE

Page 96 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22128	35308	0.84	1.8E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	0.81	1.8E-01	M28018.1	NT	S communs oxidine-5-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	M28018.1	NT	S communs oxidine-5-phosphate decarboxylase (URA1) gene, complete cds
9579	22331	35526	0.75	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9583	22335	35530	0.71	1.8E-01	U07548.1	NT	Methanococcus jannaschii section 86 of 150 of the complete genome
10033	22681		0.78	1.8E-01	AF200252.1	NT	Aquarius eplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10280	22914	39124	1.48	1.8E-01	XG3440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	35465	3.08	1.8E-01	X77336.1	NT	A. italiana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U38908.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, helix and lysin genes, complete cds
10637	19644	32689	2.61	1.8E-01	AB018581.1	NT	Citrus latifolius mRNA for wus, complete cds
10637	19644	32690	2.61	1.8E-01	AB018581.1	NT	Citrus latifolius mRNA for wus, complete cds
10638	23329	35557	5.69	1.8E-01	AF019107.1	NT	Dicystosium discoidium unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X67033.1	NT	B. laurus mRNA for potassium channel
11767	24398	37691	3.45	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx22), mRNA
11967	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019528FT NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4158318 5'
12476	24839		3.26	1.8E-01	Q95682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12565	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	Y48H10.1 Soares placenta N22P Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hbx1)
12745	25234		1.61	1.8E-01	X16535.1	NT	Rattus norvegicus Cef3P9k gene
563	13345	25972	1.57	1.7E-01	BE385164.1	EST_HUMAN	601274804F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815768 5'
787	13559	26221	2.32	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1039	13796	26455	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1039	13796	26456	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1974	14710		2.6	1.7E-01	AF255051.1	NT	Homo sapiens BNP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28278	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

Page 97 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2863	15631	28276	2.20	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15693	28338	1.55	1.7E-01	AA339609.1	EST_HUMAN	EST141651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cdc-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cdc-1 gene, exons 1-3
3103	16688	28508	1.24	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ269505.1	NT	Anelasma sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3595	16348	28989	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hapt1 gene, complete CDS
3616	16369		0.92	1.7E-01	5031888	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16688	29309	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4822	17257		1.69	1.7E-01	X52936.1	NT	Schistosoma peregina alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	AJ247695.1	EST_HUMAN	q157600x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848908 3' similar to contains OPR.b1 OPR repetitive element;
6054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5122	17840	30455	0.75	1.7E-01	D57851.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18126	30785	2	1.7E-01	AA470896.1	EST_HUMAN	nt13a02.at1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:U17885.60S
5323	18126	30786	2	1.7E-01	AA470896.1	EST_HUMAN	nt13a02.at1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:U17885.60S
5506	18304	31205	0.62	1.7E-01	U43598.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6237	19011	31989	13.23	1.7E-01	HT2118.1	EST_HUMAN	Brugia pahangi microfilarial alpha3 protein SHP3 (shp3) gene, complete cds
6293	19066	32048	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ys02005.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19066	32048	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6763	17622	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6763	17622	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
9780	19524		2.28	1.7E-01	AF028552.3	NT	Macrorhynchus auratus oviductin precursor (OVI) gene, complete cds
6602	19640		0.88	1.7E-01	Z82810.1	NT	Homo sapiens HFE gene
7120	19608	32874	1.1	1.7E-01	AF005422.1	NT	Escherichia coli O157:H7 genomic DNA, Salai-V72 prophage inserted region
7197	19683	32957	8.8	1.7E-01	BE734776.1	EST_HUMAN	bt01589022.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7380	20060	33139	1.37	1.7E-01	PI16724	SWISSPROT	PROBABLY PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
7396	25112	33153	0.71	1.7E-01	Q01865	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7760	20466	33580	1.32	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7893	20558	33684	0.82	1.7E-01	AF150089.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (lactD) gene, complete cds
8175	20889	34001	6.19	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8176	20889	34002	6.19	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8593	21230	34431	0.47	1.7E-01	AW692873.1	EST_HUMAN	Human sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8593	21230	34431	0.47	1.7E-01	AW692873.1	EST_HUMAN	Human sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8528	21320	34462	2.09	1.7E-01	D00384.1	NT	Rat (SHR strain) SVT gene
8743	21435	34580	0.76	1.7E-01	AF217413.1	NT	Homo sapiens neuregulin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.76	1.7E-01	AF217413.1	NT	Homo sapiens neuregulin 3 isoform gene, complete cds, alternatively spliced
9069	21765	34916	0.48	1.7E-01	BE283142.1	EST_HUMAN	Human sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9069	21765	34917	0.48	1.7E-01	BE283142.1	EST_HUMAN	Human sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9490	22143	35323	7.86	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22250	35435	0.51	1.7E-01	AW677455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9597	22250	35436	0.51	1.7E-01	AW677455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9815	22268	35435	3.14	1.7E-01	U16285.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22359	35555	0.63	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (epd gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10285	22942	36156	1.72	1.7E-01	AA627572.1	EST_HUMAN	rg6007.71 NQ1 CGAP_C03 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbl.25081
10501	23147	36511	0.45	1.7E-01	AL101542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN).
10579	23274	36511	8.78	1.7E-01	BE330035.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10709	23398	36937	2.65	1.7E-01	AA814617.1	EST_HUMAN	601288547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11059	23725	36935	8.13	1.7E-01	71063300	NT	orf43a03.81 NQ1 CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11055	23725	36936	8.13	1.7E-01	71063300	NT	Mus musculus adenomatous polyposis coli binding protein Ebt1 (Ebt1), mRNA
11146	23813	37066	1.62	1.7E-01	Y08391.1	NT	Mus musculus adenomatous polyposis coli binding protein Ebt1 (Ebt1), mRNA
11348	24038	37341	1.69	1.7E-01	AA883375.1	EST_HUMAN	S. pombe pcp1+ gene
11712	24307		1.83	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
11746	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR)
11746	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR)
11874	24453	37789	2.62	1.7E-01	11418157	NT	IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN
12000	25320		1.85	1.7E-01	AL163278.2	NT	Homo sapiens sodium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA

Page 99 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12886	25167		1.85	1.7E-01	AB24404.1	EST_HUMAN	659905.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2274872.3 similar to gb:U7379 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12852	24889	30998	16.27	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
122	12940	25582	2.39	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
694	19518	26081	1.51	1.6E-01	R31497.1	EST_HUMAN	vt7512.1.1 Soares placenta h2HP Homo sapiens cDNA clone IMAGE:135593.5'
1493	14240	28927	1.16	1.6E-01	AA548983.1	EST_HUMAN	nt28412.1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014839.3'
1612	14259	28944	3.92	1.6E-01	AF288117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1917	14654	27364	1.86	1.6E-01	P22069	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1977	14713		1.51	1.6E-01	U10334.1	NT	Craseostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2383	15503	27844	1.35	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2487	15214	27937	1.4	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	15681	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2894	15681	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3624	16377	29019	1.21	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3982	16750		2.49	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4294	17033	29681	9.42	1.6E-01	AF178980.1	NT	Homo sapiens apelin gene, complete cds
4423	17159		3.07	1.6E-01	AW968601.1	EST_HUMAN	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA
4431	17187		4.35	1.6E-01	67683310	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4859	17586	30219	0.7	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4892	17619	30237	1.38	1.6E-01	AA089343.1	EST_HUMAN	284408.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:611361.3 similar to TR:E221955
4911	17639	30253	1.54	1.6E-01	AJ000635.1	NT	E221965 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4911	17639	30254	1.54	1.6E-01	AJ000635.1	NT	Lycopodium esculentum Real Fragment 2, satellite region
5003	18108	30768	0.99	1.6E-01	L40508.1	NT	Lycopodium esculentum Real Fragment 2, satellite region
5435	18234	30947	2.86	1.6E-01	AW197496.1	EST_HUMAN	Pharmodium falcatum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5435	18234	30948	2.86	1.6E-01	AW197496.1	EST_HUMAN	hm4301.x1 NCI_CGAP_CG8 Homo sapiens cDNA clone IMAGE:2898989.3 similar to TR:O75984 O75984
5447	18246	31134	2.15	1.6E-01	AF034716.1	EST_HUMAN	HYPOPHYSICAL 127.6 KD PROTEIN ;
5038	18720	31679	0.83	1.6E-01	BE925803.1	EST_HUMAN	HYPOPHYSICAL 127.6 KD PROTEIN ;
6162	18939	31906	0.71	1.6E-01	BF183584.1	EST_HUMAN	Rattus norvegicus GCAT1 enhancer binding protein epsilon (cbpse) gene, complete cds
6162	18939	31910	0.71	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-31080G-113-h01 BN0034 Homo sapiens cDNA
							601809728R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335.3'
							601809728R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335.3'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6334	19104	32082	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6334	19104	32083	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6885	19802	32841	0.55	1.6E-01	AA398047.1	EST_HUMAN	z18904.71 Soares testis, NIH Homo sapiens cDNA clone IMAGE:728511 5'
6887	17044	30639	5.32	1.6E-01	AW291215.1	EST_HUMAN	U-H-B12-agi-B-06-U1 at NCJ CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7676	20340	33433	1.68	1.6E-01	AW246359.1	EST_HUMAN	2822248 EpH4 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.6E-01	AI196525.1	EST_HUMAN	AUT35623 PLACE1 Homo sapiens cDNA clone PLACE100466 5'
7769	20464	33559	1.81	1.6E-01	L49349.1	NT	Gonilla gonilla androgen receptor gene, partial exon
7924	20819		0.61	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1/EO607 Pediatric pre-B cell acute lymphoblastic leukemia Baylör-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8018	20713	33844	0.87	1.6E-01	U98243.1	NT	Bacteroides vulgatus beta-lactamase (bla) gene, complete cds and mobilization protein (mobA) gene, complete cds
8530	21222	34364	0.88	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 18 of 21): from 2897771 to 3213410
8725	21417	34561	0.63	1.6E-01	R13673.1	EST_HUMAN	yf60h08.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:28873 5'
8831	21523		0.59	1.6E-01	L35681.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21581	34706	1.72	1.6E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR0011w
9009	21699		0.83	1.6E-01	AF11187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds, cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041169-011-H01 ST0200 Homo sapiens cDNA
9554	22207	35391	1.7	1.6E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR0011w
9583	22242		0.97	1.6E-01	BE16584.1	EST_HUMAN	PV23-H10353-270100-004.F11 HT0363 Homo sapiens cDNA
10553	23249	36488	3.3	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-11169-028-G01 CT0220 Homo sapiens cDNA
10918	23598	38845	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	38846	1.69	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	38852	1.55	1.6E-01	BE269949.1	EST_HUMAN	601145789.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3181183 5'
11059	23729		4.28	1.6E-01	AF105084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23994	37298	7.28	1.6E-01	6871652	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aplb1), mRNA
11706	24301		1.26	1.6E-01	BF527237.1	EST_HUMAN	60203948F2 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177073 5'
11885	25331		1.64	1.6E-01	6879466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12002	24538	37273	5.28	1.6E-01	AV716385.1	EST_HUMAN	AV719485 GLC Homo sapiens cDNA clone GLCEMF07 5'
12292	24721	31052	1.72	1.6E-01	L14933.1	NT	Rat convezatae P05 mRNA, 5' end
12321	24740		1.5	1.6E-01	AW839711.1	EST_HUMAN	RG1-L10074-H10200-014-H01_1 L10074 Homo sapiens cDNA
12418	25149		287.78	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for anti-laurene synthase, complete cds
12574	24901		2.4	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12661	24981		1.72	1.E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 84208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12687	24973	30692	1.7	1.E-01	9606522	NT	Rattus norvegicus chondroitin sulfatase proteoglycan 5 (neuroglycan 5) (Cspg5), mRNA
12766	25046		1.52	1.E-01	BF672698.1	EST_HUMAN	902152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
241	13050	25639	1.4	1.E-01	BE710087.1	EST_HUMAN	IL3-H10619-040700-197.E05 HT0619 Homo sapiens cDNA
241	13050	25690	1.4	1.E-01	BE710087.1	EST_HUMAN	IL3-H10619-040700-197.E05 HT0619 Homo sapiens cDNA
673	15517		9.31	1.E-01	AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH06 5'
768	13339	26198	1.09	1.E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1076	13833	26491	2.75	1.E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1091	13949		1.42	1.E-01	L36725.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13946	26610	0.82	1.E-01	AW195516.1	EST_HUMAN	nt33811.x1 NC1 CGAP Xcl11 Homo sapiens cDNA clone IMAGE:2696089 3'
1252	14001	26698	2.66	1.E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1252	14001	26699	2.66	1.E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1465	14212	26901	1.88	1.E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mdkk1) mRNA, complete cds
1901	14038	27347	1	1.E-01	AW444451.1	EST_HUMAN	UI-H-B13-ald-b-06-0-UI.s1 NC1 CGAP Pan1 Homo sapiens cDNA clone IMAGE:2733641 3'
2718	15423	28162	1.88	1.E-01	BF695381.1	EST_HUMAN	902083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2814	15680		1.15	1.E-01	AW572516.1	EST_HUMAN	xx569402.x2 NC1 CGAP Pan1 Homo sapiens cDNA clone IMAGE:2831078 3' similar to gb-X55072_mn1
3048	15614	28459	0.74	1.E-01	OT6857	SWISSPROT	THYD-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3347	16108	28761	5.06	1.E-01	AA695049.1	EST_HUMAN	0668405.x1 NC1 CGAP GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gbM11433
3381	16108	28777	0.82	1.E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3381	16120	28778	0.82	1.E-01	Z23104.1	NT	Lysagallia mRNA for G protein-coupled receptor
3738	16491	28126	2.11	1.E-01	U09964.1	NT	Lysagallia mRNA for G protein-coupled receptor
3752	16504	29140	0.74	1.E-01	7108358	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3848	16669	29236	2.65	1.E-01	AW655963.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4028	16773	29405	1.7	1.E-01	AW556859.1	EST_HUMAN	h1006.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4151	16801	29530	8.35	1.E-01	AL163284.2	NT	RC2-HT0749-19109-012-09 HT0148 Homo sapiens cDNA
4676	17410	30046	1.57	1.E-01	BF687665.1	EST_HUMAN	RC2-HT0749-19109-012-09 HT0148 Homo sapiens cDNA
4703	15423	28162	1.92	1.E-01	BF695381.1	EST_HUMAN	602087182F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4006223 5'
5132	17860	30467	1.55	1.E-01	Z72608.1	NT	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
							S.cerevisiae chromosome VII reading frame ORF YOL086w

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5145	17684	30480	1.05	1.5E-01	AF06613.1	NT	Merone exocytic gonadotropin-releasing hormone type II gene, complete cds
5175	17684	30489	2.18	1.5E-01	P07995	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	AF256652.1	NT	Calman crocodilian MHC class II beta chain (ncilbeta) gene, complete cds
5245	18051		6.92	1.5E-01	P15195	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5451	18250	31139	5.08	1.5E-01	AW850754.1	EST_HUMAN	IL3-C10219-160200-064-F10 C10219 Homo sapiens cDNA
5492	18291	31189	8.42	1.5E-01	U65018.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5492	18291	31189	8.42	1.5E-01	U65018.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5915	18700	31653	3.09	1.5E-01	6753550	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5915	18700	31654	3.09	1.5E-01	6753550	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5952	18734	31663	1.93	1.5E-01	AJ276503.1	NT	Mus musculus genomic fragment, 278 Kb, chromosome 7
6102	18880	31847	3.1	1.5E-01	BE727658.1	EST_HUMAN	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6152	18929		1.77	1.5E-01	4506386	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6251	19025	31999	2.09	1.5E-01	AF134007.1	NT	Influenza B virus (BANachang/480/94) NB protein gene, complete cds, and neuraminidase gene, partial cds
6409	19099	32178	2.21	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6437	19205	32201	4.99	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (OSORF3), mRNA
6448	19214	32214	1.95	1.5E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6403	19259	32250	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6555	19348	32351	1.25	1.5E-01	AA714760.1	EST_HUMAN	hw30070.st NCI CGAP GCB0 Homo sapiens cDNA clone IMAGE:1241871 3'
6612	19375	32359	1.68	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF6)
6892	17658	30554	6.82	1.5E-01	AW970295.1	EST_HUMAN	EST1382376 IMAGE resequences, MAGK Homo sapiens cDNA
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	cb7302.st NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7115	19803		2.07	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7250	19873	33051	2.95	1.5E-01	AI973157.1	EST_HUMAN	wf52608.st NCI CGAP_UIT Homo sapiens cDNA clone IMAGE:2491310 3'
7490	20162	33254	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7490	20162	33255	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33262	2.04	1.5E-01	AIW500511.1	EST_HUMAN	UIHF-BNC-akc-d05-0-UIIT NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7499	20171	33263	2.04	1.5E-01	AIW500511.1	EST_HUMAN	UIHF-BNC-akc-d05-0-UIIT NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	U46500.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
7957	20652	33775	0.96	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK68 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	0055g12.11 NC1 CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8211	20905		0.95	1.5E-01	BE884760.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8299	20993		11.54	1.5E-01	C16900.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8332	21025	34162	1.8	1.5E-01	L27535.1	NT	C16900 Clontech human aorta polyA+ mRNA (R6372) Homo sapiens cDNA clone GEN:529H09 5'
8491	21183	34325	1.85	1.5E-01	D84478.1	NT	Parguesolamin gila growth hormone (GH) mRNA, complete cds
8512	21204		0.71	1.5E-01	P43449	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8737	21429	34575	1.19	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9002	21602	34842	2.88	1.5E-01	N74228.1	EST_HUMAN	Homo sapiens adipoon-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9092	21781	34945	1	1.5E-01	BF585465.1	EST_HUMAN	z559016.g1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:266856 3' similar to
9100	21788		2.3	1.5E-01	AV754818.1	EST_HUMAN	PIR-S44443 S44443 RAD23 protein homolog - human;
9305	21872		0.74	1.5E-01	AU130007.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	AV754818 TP Homo sapiens cDNA clone TPAAB12 5'
							AU130007 NT2P23 Homo sapiens cDNA clone NT2RP3000080 5'
							Adipenser transmontano vitellogenin mRNA, partial cds
9717	22368	35568	0.53	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9821	22472	35674	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
9821	22472	35678	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10103	22751	35995	2.92	1.5E-01	X98952.1	NT	P1 lentuaculus mRNA for integrin beta subunit
10207	22855	36070	2.16	1.5E-01	A1814048.1	EST_HUMAN	wk53h12.11 NC1 CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
							GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10207	22856	36071	2.16	1.5E-01	A1814048.1	EST_HUMAN	wk53h12.11 NC1 CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10265	22933	36148	2.01	1.5E-01	U40592.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36311	1.43	1.5E-01	AJ011884.1	NT	Danio rerio transcription factor Pax6 (Pax6) mRNA, complete cds
10438	23084	36312	1.43	1.5E-01	AJ011884.1	NT	Claviceps purpurea psi gene
10595	23289	36526	1.62	1.5E-01	BE098492.1	EST_HUMAN	CM2-BT0886-210300-122-F11 BT0886 Homo sapiens cDNA
10595	23289	36527	1.62	1.5E-01	BE098492.1	EST_HUMAN	CM2-BT0886-210300-122-F11 BT0886 Homo sapiens cDNA
10729	23414	36554	7.31	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10729	23414	36555	7.31	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10898	23476		1.7	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
11012	23684	36944	1.6	1.5E-01	AW641915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
							zw45d02.r1 Soares, total, fous, Nb2HF8, 8y Homo sapiens cDNA clone IMAGE:773091 5' similar to
11057	23727	36999	1.85	1.5E-01	AA425488.1	EST_HUMAN	contains element MER22 repetitive element;

Page 104 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11119	19973	33051	1.66	1.5E-01	AI0731167.1	EST_HUMAN	wf5208.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2481310.3
11625	24222		1.66	1.5E-01	AI193704.1	EST_HUMAN	q672401.x1 Soares_fair_NHL19W Homo sapiens cDNA clone IMAGE:1744536.3 similar to
11959	26202		11.07	1.5E-01	BF70692.1	EST_HUMAN	g5m17687.605 ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12320	24739		1.37	1.5E-01	AF030359.2	NT	90212875F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285540.6
12324	24743		1.77	1.5E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3G mRNA, complete cds
12369	24771		5.36	1.5E-01	AB028898.1	NT	Mus musculus mRNA for death inducer-inhibitor-1 (Dio-1)
12385	25220		9.97	1.5E-01	R83077.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12472	25241		2.63	1.5E-01	AV741272.1	EST_HUMAN	y6787604.r1 Soares fetal liver spleen TNF.L3 Homo sapiens cDNA clone IMAGE:194430.6
12573	25150	30697	9.2	1.5E-01	AL138074.2	NT	AV741272 CB Homo sapiens cDNA clone CBDA004.5
12783	25036	30655	1.89	1.5E-01	AJ278242.1	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
292	13098		1.72	1.4E-01	AF006653.1	NT	Sus scrofa mRNA for sodium iodide symporter
890	13659		3.62	1.4E-01	D78693.1	NT	Homo sapiens T cell receptor beta locus, TCRBV/85SP to TORBV/21S2A2 region
1236	13955		2.48	1.4E-01	T91894.1	EST_HUMAN	Xenopus laevis mRNA for DNA (cytosine-5-methyltransferase, complete cds)
1742	14484		1.5	1.4E-01	6876980	NT	y54601.x1 Soares fetal liver spleen TNF.L3 Homo sapiens cDNA clone IMAGE:112032.3
1745	14487	27186	1.71	1.4E-01	AE001710.1	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1898	14635		0.86	1.4E-01	AW135741.1	EST_HUMAN	Thermoga melittina section 22 of 136 of the complete genome
1978	14714		9.33	1.4E-01	AA720615.1	EST_HUMAN	UHH-BIT-act9-Q-U1.s1 NCL CGAP_Su63 Homo sapiens cDNA clone IMAGE:2714009.3
2478	15193	27835	1.38	1.4E-01	P30706	SWISSPROT	hy2307.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1263921.3
2795	15500	28241	4.23	1.4E-01	AI933469.1	EST_HUMAN	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
3879	16529	29267	0.86	1.4E-01	R56232.1	EST_HUMAN	wn7401.x1 NCL CGAP_L12 Homo sapiens cDNA clone IMAGE:2441665.3
3879	16529	29268	0.96	1.4E-01	R56232.1	EST_HUMAN	y6787603.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:41467.5
4153	19855	29524	8.69	1.4E-01	AI695094.1	EST_HUMAN	y6787603.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:41467.5
4153	19855	29525	8.69	1.4E-01	AI695094.1	EST_HUMAN	y6787602.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570.3
4212	19953	29577	3.79	1.4E-01	AE001710.1	NT	y6787602.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570.3
5014	17755	30342	0.94	1.4E-01	UI2283.1	NT	Thermoga melittina section 22 of 136 of the complete genome
5223	19300	30656	5.48	1.4E-01	T80677.1	EST_HUMAN	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5246	18052	30678	4.6	1.4E-01	AB004656.1	NT	y615611.s1 Stratiotes lung (937210) Homo sapiens cDNA clone IMAGE:117812.3
5246	18052	30680	4.6	1.4E-01	AB004656.1	NT	Candida tropicalis DNA for mitochondrial NAOP-linked isocitrate dehydrogenase, complete cds
6205	19980	31959	3	1.4E-01	BE328991.1	EST_HUMAN	Candida tropicalis DNA for mitochondrial NAOP-linked isocitrate dehydrogenase, complete cds
6391	19160	32160	5.6	1.4E-01	AI117147.1	EST_HUMAN	h67602.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538.3
6391	19160	32161	5.6	1.4E-01	AI117147.1	EST_HUMAN	AI117147 HEMBA1 Homo sapiens cDNA clone HEMBA100769.5
6477	19244	32244	3.14	1.4E-01	AW082766.1	EST_HUMAN	AI117147 HEMBA1 Homo sapiens cDNA clone HEMBA100769.5
							y671612.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881751.3

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6460	19287		1.64	1.4E-01	BE265536.1	EST_HUMAN	801193523.F1.NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537561.5'
6509	19274	32275	2.45	1.4E-01	BF375833.1	EST_HUMAN	QV14JUN00309-00309-13-049 UM0038 Homo sapiens cDNA
7026	19178		0.85	1.4E-01	AL118588.1	EST_HUMAN	DKF75761A09.0.1.761 (synonym: hmy2) Homo sapiens cDNA clone DKF75761A09.0.1.761
7284	19867		1.51	1.4E-01	AW015373.1	EST_HUMAN	U14810-aak-09-Q-0.1.1 NCL CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710289.3'
7521	20182	33283	1.19	1.4E-01	U85645.1	NT	Oxydolagus cuticulus fructose 1,6-bisphosphate aldolase (Ald6) gene, complete cds
7653	20317	33427	0.98	1.4E-01	A3905192.1	EST_HUMAN	Q36012.X1 Soares_NHMP-U.S1 Homo sapiens cDNA clone IMAGE:1879583.3'
8373	21068		1.23	1.4E-01	AV659047.1	EST_HUMAN	AB59047 GLC Homo sapiens cDNA clone GLOC:SH06.3'
8683	21375		0.57	1.4E-01	AA360983.1	EST_HUMAN	1982612.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111.3' similar to TR-002710.002710 GAG POLYPROTEIN.1
8811	21503	34650	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8882	21583	34722	0.59	1.4E-01	AW023630.1	EST_HUMAN	AF58903.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487465.5'
8021	21711	34864	0.97	1.4E-01	R62746.1	EST_HUMAN	Y10H05.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873.5'
8021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	Y10H05.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873.5'
8085	21774	34638	8.81	1.4E-01	BF310559.1	EST_HUMAN	801895459.F1.NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824.5'
9175	21845	35011	1.24	1.4E-01	W63411.1	EST_HUMAN	348404.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102.5' similar to contains element KER repetitive element.1
9246	21925	35098	0.46	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9246	21925	35098	0.46	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9258	21937	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9258	21937	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.86	1.4E-01	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la (JAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35651	0.97	1.4E-01	X66092.1	NT	C.parfingens ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023613.1	NT	Macromitrium levalum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9998	22638	35846	0.66	1.4E-01	AW021608.1	EST_HUMAN	AF29H08.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485064.5'
9988	22636	35847	0.56	1.4E-01	AW021608.1	EST_HUMAN	AF29H08.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485064.5'
10157	22805	35022	0.81	1.4E-01	BF376285.1	EST_HUMAN	WFR3-S10216-211259-013-408 S10218 Homo sapiens cDNA
10157	22805	35023	0.81	1.4E-01	BF376285.1	EST_HUMAN	WFR3-S10216-211259-013-408 S10218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84203.1	EST_HUMAN	Yd47003.11 Soares fetal liver spleen INF18 Homo sapiens cDNA clone IMAGE:111366.5'
10469	23148	36372	0.62	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2559451 to 2812870
10607	23301		1.64	1.4E-01	AA811480.1	EST_HUMAN	AF59803.31 NCL CGAP GC81 Homo sapiens cDNA clone IMAGE:1320364.3'
10746	23433	35676	3.24	1.4E-01	R63400.1	EST_HUMAN	Y70C05.11 Soares breast 2NB-Hat Homo sapiens cDNA clone IMAGE:154088.5'
10954	23631	35679	1.31	1.4E-01	AW104982.1	EST_HUMAN	Yd73610.X1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274.3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11038	23707	36976	1.3	1.4E-01	T66102.1	EST_HUMAN	ye47g10.11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23707	36976	1.3	1.4E-01	T66102.1	EST_HUMAN	ye47g10.11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23708	36979	2.36	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-3 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (ALA-9) (CD49E)
11282	23924	37215	1.69	1.4E-01	X69092.1	NT	C-perfringens ORF for putative membrane transport protein
11301	19867		1.41	1.4E-01	AW015373.1	EST_HUMAN	U1-H-BIO-act-c-09-0-U1 s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36446	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldhyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11512	24112		1.82	1.4E-01	X62102.1	NT	M.musculus p16K gene for 16 kDa protein
11743	24335	37661	1.83	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; IPHLP (Tolpo) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and HBAR (Hbar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW654572.1	EST_HUMAN	ht4r08.x1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2872318 3'
11827	24411	37748	1.31	1.4E-01	AW684572.1	EST_HUMAN	ht4r08.x1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2872318 3'
12213	25172	30904	1.68	1.4E-01	A300080.1	NT	Ephydella fluviatilis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P.salina plasmid gene secY
12275	24714		2.2	1.4E-01	11868117	NT	Rattus norvegicus desmin (Des), mRNA
12318	25393		2.84	1.4E-01	BE513502.1	EST_HUMAN	60131938F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3634326 5'
12413	24794		1.35	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D84004.1	NT	Synochysis sp. POC893 complete genome, 23/27 2658767-3002985
12500	25407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		6.26	1.4E-01	D82863.1	NT	Mus musculus mRNA for prolifase, complete cds
12779	25033		2.37	1.4E-01	AW377888.1	EST_HUMAN	MRO-HT0206-221299-204-008 HT0208 Homo sapiens cDNA
314	13118	25756	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25767	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25632	2.8	1.3E-01	A5013139.1	NT	Homo sapiens gene for NPS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
824	13594	26264	0.92	1.3E-01	X63330.1	NT	P. dumetili histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13769	26423	1.31	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Page 107 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1105	13862		2.6	1.3E-01	AL116285.1	NT	Bovine chimeric strain T4 cDNA library under conditions of nitrogen deprivation
1183	13948	26809	1.13	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF03 5'
1425	14172		1.18	1.3E-01	AF148277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1850	14598	27303	0.97	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Col1a1), mRNA
1852	14687	27400	2.18	1.3E-01	AL117078.1	NT	Bovine chimeric strain T4 cDNA library under conditions of nitrogen deprivation
							Rhodospirillum rubrum acidophilum pucB5, pucA6, pucB6, pucA7, pucB7, pucA8 and pucC genes and ORF151
2167	14806		1.22	1.3E-01	AJ248678.1	NT	RC4-S10173-181098-032-012 S10173 Homo sapiens cDNA
2298	15013		1.2	1.3E-01	AW612104.1	EST_HUMAN	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2376	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15306	28042	4.76	1.3E-01	M88918.1	NT	Carcinus auratus keratin type I mRNA, complete cds
3005	15531	28474	1.01	1.3E-01	AF163207.2	NT	Homo sapiens chromosome 21 segment HS210007
3443	16198	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolycopolyl transacylase mRNA, complete cds
3688	16718		1.43	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SP3a2 complete genome
4137	16879		4.24	1.3E-01	AV384341.1	EST_HUMAN	OY3-DT0018-081288-036-003 DT0018 Homo sapiens cDNA
4145	16887	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	XG2310.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2813893 3'
4257	16938	29627	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4257	16938	29628	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.78	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS210080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolycopolyl transacylase mRNA, complete cds
4497	17233	29953	2.68	1.3E-01	BE272336.1	EST_HUMAN	BM126088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4863	17688		0.74	1.3E-01	BF091880.1	EST_HUMAN	RC4-TN0077-180300-012-c05 TN0077 Homo sapiens cDNA
							hcd708.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872879 3' similar to contains L1,b1 L1
							L1 repetitive element
5242	18048	30877	0.83	1.3E-01	AV1466888.1	EST_HUMAN	QVQ-UM0093-100400-189-a08 UM0093 Homo sapiens cDNA
5278	18093	30739	2.23	1.3E-01	AV804417.1	EST_HUMAN	EMERICELLA nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5414	18213		0.77	1.3E-01	AF107793.1	NT	Emmericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5497	18295		0.75	1.3E-01	AF056880.1	NT	Hepatitis C virus 5' UTR, Cl.10 genome polyprotein gene, partial cds
5538	18433	31346	0.97	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5586	18691	31628	0.57	1.3E-01	BF527281.1	EST_HUMAN	60203937F2 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4172233 5'
5868	18881	31629	0.57	1.3E-01	BF527281.1	EST_HUMAN	60203937F2 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4172233 5'
6392	19161	32162	15.12	1.3E-01	AB031326.1	NT	Schistosoma cercariae pomb gene for Alp41, complete cds
8474	19241	32241	1.95	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6891	19508		0.75	1.3E-01	W25367.1	EST_HUMAN	2863 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Page 108 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6814	19661		0.89	1.3E-01	BF529560.1	EST_HUMAN	602044348FT NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181866 5'
7162	19849		1.96	1.3E-01	H48684.1	EST_HUMAN	Y330202.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:207075 5'
7859	20554		0.88	1.3E-01	BE272390.1	EST_HUMAN	61126068FT NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2990063 5'
7873	20568	33694	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7922	20597	33727	1.17	1.3E-01	BF690522.1	EST_HUMAN	602187016T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4299074 3'
8138	20630		0.51	1.3E-01	BE562528.1	EST_HUMAN	60135828FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:388934 5'
8172	20666	33958	0.64	1.3E-01	11421559	NT	Homo sapiens TED protein (TED), mRNA
8243	20937		4.47	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDLO54c
8285	20979		4.44	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8428	21119	34258	1.02	1.3E-01	BF60522.1	EST_HUMAN	602187016T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4299074 3'
8847	21538	34583	0.59	1.3E-01	R11172.1	EST_HUMAN	Y09911.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN :
8847	21538	34694	0.58	1.3E-01	R11172.1	EST_HUMAN	Y09911.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN :
8119	21807	34973	0.81	1.3E-01	11068003	NT	P10214 Xystella granulovirus, complete genome
8119	21807	34974	0.81	1.3E-01	11068003	NT	P10214 Xystella granulovirus, complete genome
8972	21847	35120	3.71	1.3E-01	AF023126.1	NT	Oryctolagus cuniculus H-K-ATPase alpha 2c subunit mRNA, complete cds
9671	22323		0.59	1.3E-01	N86348.1	EST_HUMAN	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9951	22599		0.99	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deaminase, type IV (Pd4), mRNA
10030	22678	35884	0.85	1.3E-01	AW851598.1	EST_HUMAN	MR2-CT022Z-207089-001-401 CT0222 Homo sapiens cDNA
10291	25128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36280	0.64	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HENBB1 Homo sapiens cDNA clone HENBB1002387 5'
10471	23117	36347	0.52	1.3E-01	AW247635.1	EST_HUMAN	2820437 3prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2820437 3'
10528	23225		2.93	1.3E-01	BF330899.1	EST_HUMAN	MR4-B10358-130 700-010-K03 B10358 Homo sapiens cDNA
10776	23459	36701	1.56	1.3E-01	H01893.1	EST_HUMAN	Y32809.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:150149 5'
11039	23710	36980	1.33	1.3E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23876		3.28	1.3E-01	6671745	NT	Mus musculus colicin 2, muscle (Col2), mRNA
11304	23953	37253	1.42	1.3E-01	BF677325.1	EST_HUMAN	602087045FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23983	37264	1.42	1.3E-01	BF677325.1	EST_HUMAN	602087045FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37504	4.28	1.3E-01	BE278449.1	EST_HUMAN	601156055FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504904 5'
11723	24317	37640	1.84	1.3E-01	BE616934.1	EST_HUMAN	601473566FT NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3876208 5'
11755	24349	37676	1.44	1.3E-01	BF683555.1	EST_HUMAN	602139760FT NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4300363 5'
12114	24607	31058	1.37	1.3E-01	BE518346.1	EST_HUMAN	601482741FT NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866093 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12247	24695		4.43	1.3E-01	AJ242790.1	NT	Gallus gallus scyl1 gene for lympholactin, exons 1-3
12274	24713		1.51	1.3E-01	Z13694.1	NT	R. norvegicus cri2 gene for crystallin related protein 2
12806	24915		1.43	1.3E-01	AB028826.1	NT	Ephyraia furcillalis mRNA for SALK-3, complete cds
12836	24936		2.26	1.3E-01	AW001114.1	EST_HUMAN	wl24d09.x1 Scores: Dieckgraebe, colon_NHGD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:060287 O60287 KIA0539 PROTEIN. ;
374	13169	25844	8.42	1.2E-01	AI421744.1	EST_HUMAN	335902.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2096539 3' similar to gb:U05760.maf
415	12828		1.05	1.2E-01	U06812.1	NT	ANEXIN V (HUMAN);
534	13317		4.33	1.2E-01	AF039442.1	NT	Dicystostellum discoideum ORF DG1018 gene, partial cds
1365	14103	26778	3.22	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1365	14103	26779	3.22	1.2E-01	AU149148.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1362	14110		4.38	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1496	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1627	14373	27062	1.26	1.2E-01	Q14834	SWISSPROT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1646	14392	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	a48905.g1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480894 3' similar to TR:Q16871
1762	14504		20.17	1.2E-01	X89211.1	NT	Q16871 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1913	14650		1.03	1.2E-01	AW446968.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
2181	14910	27842	1.75	1.2E-01	BF248490.1	EST_HUMAN	NFAT3 (NF-ATC4) (NF-AT3)
2284	15009	27748	1.2	1.2E-01	AI163213.2	NT	q65909.x1 NCL CGAP_Eac2 Homo sapiens cDNA clone IMAGE:1950553 3'
2597	15311	28047	1.49	1.2E-01	AW695567.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	UHH-B18-alc-e-10-Q-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2847	15516	28262	1.3	1.2E-01	U18018.1	NT	801821567.F1 NH_MGC_92 Homo sapiens cDNA clone IMAGE:4048224 5'
2803	15689	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS71C013
2935	15701	28350	2.92	1.2E-01	MT6384.1	NT	QV3-BN0046-220300-128-110 BN0046 Homo sapiens cDNA
3004	15770	28418	0.97	1.2E-01	X69892.1	NT	1stB907.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2228983 3' similar to TR:Q14048 Q14048
3224	15997	28941	1.59	1.2E-01	AW370668.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] contains element PTR5 repetitive element. ;
3282	16014		1.12	1.2E-01	U07600.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
3472	16228		0.8	1.2E-01	Z59118.1	NT	a60609.x1 Barstead cdnt HPLR87 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
3511	16297	28921	0.82	1.2E-01	X69892.1	NT	605 RIBOSOMAL PROTEIN L30 (HUMAN);
							Human creatine kinase-B mRNA, complete cds
							Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
							QV1-B10259-281098-021-c05 B10259 Homo sapiens cDNA
							Methanococcus jannaschii section 142 of 150 of the complete genome
							Bacillus subtilis complete genome (section 19 of 21): from 2765131 to 3013540
							Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3511	16287	28922	0.82	1.2E-01	X56882.1	NT	W heat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	18228		1.46	1.2E-01	Z89718.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4160	16900	28528	1.97	1.2E-01	Z54255.1	NT	P clarkii mRNA, repeat region (ID ZMR17)
4160	16900	29529	1.97	1.2E-01	Z54255.1	NT	P clarkii mRNA, repeat region (ID ZMR17)
4872	17408	30041	1.1	1.2E-01	Z48183.1	NT	L esculentum mRNA for glycocalyx
4739	17471		0.92	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5170	17979	30492	0.81	1.2E-01	AA744969.1	EST_HUMAN	ny63504.s1 NO1 CGAP GGB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5217	18025	30549	1	1.2E-01	AF223394.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5227	18034	30659	2.59	1.2E-01	W33035.1	EST_HUMAN	z508d02.1 Soares parathyroid tumor_NBHPA Homo sapiens cDNA clone IMAGE:321690 5'
5284	18089	30749	2.3	1.2E-01	Z98268.1	NT	Homo sapiens gene encoding diacylglycerol kinase (exons 1-13)
5418	18217	30926	0.68	1.2E-01	Z48234.1	NT	M domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.83	1.2E-01	BE620945.1	EST_HUMAN	601453518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6153	18930	31868	1.36	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6205	18981	31960	2.35	1.2E-01	AW845275.1	EST_HUMAN	IL-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6337	19107	32097	0.57	1.2E-01	AA747935.1	EST_HUMAN	ny6501.s1 NO1 CGAP GGB1 Homo sapiens cDNA clone IMAGE:1268024 3'
6550	19315	32321	1.14	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NO1 CGAP Brn67 Homo sapiens cDNA clone IMAGE:4159385 5'
6700	19816	32656	0.69	1.2E-01	AF265739.1	NT	LC virus glycoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20468		1.4	1.2E-01	BE507072.1	EST_HUMAN	PM3-BN0137-260300-002-009 BN0137 Homo sapiens cDNA
7862	20557	33683	4.36	1.2E-01	AI013753.1	EST_HUMAN	wc59g03.x1 NO1 CGAP C33 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
7905	20901	33731	0.67	1.2E-01	Q02369	SWISSPROT	Q9735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8208	20902	34037	0.73	1.2E-01	AI032681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX II-B22) (CH-B22)
							at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
8295	20986		10.29	1.2E-01	AW039852.1	EST_HUMAN	xc46d07.x1 NO1 CGAP Ewe2 Homo sapiens cDNA clone IMAGE:2567597 3' similar to gb:M13452 LAMIN A (HUMAN);
8315	21008		3.34	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34184	0.59	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 57 kD subunit (vme-2) gene, complete cds
8354	21047	34185	0.59	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 57 kD subunit (vme-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271786.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
8559	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 28 of 163 of the complete genome

Page 111 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8623	21316		0.62	1.2E-01	X15101.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9471	22060	36252	2.93	1.2E-01	X77861.1	NT	S. cerevisiae HXT5 gene
9908	22556	36750	1.69	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cui Homo sapiens cDNA clone CUAKE08 5'
10511	23305	36843	1.38	1.2E-01	BF314481.1	EST_HUMAN	601600763FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4130103 6'
10801	23484		2.17	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10899	23672		3.18	1.2E-01	BE362234.2	EST_HUMAN	601655578R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
11094	23764		1.68	1.2E-01	BF314481.1	EST_HUMAN	601600763FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF190463.1	NT	Homo sapiens dyenin intermediate chain DNAT1 (DNAT1) gene, exon 17
11283	23944	37238	1.65	1.2E-01	R40246.1	EST_HUMAN	Y60002.87 Soares Infant brain T1B1B Homo sapiens cDNA clone IMAGE:28890 3'
11492	24003		1.67	1.2E-01	M65108.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11892	24462		2.53	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLC1B12 3'
12200	24683		3.52	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04812	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW196) (CD138 ANTIGEN)
12417	24706		3.16	1.2E-01	AF168992.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; end syntaxin gene, partial cds
12419	13317		3.18	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X63681.1	NT	R. norvegicus NF66 gene for 68kDa neurofilament
12586	25384	30611	1.44	1.2E-01	BE061418.1	EST_HUMAN	QV4-B10234-111196-031-g10 B10234 Homo sapiens cDNA
12610	24917	31007	5.89	1.2E-01	AI269503.1	EST_HUMAN	q12005.x1 NQI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	O96433	SWISSPROT	GYGLIN T
12693	24982	30889	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
12800	16228		1.81	1.2E-01	Z69118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
12812	26372	30614	1.39	1.2E-01	9845282	NT	Mus musculus protein (16kDa) similar to human SYK interacting protein (p16K), mRNA
557	13334	25864	0.8	1.1E-01	AI661003.1	EST_HUMAN	h18008.X1 NQI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
601	13379	28010	1.65	1.1E-01	AA569008.1	EST_HUMAN	hmdg11.51 NQI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059920 3' similar to gb-X06995 .ms1
1032	13792	26452	2.03	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	13821		1.3	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1136	15581	26552	4.82	1.1E-01	AV1972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1227	13977	26648	3.01	1.1E-01	D64004.1	NT	EST1384142 MAGE sequences, MAGL Homo sapiens cDNA
1511	14257	26943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synedochysis sp. FCC8803 complete genome, 23/27, 268767-3002965
2312	15037		1.85	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (P16a), mRNA

Page 112 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2540	15530		1	1.1E-01	6978676	NT	Rattus norvegicus Procollagen I alpha 1 (Col2a1), mRNA
2572	15286		1.17	1.1E-01	AW821009.1	EST_HUMAN	RCO-ST0376-210100-032-g04 S10376 Homo sapiens cDNA
3030	15768	28442	0.82	1.1E-01	F03285.1	EST_HUMAN	HSC-IRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
3336	19306		1.76	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caen1a1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393186.1	EST_HUMAN	601306878F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3444	16200	28850	1.21	1.1E-01	X62193.1	NT	Chenhardt nuclear gene on linkage group XIX
3570	16325	28972	0.77	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEKIN XI (CALCYCLIN-ASSOCIATED ANNEKIN 80) (CAP-50)
3698	16450	29089	1.47	1.1E-01	X52708.1	NT	G.ellus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4090	16833	29458	1.28	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4090	16833	29457	1.28	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4226	16937		8.78	1.1E-01	AF167066.1	NT	Drosophila melanogaster Karsicht protein (kar) mRNA, complete cds
4254	16935	29624	0.77	1.1E-01	AW802058.1	EST_HUMAN	LS-LM0070-020500-069-g03 LM0070 Homo sapiens cDNA
4394	17329	29656	0.96	1.1E-01	S44957.1	NT	Tape-1 integral membrane protein TAPA-1 [rice, B cell lymphoma line 35C13, Genomic, 1973 nt, segment 1 of 7]
4780	17612	30134	1.2	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
4957	18339		0.65	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II region/butyrophilin-like protein gene, partial cds; Nucleo4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-FP, and tenascin X (TNX) genes, complex
5077	17759	30412	1	1.1E-01	P70281	SWISSPROT	SYNAPTOMIAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18341		1.4	1.1E-01	AA747216.1	EST_HUMAN	nc76603.s1 NCL_CGAP_Ewt Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element/contains element MER35 repetitive element.
5593	18498	31391	1.23	1.1E-01	AF020827.1	NT	G Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5697	18490	31399	0.58	1.1E-01	AL110985.1	NT	Borvita chinea strain T4 cDNA library under conditions of nitrogen deprivation
5745	19537	31459	1.81	1.1E-01	X68851.1	NT	S. pombe sub gene encoding protein kinase
5781	19572	31500	6.31	1.1E-01	M65533.1	NT	Providencia reitgeri penicillin G amidase gene
5836	18737	31676	1.67	1.1E-01	AJ007873.1	NT	Homo sapiens LGMD25 gene
5855	18737	31668	1.75	1.1E-01	BE769762.1	EST_HUMAN	PM3-F10024-130000-004-f12 F10024 Homo sapiens cDNA
5975	18757	31719	8.4	1.1E-01	AW855899.1	EST_HUMAN	RC3-C02054-290398-011-e01 C02054 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	AF163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.26	1.1E-01	AF1635746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6381	19150	32149	0.72	1.1E-01	A1216307.1	EST_HUMAN	q97600.x1 Saccharomyces cerevisiae NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841089 3'
6512	19277	32278	3.71	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6804	19397		3.03	1.1E-01	AF032822.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6697	19814	32685	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6648	19430	32445	0.7	1.1E-01	AE002105.1	NT	Ureaplasma urealyticum section 59 of 59 of the complete genome
6648	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 59 of 59 of the complete genome
7087	25423	32875	0.89	1.1E-01	BF382758.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7203	25107	32884	0.84	1.1E-01	AF000005.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 116901-148500 nt, position (87)
7435	20112	33109	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.83	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7595	20283	33371	3.35	1.1E-01	AA788784.1	EST_HUMAN	at31b08.s1 Scores, parathyroid, tumor, NHPA Homo sapiens cDNA clone 12/0403 3' similar to gb.J03483
7698	20663	33660	0.8	1.1E-01	U87462.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8047	20601	33933	1.7	1.1E-01	AA463574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20601	33934	1.7	1.1E-01	AA463574.1	EST_HUMAN	nt04910.t1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X61233.1	NT	nt04910.t1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8183	20887	34081	1.14	1.1E-01	AA1817818.1	EST_HUMAN	H.sapiens IL15 gene
8246	20943	34081	1.45	1.1E-01	AL134346.1	EST_HUMAN	PX1-ST0270-08020-001-f09 ST0270 Homo sapiens cDNA
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	DKFZp447P194.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp447P194.1 5'
8810	21602	34649	0.68	1.1E-01	AI807474.1	EST_HUMAN	Pedibacillus acidilactici H plasmid pSMB74 pediclin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8908	21597	34759	0.47	1.1E-01	AF000081.1	NT	wf48d01.x1 Scores, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
8941	21632	34776	2.04	1.1E-01	AA182153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34776	2.04	1.1E-01	AA182153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9033	21723	34877	0.74	1.1E-01	Y12727.1	NT	z063b12.r1 Stratiogene muscle 637209 Homo sapiens cDNA clone IMAGE:827743 5'
9063	21762	34912	2.04	1.1E-01	TT2876.1	EST_HUMAN	z063b12.r1 Stratiogene muscle 637209 Homo sapiens cDNA clone IMAGE:827743 5'
9090	21778	34912	0.8	1.1E-01	BE693260.1	EST_HUMAN	P. fulvus partial dph5 gene and argf gene
9322	21889	35189	0.88	1.1E-01	BE142905.1	EST_HUMAN	cd19003.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9366	22058	35189	0.88	1.1E-01	BE142905.1	EST_HUMAN	gb.M818181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9810	22461	35189	0.88	1.1E-01	BF085149.1	EST_HUMAN	601438972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
10017	22655	35189	0.88	1.1E-01	BF085149.1	EST_HUMAN	CM3-HT0142-271 089-026-p11 HT0142 Homo sapiens cDNA
10108	22764	35189	0.88	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040500-005-008 GN0027 Homo sapiens cDNA
10235	22863	35189	0.88	1.1E-01	BF085149.1	EST_HUMAN	Arabisopsis italica DNA chromosome 4, contig fragment No. 43
10708	15798	28442	2.05	1.1E-01	F03265.1	EST_HUMAN	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
							y06600.s1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:147084 3'
							Cerebellar capillary vovo retinoblastoma gap-like, pol-like and env-like genes, complete cds
							HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1702 3'

Page 114 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
10840	23622		2.75	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
10874	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	Y35F12.11 Soares placenta NizCHP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
10983	23658	36911	1.39	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Borytes ciferrea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37018	1.68	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11169	23896	37117	3.21	1.1E-01	Z171910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11169	23936	37118	3.21	1.1E-01	Z171910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11277	23938	37220	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24269		1.65	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11690	24529		1.36	1.1E-01	AA182153.1	EST_HUMAN	Zp33b12.11 Stizalagene muscle 937209 Homo sapiens cDNA clone IMAGE:927743 5'
12086	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112:120800.014-03 NT0112 Homo sapiens cDNA
12341	25160		1.97	1.1E-01	BE974958.1	EST_HUMAN	607680551R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4134085 3'
12750	25012	30977	3.15	1.1E-01	BF239753.1	EST_HUMAN	607680551R2 NIH_MGC 84 Homo sapiens cDNA clone IMAGE:4134085 6'
1178	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13998	26855	2.83	1.0E-01	AI985459.1	EST_HUMAN	ws08401.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 MER7 repetitive element;
1371	14119	26784	1.95	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2493	15210	27952	1.11	1.0E-01	AW451365.1	EST_HUMAN	UHH-BB-dic-07-Q-U1s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3593	16259	28913	1.19	1.0E-01	BF093391.1	EST_HUMAN	60146501F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3859849 5'
3708	16461	29100	1.03	1.0E-01	BF239518.1	EST_HUMAN	601608489F1 NIH_MGC 84 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16569	29200	0.98	1.0E-01	AF237051.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3817	16569	29201	0.98	1.0E-01	AF237051.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	16685	29320	2.53	1.0E-01	BF369703.1	EST_HUMAN	QY2-NT0048:160800-318-e05 NT0048 Homo sapiens cDNA
4318	17263		0.95	1.0E-01	AI792349.1	EST_HUMAN	an320a.y5 Geassier Wilms tumor Homo sapiens cDNA clone IMAGE:1700359 5'
4684	17308	30032	1.19	1.0E-01	U60450.1	NT	Drosophila melanogaster tyrosine kinase p45 lacform (fry) mRNA, complete cds
4686	17694	30217	2.35	1.0E-01	AW952344.1	EST_HUMAN	EST36414.4 IMAGE:160800-318-e05 NT0048 Homo sapiens cDNA
5235	18044		9.73	1.0E-01	W66490.1	EST_HUMAN	ZH62ND4.s1 Soares_Yield_liver_spleen_TNF1S_5T Homo sapiens cDNA clone IMAGE:416859 3'
5789	18590		1.21	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
5834	18717	31675	14.15	1.0E-01	AF274975.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6243	19017	31691	0.99	1.0E-01	AA481979.1	EST_HUMAN	zw41010.s1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:756259 3' similar to contains
6259	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	L1.13.L1 repetitive element;
							z6167612.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'

Page 115 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6824	18660		1.81	1.0E-01	R23821.1	EST_HUMAN	yh34hd08.1 Scores placenta Nb2HP Homo sapiens cDNA IMAGE:131675 5' similar to contains Alu repetitive element;
7635	20300		2.67	1.0E-01	Y12488.1	NT	M musculus with gene
7709	20373	33488	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7708	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20529	33686	0.65	1.0E-01	AA061091.1	EST_HUMAN	alc2p01.s1 Scores_basla_NHT Homo sapiens cDNA clone IMAGE:1407668 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	47583555	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.96	1.0E-01	AW189787.1	EST_HUMAN	x08b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN) contains TAR1.13 TAR1 repetitive element;
8084	21773	34637	1.04	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synanon mRNA, complete cds
8395	22057	35228	0.51	1.0E-01	R44863.1	EST_HUMAN	y53hd04.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34649 3'
9407	22069		1.6	1.0E-01	M76728.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
8450	22000		3.02	1.0E-01	AE001501.1	NT	Helicobacter pylori strain J99 section 62 of 132 of the complete genome
8464	22074	35245	0.75	1.0E-01	W01955.1	EST_HUMAN	z08610.s1 Scores_fetal_Heart_NBH19W Homo sapiens cDNA clone IMAGE:327282 3'
8721	22372	35571	1.67	1.0E-01	BF240154.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046769.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046769.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST356915 IMAGE resequences, IMAGE Homo sapiens cDNA
10048	22696	35912					y52hd03.s1 Striatagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10228	22877	36089	0.51	1.0E-01	T51952.1	EST_HUMAN	contains Alu repetitive element
10554	23250		0.89	1.0E-01	BE782760.1	EST_HUMAN	601564604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3930366 5'
10358	23534	36884	1.95	1.0E-01	AU169127.1	EST_HUMAN	AU169127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10358	23534	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10358	23534	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23983	37283	5.22	1.0E-01	BE780343.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
11510	24110		1.52	1.0E-01	AF000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain RIMD 0509952
11594	24193	37511	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for GLC-b chloride channel protein
11594	24193	37512	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for GLC-b chloride channel protein
11832	24416	37755	1.89	1.0E-01	AY048035.1	EST_HUMAN	AY048035 GLC Homo sapiens cDNA clone GLCSPG01 3'
11832	24416	37756	1.89	1.0E-01	AY048035.1	EST_HUMAN	AY048035 GLC Homo sapiens cDNA clone GLCSPG01 3'
12083	24921		4.32	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3461593 5'
12300	24725		1.71	1.0E-01	7862195	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

Page 118 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12317	24798		2.22	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12814	24821		2.74	1.0E-01	BE537718.1	EST_HUMAN	901005554FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12877	25318		5.03	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25502		9.8	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15488	28224	1.27	9.8E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2790	15495	28235	1.53	9.8E-02	BE545554.1	EST_HUMAN	901070219FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455365 5'
2790	15495	28235	1.53	9.8E-02	BE545554.1	EST_HUMAN	901070219FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455365 5'
3260	16022	26871	1.32	9.8E-02	AF009810.1	NT	Homo sapiens neurexin III alpha gene, partial cds
3653	16583	29324	0.73	9.8E-02	AB21637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor Nkx-HOT Homo sapiens cDNA clone IMAGE:740532 3'
4632	17387	30003	0.93	9.8E-02	BE574249.1	EST_HUMAN	7d77c12.x1 NCL CGAP_L024 Homo sapiens cDNA clone IMAGE:3278998 3'
8875	17951	30547	9.17	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7815	20510	33534	0.83	9.8E-02	AW103088.1	EST_HUMAN	repetitive element; contains element MIR MIR repetitive element ;
7815	20510	33535	0.93	9.8E-02	AW103088.1	EST_HUMAN	repetitive element; contains element MIR MIR repetitive element ;
9150	21897	35055	0.98	9.8E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O sativa RAmv3C gene for alpha-amyase
3100	15865		0.9	9.8E-02	4504578	NT	Homo sapiens 1 factor (complement) (IF) mRNA
3142	15908	28550	3.84	9.8E-02	AF184274.1	NT	Daucus carota leucocoryneidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4168	16538	29564	6.24	9.8E-02	AF257329.1	NT	Leptospheria maculans beta-tubulin mRNA, complete cds
4168	16538	29565	6.24	9.8E-02	AF267329.1	NT	Leptospheria maculans beta-tubulin mRNA, complete cds
7381	20091		0.77	9.8E-02	X54133.1	NT	Human HPTF delta mRNA for protein tyrosine phosphatase delta
9153	21894		1.18	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11437	22204	36438	2.05	9.8E-02	BF037421.1	EST_HUMAN	901480793FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
12052	24570		1.78	9.8E-02	8393761	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1328	14077	26752	1.31	9.7E-02	AB006808.1	NT	Alice arborensis mRNA for NADP-malic enzyme, complete cds
1580	14328		1.49	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), mRNA
2257	14384	27724	2.08	9.7E-02	BE168600.1	EST_HUMAN	OV14-HT0516(6-070306-095-c04) HT0516 Homo sapiens cDNA
3965	16714		3.49	9.7E-02	Q39795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18097	30695	0.94	9.7E-02	AF009189.1	NT	Caulobacter crescentus thymellate kinase (tkm) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripior
5261	18097	30896	0.94	9.7E-02	AF069189.1	NT	Caulobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnac) genes, complete cds
5924	18708	31662	1.43	9.7E-02	AF065447.1	EST_HUMAN	EST1365546 IMAGE resequences, MAGC Homo sapiens cDNA
7198	18934	32958	3.24	9.7E-02	Z69118.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
7882	20577	33705	1.28	9.7E-02	N22768.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22768.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	AI065398.1	EST_HUMAN	wf78606.x1 NCI_OGAP_Ov48 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:52851_nai PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11162	23819	35837	2.84	9.7E-02	U58337.1	NT	Mus musculus Igalpha (Lgln) mRNA, partial cds
2009	14744	27470	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47411.x1 Soares NIH/NIH/NIH S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2009	14744	27471	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47411.x1 Soares NIH/NIH/NIH S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4311	17050	29875	5.8	9.6E-02	Z32688.2	NT	Protein fibrillin fibrillar protein, strain H14320
4940	17698	30276	0.99	9.6E-02	AV066230.1	EST_HUMAN	EST1378303 IMAGE resequences, MAGC Homo sapiens cDNA
8014	18795	30276	3.13	9.6E-02	BE910039.1	EST_HUMAN	601489089FT NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3900165 5'
8274	20888	35300	0.8	9.6E-02	AI0137084.1	EST_HUMAN	AI0137084 PLACE1 Homo sapiens cDNA clone IMAGE:1005740 5'
9444	22121	35300	1.31	9.6E-02	AV067898.1	EST_HUMAN	AV067898 GKC Homo sapiens cDNA clone IMAGE:3919963 5'
9772	22423	35760	1.12	9.6E-02	BE884896.1	EST_HUMAN	601434080FT NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3919963 5'
9839	22597	35760	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
9839	22597	35761	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22658	35884	0.5	9.6E-02	BE077270.1	EST_HUMAN	602086769FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4250969 5'
10051	22698	35915	1.54	9.6E-02	AB013965.1	NT	Antirrhinum majus transposon Tami3 pseudogene for transposase (in S-5 copy)
10051	22698	35916	1.54	9.6E-02	AB013965.1	NT	Antirrhinum majus transposon Tami3 pseudogene for transposase (in S-5 copy)
10158	22806	36024	3.35	9.6E-02	PC08174	SWISSPROT	COMPLEMENT DECAT-ACCELERATING FACTOR PRECURSOR (CD55)
10643	23334	34572	7.22	9.6E-02	Z78702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102162
12852	24954	39442	3.34	9.6E-02	HI4590.1	EST_HUMAN	INT19003.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'
4081	16625	29442	2.1	9.5E-02	AV092398.1	EST_HUMAN	GM2-9N0023-05020-087-f12 BN0023 Homo sapiens cDNA
5979	18376	31289	0.85	9.5E-02	PF1654	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
6988	19691	32729	0.85	9.5E-02	AA780728.1	EST_HUMAN	ac86908 at 1 Stradegene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7202	19698	32663	4.72	9.5E-02	AB003473.1	NT	Trimeric virus flavivirus DNA for phospholipase A2 inhibitor, complete cds
7467	20141	33234	7.68	9.5E-02	AI161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7597	19376	31289	0.84	9.5E-02	PF1654	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7780	20476	33600	1.83	9.5E-02	BF038861.1	EST_HUMAN	601453942F NIH_MGC 96 Homo sapiens cDNA clone IMAGE:3857243 5'
7780	20476	33601	1.83	9.5E-02	BF038861.1	EST_HUMAN	601453942F NIH_MGC 96 Homo sapiens cDNA clone IMAGE:3857243 5'
10578	23273	36508	2.36	9.5E-02	BF035661.1	EST_HUMAN	601453942F NIH_MGC 96 Homo sapiens cDNA clone IMAGE:3857243 5'

Page 118 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10578	23273	38510	2.38	9.5E-02	BF035891.1	EST_HUMAN	60145382F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857249 5'
1825	14584	27278	2.82	9.4E-02	BF871093.1	EST_HUMAN	602150083F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281617 5'
1857	14595	27310	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14595	27311	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	16910	23249	4.43	9.4E-02	Z33059.1	NT	M. capricornus DNA for CONTIG MC073
6225	18959	31978	0.83	9.4E-02	AF087383.1	NT	Triticum aestivum heat shock protein 101 [Hsp101a] mRNA, complete cds
8498	21190		2.48	9.4E-02	Z46953.1	NT	Acinetobacter sp. cysD, cobQ, cobM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
10851	20186	33258	2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p135 gene, partial cds
11941	25255		1.78	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12571	24985		1.92	9.4E-02	AF186036.1	NT	Mycoplasma pulmonis hypothetical membrane protein P93 gene, complete cds
2886	15784		1.97	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3026	15782		6.32	9.3E-02	6912526	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3251	16013	28695	1.85	9.3E-02	BF575511.1	EST_HUMAN	602133089F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	29502	3.51	9.3E-02	BE331943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4132	16874	29503	3.51	9.3E-02	BE331943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4695	17419		2.04	9.3E-02	AY732224.1	EST_HUMAN	AY732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5576	18373		0.67	9.3E-02	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8146	20840	33972	0.62	9.3E-02	AW566007.1	EST_HUMAN	EST169 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
8910	22283	35449	2.15	9.3E-02	BE902831.2	EST_HUMAN	60165988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10091	22739	35953	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10091	22739	35954	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22866		3.5	9.3E-02	AW208117.1	EST_HUMAN	U11H-B11-afix-H65-Q-U1st NCL CGAP_S033 Homo sapiens cDNA clone IMAGE:2723553 3'
12194	25181		2.61	9.3E-02	AJ248850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA pyrase B subunit
12560	25209		8.43	9.3E-02	AW458950.1	EST_HUMAN	h22812.1 Soares_NFL_T_GBG_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Blnp1 (BING1), tapasin (tapasin), RaGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), belar1, 3-galactosyl transferase (belar1.3-galactosyl t-)
12752	25254		2.1	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25668	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25669	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2224	14852		1.88	9.2E-02	R64155.1	EST_HUMAN	Y69807.7 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:41618 5'
3175	15938	28587	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16081	28709	0.85	9.2E-02	A4534354.1	EST_HUMAN	nt7990.1st NCL_CGAP_C033 Homo sapiens cDNA clone IMAGE:923135 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3573	16328		1.28	9.2E-02	6755216	NT	Mus musculus pre T-cell antigen receptor alpha (Piera), mRNA
4213	19594		0.99	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4274	17013		0.78	9.2E-02	BE289722.1	EST_HUMAN	600844365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
7807	20802	33732	1.88	9.2E-02	T48920.1	EST_HUMAN	y99008.1 Stratagene placenta (8937225) Homo sapiens cDNA clone IMAGE:68908 5' similar to gb-X56509 GUANINE NUCLEOTIDE-BINDING PROTEIN G(9), ALPHA SUBUNIT (HUMAN)
8076	20770	33659	2.2	9.2E-02	X95256.1	NT	H valera 3 case isomerase gene
11695	24280	37614	1.27	9.2E-02	AF026852.3	NT	Mesocricetus auratus oxidochlorin precursor (OVI) gene, complete cds
12739	25412		1.4	9.2E-02	11498872	NT	Podiceps anserinus mitochondrion, complete genome
414	12825	25438	4.19	9.1E-02	X77955.1	NT	O. cuniculus k12 keratin gene
4451	17187	26812	1.33	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5843	18438	31352	1.44	9.1E-02	AF128756.1	NT	Homo sapiens MSH455 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TC7, LST-1, LTB, TNF, and LTA genes, complete cds
7285	19588	33045	14.94	9.1E-02	AW160658.1	EST_HUMAN	au74605.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7575	20244	33349	0.78	9.1E-02	AF000051.1	NT	Aeropyrum pernix genomic DNA, section 47
7609	20275	33363	0.72	9.1E-02	U86073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
8822	21614	34659	0.88	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10327	22974		1.37	9.1E-02	T02984.1	EST_HUMAN	FB18F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
10354	23001	36218	1.25	9.1E-02	S74050.1	NT	Tg918-CyJ actin (Tripleneustes grillaxia-sea urchins, embryos, Genomic, 5275 nt)
10383	23029	36244	1.19	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12110	23548		1.4	9.1E-02	AA179901.1	EST_HUMAN	z38b12.31 Stratagene muscle 037209 Homo sapiens cDNA clone IMAGE:811783 3' similar to SW-TRT3_HUMAN P43378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA1 ;
12181	24653		2.12	9.1E-02	AF052893.1	NT	Rattus norvegicus cell cycle protein p56CDC gene, complete cds
12837	25204		1.93	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	13801	26155	4.3	9.0E-02	P15528	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED RECEPTOR MOV19) (KB CELLS FBP)
1631	14377	27064	5.28	9.0E-02	BE220482.1	EST_HUMAN	h93910.1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2806	15511	28252	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8095-05 from USA envelope glycoprotein (env) gene, partial cds
2808	15511	28253	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8095-05 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28144	0.84	9.0E-02	AF276735.1	NT	Dicystidium discidium spore coat structural protein SP65 (cds) gene, complete cds
4619	17354	29959	3.27	9.0E-02	X65740.2	NT	Plasmidium talcitarum P-type ATPase 3 gene

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5908	18691	31940	5.21	8.0E-02	W59037.1	EST_HUMAN	z68642.7 Soares_fetal_lung_NH-L19W Homo sapiens cDNA clone IMAGE:297694 5' similar to
6819	19381		1.14	9.0E-02	BF062651.1	EST_HUMAN	PIR35521Y1 S52171 small G protein - human ;
6868	19535	32619	0.72	8.0E-02	R62805.1	EST_HUMAN	7h33033.x1 NCL_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
12486	24845		2.01	9.0E-02	AF022238.1	NT	X11508.s1 Soares placenta Nk2H2P Homo sapiens cDNA clone IMAGE:138903 3'
1418	14165	26849	1.99	8.9E-02	BF701593.1	EST_HUMAN	Escherichia coli strain E2348/69 pathogenicity island, rOrt1 (rOrt1), rOrt2 (rOrt2), EsecR (escR), EsecS (escS), EsecT (escT), EsecU (escU), CseD (cseD), EsecQ (escQ), EsecJ (escJ), SepZ (sepZ), EsecV (escV), EsecN (escN), SepD (sepD), Tr (tr), OrfU (orfU), >
1418	14166	26850	1.99	8.9E-02	BF701593.1	EST_HUMAN	602126030.F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285551 5'
2396	15107	27846	1.22	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT03039-251169-003-001 HT03039 Homo sapiens cDNA
4175	16915		1.93	8.9E-02	AF266055.1	NT	Aurichum angustatum AtranF62 protein (AtranF62) gene, partial cds
5760	18552	31474	3.22	8.6E-02	AW462122.1	EST_HUMAN	U1-H818-4b-f08-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5760	18552	31475	3.22	8.6E-02	AW462122.1	EST_HUMAN	U1-H818-4b-f08-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5776	18567	31496	3.39	8.6E-02	11433478	NT	Homo sapiens similar to endoxyean (H. sapiens) (LOC83107). mRNA
7093	19782	32848	1.64	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE: METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7458	20132		2.06	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6PA2078
7849	20644	33768	1.08	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
8030	20725	33858	0.72	8.9E-02	BF701685.1	EST_HUMAN	602126111.F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285527 5'
8030	20725	33859	0.72	8.9E-02	BF701685.1	EST_HUMAN	602126111.F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285527 5'
8466	21188	34331	4.72	8.9E-02	AA309319.1	EST_HUMAN	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9520	22173	35356	0.8	8.9E-02	AI285927.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_LymB Homo sapiens cDNA clone IMAGE:1988890 3' similar to contains MER10.b1 MER10 repetitive element ;
9520	22173	35357	0.8	8.9E-02	AI285927.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_LymB Homo sapiens cDNA clone IMAGE:1988890 3' similar to contains MER10.b1 MER10 repetitive element ;
9632	22284	35477	0.79	8.9E-02	AA339355.1	EST_HUMAN	EST144544 Fetal brain 1 Homo sapiens cDNA 5' end
11592	25173		1.49	8.9E-02	P30143	SWISSPROT	HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (HGPRT) (HGPRT) (HGPRT)
11940	26207		1.48	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12085	24591		3.08	8.9E-02	BF686918.1	EST_HUMAN	602126832.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12984	24716		1.67	8.9E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1352	14100	28775	1.59	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3893	19533	29272	1.03	8.6E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TF1D 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII100)
4214	16955		0.99	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4259	17009		1.27	8.8E-02	4590423	NT	Homo sapiens paired box gene 6 (enfilid, keratilis) (PAX6), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8868	21577	34719	1.07	8.8E-02	A4151872.1	EST_HUMAN	z55905.s1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE264455.1	EST_HUMAN	8071191770F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3335648 5'
11062	23732	37004	2.7	8.8E-02	BE264455.1	EST_HUMAN	8071191770F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3335648 5'
11228	23891	37178	6.92	8.8E-02	AL040120.1	EST_HUMAN	DKFZp434D1313.1 t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24641	31098	2.66	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL283w
1642	14388	27077	1.15	8.7E-02	A167281.1	EST_HUMAN	ox65801.s1 Soares_NHHMPQ.S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3681	19434	28077	3.66	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	19434	28078	3.66	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178635.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
6231	18037	30663	5.89	8.7E-02	AA268975.1	EST_HUMAN	z55503.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6231	18037	30664	5.88	8.7E-02	AA268975.1	EST_HUMAN	z55503.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32812	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcng1 gene for potassium channel protein, exons 10-14
8748	19578	32813	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcng1 gene for potassium channel protein, exons 10-14
6943	19425	32440	0.71	8.7E-02	AF281342.1	NT	Oncofynchus mykiss TAT-binding protein 1 mRNA, partial cds
7161	20457		0.45	8.7E-02	AA264532.1	EST_HUMAN	z20a03.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:713692 3'
8413	21106	34245	0.9	8.7E-02	AE034787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10810	23304		2.46	8.7E-02	LO4758.1	NT	Oryctolagus cuniculus cyclochrome P-450 (CYP4A4) gene, 5' end
11282	23943	37237	2.55	8.7E-02	AJ007763.1	NT	Glucobacter oxydans RNA-III and RNA-IIIa genes
12145	24633		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	6879037	NT	Mus musculus nidogen 2 (Nid2), mRNA
1230	13979	28649	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region, segment 2/2
2240	14888	27706	1.82	8.6E-02	BE408687.1	EST_HUMAN	801304016F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3639643 5'
3183	15946	28568	4.57	8.6E-02	LD5468.1	NT	Trichomonas vaginalis beta-tubulin (btu51) gene, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3635	18988		3.77	8.6E-02	AF163932.1	NT	Dichyetalium discoidium adenyl cyclase (aca) gene, complete cds
5134	17852		0.86	8.6E-02	BF570280.1	EST_HUMAN	60218716T1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4310289 3'
6003	17874	31748	4.75	8.6E-02	Y10828.1	NT	Homo sapiens LCNTb gene
6281	19054	32033	1.58	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6281	19054	32034	1.58	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7481	20153	33248	1.34	8.6E-02	P14818	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (R-RELATED RECEPTOR)
7831	20526	33651	1.25	8.6E-02	5730068	NT	Homo sapiens Smr2-related GTP activator protein (SRGAP) mRNA
7831	20526	33652	1.25	8.6E-02	5730068	NT	Homo sapiens Smr2-related GTP activator protein (SRGAP) mRNA
7669	20664	33788	0.62	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8031	20726		0.81	8.6E-02	U80168.1	NT	Dichyetalium discoidium proteasome subunit C2 homolog P4C (p4C) gene, complete cds
8037	22268	35482	1.78	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 legged2 gene, complete cds; and unknown gene
8672	22325		0.58	8.6E-02	AW682183.1	EST_HUMAN	h120D08.x1 NCL_CGAP_17 Homo sapiens cDNA clone IMAGE:2872846 3'
10053	22701	35918	0.81	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10865	23545	38782	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10865	23545	38793	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	23877	37163	4.64	8.6E-02	BF305906.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138216 5'
11214	23877	37164	4.64	8.6E-02	BF305906.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138216 5'
11417	23184	38414	5.97	8.6E-02	AE01073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11568	24187	37481	2.11	8.6E-02	AF283860.1	NT	Bacillus stearothermophilus BarF methylase (FM) and BarF1 restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.6E-02	AE000862.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.6E-02	AA985491.1	EST_HUMAN	q83607.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA
5821	18417		1.29	8.6E-02	P08089	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5921	18706	31659	6.95	8.6E-02	AF283865.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8904	21199	34340	1.65	8.6E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35591	2.81	8.6E-02	BE833054.1	EST_HUMAN	RCA-OT0037-200700-014-05 OT0037 Homo sapiens cDNA
9736	22387	35592	2.81	8.6E-02	BE833054.1	EST_HUMAN	RCA-OT0037-200700-014-05 OT0037 Homo sapiens cDNA
10261	22809	36119	0.54	8.6E-02	X76731.1	NT	Vammodys gene for ammodys C
10382	23028	36243	0.87	8.6E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11105	23775		8.87	8.6E-02	AF155310.1	NT	Homo sapiens leparinase precursor, mRNA, complete cds
11125	23764	37070	4.43	8.6E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12700	24981		3.8	8.5E-02	AA322934.1	EST_HUMAN	EST127236 Ovary II Homo sapiens cDNA 5' end
2872	15902	28121	3.73	8.4E-02	W69330.1	EST_HUMAN	zf44611.1 Soares_Yeai1.NBH19W Homo sapiens cDNA clone IMAGE:343532 5'
3301	18535	29184	1	8.4E-02	A1827588.1	EST_HUMAN	W01011.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSK1 repetitive element.
4321	17060	29685	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycocortin alpha-subunit mRNA, complete cds
4321	17060	29686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycocortin alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042565.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5229	19035	30661	9.84	8.4E-02	BE287153.1	EST_HUMAN	601190439F1 NIH_JGCC_7 Homo sapiens cDNA clone IMAGE:3534383 5'
6590	18353	32368	1.72	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7028	20623	33751	7.18	8.4E-02	BE086074.1	EST_HUMAN	CX3-BT0700-260400-152-05 BT0700 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218690.1	NT	Homo sapiens atratin precursor (ATRIN) gene, exon 2
10260	22608	38118	1.83	8.4E-02	A1735184.1	EST_HUMAN	aa88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
12070	24584	31122	1.68	8.4E-02	R79408.1	EST_HUMAN	y83112.1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27485	0.92	8.3E-02	5535680	NT	hodes hexagonus mitochondrion, complete genome
2005	14741	27486	0.92	8.3E-02	5535680	NT	hodes hexagonus mitochondrion, complete genome
3660	16935	29680	6.91	8.3E-02	P75334	SWISSPROT	HYPOPHYSICAL LIPOPROTEIN MG3099 HOMOLOG PRECURSOR
3607	16360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	h82g08.x1 Soares_NHMP1_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3607	16360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	h82g08.x1 Soares_NHMP1_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6168	18943	31814	1.05	8.3E-02	A1942338.1	EST_HUMAN	w078f1.x1 NGL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:2481581 3'
6273	19046	32023	3.05	8.3E-02	AF052933.1	NT	Homo sapiens proteasome 43 gene, exon 1
7880	20375	33702	2.98	8.3E-02	AF165787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
7911	20606		1.46	8.3E-02	AA845295.1	EST_HUMAN	q88g08.x1 NGL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1458422 3' similar to contains L1:1 L1 L1
8198	20892		1.32	8.3E-02	AA987873.1	EST_HUMAN	q81f10.s1 NGL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1592779 3'
9438	22116	35291	1.41	8.3E-02	AW893503.1	EST_HUMAN	la05110.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q16332 Q15332 GAMMA
9451	22001		1.88	8.3E-02	AL161595.2	NT	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
10240	22688		0.49	8.3E-02	AF020408.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
12158	23553		1.67	8.3E-02	BE585458.1	EST_HUMAN	Dicotyledon discoidium DocA (dca) mRNA, complete cds
1357	14105		7.15	8.2E-02	Y08170.2	NT	60164470F1 NIH_JGCC_56 Homo sapiens cDNA clone IMAGE:3929863 5'
1481	14228	28914	1.69	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
3071	15837		2.07	8.2E-02	AL163205.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3784	18536		1.35	8.2E-02	AL161488.2	NT	Homo sapiens chromosome 21 segment HS21C008
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3988	16737	28371	1.07	8.2E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C006
4251	16892	28617	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
4251	16892	28618	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16892	28619	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76003.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5070	17789		2.39	8.2E-02	Z66893.1	NT	T. infantum transposon Resides DNA
5252	19068	30687	1.49	8.2E-02	BE697030.1	EST_HUMAN	6014936576T NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	19691	32707	3.09	8.2E-02	AF306555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20288		0.57	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8670	21382	34509	2.95	8.2E-02	AW875128.1	EST_HUMAN	RC2-PT0004-031.295-011-405 PT0004 Homo sapiens cDNA
8498	22162	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9653	22316	35512	2.24	8.2E-02	BE254318.1	EST_HUMAN	601175055F1 NIH_VGCG 16 Homo sapiens cDNA clone IMAGE:3355598 5'
12164	24646	31102	4.03	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12554	25138		3.65	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6688	18463	31378	0.79	8.1E-02	AE004008.1	NT	Xyella fastidiosa, section 152 of 229 of the complete genome
6286	18059	32040	1.19	8.1E-02	T11632.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7097	19786		0.66	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
7482	20154		1.25	8.1E-02	A1692681.1	EST_HUMAN	w38808.x1 NCL CGAP LU24 Homo sapiens cDNA clone IMAGE:2338503 3'
8288	20932	34097	0.81	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060). mRNA
8238	20932	34088	0.81	8.1E-02	AY006150.1	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060). mRNA
9812	22463		1.64	8.1E-02	AY006150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	16534	25447	5.03	8.0E-02	AV954663.1	EST_HUMAN	EST366723 IMAGE resequences, MAGC Homo sapiens cDNA
915	13682	28344	0.78	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1694	15576	27134	9.85	8.0E-02	D26633.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1894	14576	27135	9.85	8.0E-02	D26633.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1996	14633	27343	3.27	8.0E-02	BE063719.1	EST_HUMAN	PM3-BT10347-170200-001-B08 BT10347 Homo sapiens cDNA
2374	15006	27635	1.09	8.0E-02	D09915.1	NT	Synschoyocytis sp. POC8603 complete genome, 1727 2137259-2287259
2374	15006	27636	1.09	8.0E-02	D09915.1	NT	Synschoyocytis sp. POC8603 complete genome, 1727 2137259-2287259
2473	15191		4.2	8.0E-02	BF298744.1	EST_HUMAN	601855546F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4075618 5'
2823	13827	28486	0.98	8.0E-02	M23449.1	NT	Dicyleosellum cylindricum cyclic nucleotide phosphodiesterase gene, complete cds
2901	15687	28315	1.45	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3797	16549	29182	1.01	8.0E-02	AV9566118.1	EST_HUMAN	EST378181 IMAGE resequences, MAG1 Homo sapiens cDNA

Page 125 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4725	17457	30083	1.43	8.0E-02	AI034202.1	EST_HUMAN	531g02.21 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4764	17498		6.33	8.0E-02	X72794.1	NT	Musculus gene for gelatinase B
5108	17828	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	U1-H-B1-and-4-TD-U1.x1 NCI_CGAP_SUD3 Homo sapiens cDNA clone IMAGE:2721947 3'
5901	18591	31516	3.15	8.0E-02	AF275043.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18591	31516	1.82	8.0E-02	AF275043.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114993.1	NT	Bovine chaperonin 14 cDNA library under conditions of nitrogen deprivation
9289	21956	35127	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9289	21956	35128	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10058	22706		0.65	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10592	23883	36823	2.27	8.0E-02	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12185	24655	31070	6.39	8.0E-02	AL006375.1	NT	Drosophila orexin hunchback region
12748	17903		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.6E-02	BE250008.1	EST_HUMAN	600943161 FTI NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2959510 5'
2978	15744	28392	7.25	7.9E-02	AI050209.1	EST_HUMAN	605 RIBOSOMAL PROTEIN L38 (HUMAN); p98-08.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3771	16529	29168				NT	Plasmidum falcatum strain Dd2 heat shock protein 88 (HSP88), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG5 (cg5), putative chloroquine resistance transporter (ert), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3822	15583	29217	0.97	7.9E-02	AF030694.2	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	15583	29218	5.01	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4945	17378	30011	0.99	7.9E-02	BF348454.1	EST_HUMAN	6020187071 NCI_CGAP_Bmt67 Homo sapiens cDNA clone IMAGE:4155401 5'
4760	17402		1.31	7.9E-02	AB008016.1	NT	Arabidopsis thaliana RXW24L, mRNA, partial cds
4851	17591	30204	1.02	7.9E-02	L24757.1	NT	Human bone alyoprotein (BNSP) gene, exons 2, 3 and 4
6597	19360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
7931	20528	33764	2.79	7.9E-02	U27832.1	NT	Securinomyces cerevisiae suppressor of Mif2 SmkAp (SMK4) gene, complete cds
9927	22575	35773	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou033005.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:G37A2.2 CE09891.1
9927	22575	35774	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou033005.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:G37A2.2 CE09891.1
1188	13940	28604	1.77	7.8E-02	AI783275.1	EST_HUMAN	ou056002.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.0 L1 repetitive element
1188	13940	28605	1.77	7.8E-02	AI783275.1	EST_HUMAN	ou056002.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.0 L1 repetitive element

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression: Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943058F1 NIH_MGC_15 Homo sapiens cDNA IMAGE:2856993 5'
6976	19457	32479	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6976	19457	32480	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8984	21376	34520	0.71	7.8E-02	BE87947.1	EST_HUMAN	801440439F1 NIH_MGC_72 Homo sapiens cDNA IMAGE:3925449 5'
8778	21471	34616	0.66	7.8E-02	X78344.1	NT	S cerevisiae CAT6 gene
8951	21642	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21642	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9291	22016	35183	1.07	7.8E-02	AA469354.1	EST_HUMAN	nc88p06.r1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:771731
9701	22332	35547	0.62	7.8E-02	Z59124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3596281 to 4214814
10582	22358	35494	4.58	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12764	25016		3.82	7.8E-02	AF069349.1	NT	HIV-1 strain 97USNG30' from USA, envelope glycoprotein (env) gene, partial cds
1378	15508	26800	1.25	7.7E-02	AF161897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	18328		1.97	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5456	18235	31145	0.59	7.7E-02	AF062636.1	NT	Galus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33625	5.37	7.7E-02	AA402949.1	EST_HUMAN	zu83d1.r1 Scores ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:747177 5' similar to
9735	22386	36550	3.94	7.7E-02	P38080	SWISSPROT	TRG1173905 G173905 SPICEOSOME ASSOCIATED PROTEIN. ;
10031	22879	35935	0.85	7.7E-02	A1318662.1	EST_HUMAN	aa0008.r1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S
10031	22879	35966	0.85	7.7E-02	A1818662.1	EST_HUMAN	aa0008.r1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S
10833	23313	36893	4.51	7.7E-02	11422757	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
12389	25215		2.68	7.7E-02	11439859	NT	Homo sapiens KIAA0028 gene product (KIAA0028), mRNA
3382	18141	28768	1.97	7.6E-02	BE514432.1	EST_HUMAN	60131G28F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3403	18161	28812	1.14	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3447	18302	28952	0.71	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6008	18787	31749	0.81	7.6E-02	A1081275.1	EST_HUMAN	an25p02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6293	19037	32012	0.92	7.6E-02	BE376238.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9767	22448		1.63	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
10119	22767	33978	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-H170545-020800-017-d06 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE396938.2	EST_HUMAN	601654616F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10487	23193	38336	0.71	7.6E-02	XG2655.1	NT	Lusculentum mRNA for triose phosphate translocator
10487	23193	39360	0.71	7.6E-02	XG2655.1	NT	Lusculentum mRNA for triose phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW590845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
767	13540	28199	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	28200	1.44	7.6E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for: interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	AB048714.1	EST_HUMAN	wc24h09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472267 3'
8236	20630	34088	1.06	7.5E-02	AB84387.1	EST_HUMAN	w52602.x1 NCL CGAP_Birt25 Homo sapiens cDNA clone IMAGE:2428497 3' similar to gb:M14328 ALPHA
8405	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
6922	22580		0.54	7.5E-02	BF221730.1	EST_HUMAN	7d61cd5.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10390	23036	38252	0.71	7.5E-02	BF206039.1	EST_HUMAN	MER27 repetitive element:
10498	23134	38361	0.72	7.5E-02	X79460.1	NT	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
465	13250	25891	1.46	7.4E-02	AW838547.1	EST_HUMAN	C:flm DSM 20113 16S rDNA
1445	14192		0.92	7.4E-02	AF030027.1	NT	RC5-L70054-260100-011-H09 L70054 Homo sapiens cDNA
2585	16289		1.32	7.4E-02	6755069	NT	Equine herpesvirus 4 strain NS80357, complete genome
3581	16336	28981	0.86	7.4E-02	AB07885.1	EST_HUMAN	Mus musculus plect-like homeodomain transcription factor 1 (Pitx1), mRNA
4656	17390	30024	2.03	7.4E-02	L79810.1	NT	wf43001.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4741	17473	30108	2.94	7.4E-02	6378442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4899	17616	30235	2.1	7.4E-02	6878492	NT	Rattus norvegicus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
6403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	y91408.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:3895284 5'
7801	20496	33618	1.52	7.4E-02	BE880112.1	EST_HUMAN	601463368F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3895284 5'
8399	21092	34228	1.03	7.4E-02	U65086.1	NT	Human periodic thymoprotein 2 (PTP2) gene, exons 15 to 21, and complete cds
9064	21753	34913	1.12	7.4E-02	AW628605.1	EST_HUMAN	ih07d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.:

Page 128 of 536

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8064	21763	34814	1.12	7.4E-02	AW628605.1	EST_HUMAN	h87d11.1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2867881 5' similar to SW:SCA2_HUMAN
9339	20410	33525	0.52	7.4E-02	A1872639.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
9339	20410	33526	0.52	7.4E-02	A1872639.1	EST_HUMAN	w57402.21 Soares Dieckgraefe codon_NFICD Homo sapiens cDNA clone IMAGE:2346819 3'
9714	22365	35563	1.03	7.4E-02	U42293.1	NT	w57402.21 Soares Dieckgraefe codon_NFICD Homo sapiens cDNA clone IMAGE:2346819 3'
9841	22492	35562	0.52	7.4E-02	BF572878.1	EST_HUMAN	Human LIM-kinase1 and alternatively spliced LIM-kinase2 (LIMK1) gene, complete cds
10339	24618	36869	1.28	7.4E-02	AA059167.1	EST_HUMAN	U1H-BW7-rang-g05-05-U1.1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3068889 3'
12126	23618	36869	1.28	7.4E-02	AA059167.1	EST_HUMAN	284001.1 Soares retina N2B4RH Homo sapiens cDNA clone IMAGE:3841720 5'
12381	23326	36869	1.53	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-8), mRNA
458	13242	25881	2.21	7.4E-02	AW37043.1	EST_HUMAN	CM4-H10243-08119-037-411 HT0243 Homo sapiens cDNA
458	13242	25882	1.5	7.3E-02	BE564861.2	EST_HUMAN	60168738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:386209 3'
669	13446	26085	3.9	7.3E-02	BE564861.2	EST_HUMAN	60168738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:386209 3'
1464	15570	26900	3.62	7.3E-02	AW800281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1537	15580	26900	12.41	7.3E-02	AL163302.2	NT	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
6981	19131	32128	1.32	7.3E-02	AA776977.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
7369	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	224002.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7369	20048	33129	2.58	7.3E-02	P05143	SWISSPROT	g5L02428 26S PROTEASE SUBUNIT 4 (HUMAN);
8069	20762	36869	1.15	7.3E-02	7662107	NT	PROLINE-RICH PROTEIN MP-3
9110	21768	36869	1.14	7.3E-02	AB011090.1	NT	PROLINE-RICH PROTEIN MP-3
11179	19131	32128	2.08	7.3E-02	AA776977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
11844	24428	36869	5.07	7.3E-02	11560138	NT	224002.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
117	12937	25577	1	7.2E-02	AE000892.1	NT	g5L02428 26S PROTEASE SUBUNIT 4 (HUMAN);
117	12937	25578	1	7.2E-02	AE000892.1	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC94171), mRNA
1458	14205	26880	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1039934 (section 88 of 148) of the complete genome
1458	14205	26881	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1039934 (section 88 of 148) of the complete genome
2552	15267	26254	2.83	7.2E-02	U14794.1	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1039934 (section 88 of 148) of the complete genome
3865	16618	29678	4.65	7.2E-02	AW298322.1	EST_HUMAN	g5L02428 26S PROTEASE SUBUNIT 4 (HUMAN);
4312	17051	29678	4.65	7.2E-02	BF572307.1	EST_HUMAN	g5L02428 26S PROTEASE SUBUNIT 4 (HUMAN);
4844	17378	30010	0.7	7.2E-02	11466563	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC94171), mRNA

Page 129 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5205	18013	30635	2.89	7.2E-02	U67531.1	NT	Methanococcus jannaschii exon 73 of 160 of the complete genome
5206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58	7.2E-02	BF216086.1	EST_HUMAN	60186355BF1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5334697	NT	Strongylocentrotus purpuratus rRNA, complete genome
8087	20781	33910	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN NP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN NP-3
8962	21653		0.81	7.2E-02	Y17217.1	NT	Lactococcus lactis cepc gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22164	35346	2.32	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9559	22311	35509	3.8	7.2E-02	L14961.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35667	0.93	7.2E-02	BF125399.1	EST_HUMAN	60176352BF1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	hQ24F11.X1 NCL_OGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q82340 Q92340
10092	22740	35955	0.62	7.2E-02	AA758204.1	EST_HUMAN	at82c07.x1 NCL_OGAP_GOB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10250	22898	36108	1.63	7.2E-02	U62953.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28S1 protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	5.54	7.2E-02	BE595033.1	EST_HUMAN	60134392BF1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3451559 5'
10395	23041		3.68	7.2E-02	BE530214.1	EST_HUMAN	60105919BF1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10509	23166	36381	0.48	7.2E-02	AA706897.1	EST_HUMAN	z28h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10830	23512	36753	3.3	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor MIST1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY006090.1	NT	Homo sapiens putative transmembrane protein dedlin-1 mRNA, complete cds
12035	24560	31113	1.67	7.2E-02	AA773966.1	EST_HUMAN	af81a04.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12065	24593		4.45	7.2E-02	AJ230765.1	EST_HUMAN	AJ230765 Homo sapiens library (Seranaki P) Homo sapiens cDNA clone PS13D5 3'
12182	24594		1.73	7.2E-02	U62628.1	NT	Homo sapiens atada telangiectasia (ATA) gene, complete cds
12182	25185		8.19	7.2E-02	AF000962.1	EST_HUMAN	CMA-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12599	25392		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1897	14634	27344	2.01	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2290	15016	27751	5.07	7.1E-02	BF208902.1	EST_HUMAN	60187282BF1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7807	20502	33622	0.77	7.1E-02	AI125294.1	EST_HUMAN	q062a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'

Page 130 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11022	24483		6.41	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13299	25631	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14293		1.27	7.0E-02	X66977.1	NT	Martelliella Mitou-1 gene
1766	14408	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	28604.e1 Sra gene colon (#337224) Homo sapiens cDNA clone IMAGE:509699 3'
3027	15703	28440	2.1	7.0E-02	AW138152.1	EST_HUMAN	U1H-B1-ayc-07-04-J1.1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3878	16628	28266	0.74	7.0E-02	AA816438.1	EST_HUMAN	af55a12.1 Soares_testis_NHT Homo sapiens cDNA clone 1375675 3' similar to gb:K03002 60S
4119	16891		1.28	7.0E-02	AW792962.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4189	16930	29560	1.06	7.0E-02	AF077821.1	NT	CMB-UM001-1060300-270-012 UM001 Homo sapiens cDNA
4877	17604	30227	7.24	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5293	18068	33059	0.57	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050074 5'
7300	19983	33271	1.29	7.0E-02	AV669283.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
8598	21688	34836	1.26	7.0E-02	Y19187.1	NT	AV669285 GKC Homo sapiens cDNA clone GKCCAE06 5'
8497	22160	35331	1.24	7.0E-02	K02801.1	NT	Gallus gallus mRNA for partial eczzin, XL spliced variant (ecz gene)
9852	22502	35702	0.51	7.0E-02	U27266.1	NT	African swine fever virus, complete genome
11345	24035	37338	4.98	7.0E-02	AA724295.1	EST_HUMAN	Rat Ig germline epsilon H-chain gene C-region, 3' end
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
1310	14058		1.2	6.9E-02	4507868	NT	Homo sapiens chromosome 21 segment HS21C010
3773	16225	29163	1.41	6.9E-02	Q06364	SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2TD7)
3773	16225	29164	1.41	6.9E-02	Q06364	SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2TD7)
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	Enterococcus faecium cytolysin aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB
5127	17845	30462	1.25	6.9E-02	BE264603.1	EST_HUMAN	(bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminal (bglR), enterocin B
7518	20187		0.61	6.9E-02	AF164967.1	NT	precursor (enB), enterocin B immunity protease
7951	20648		1.12	6.9E-02	U12022.1	NT	6011192393F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3530253 5'
8451	21143	34282	1.01	6.9E-02	BE567435.1	EST_HUMAN	Canine distemper virus strain A7/517, complete genome
8451	21143	34283	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
9019	21708	34860	0.7	6.9E-02	U22987.1	NT	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
12065	24680		1.82	6.9E-02	X74315.1	NT	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
							Barbaric duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
							Xlaevia XFD2 mRNA for fork head protein

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12232	24685		1.69	6.8E-02 P44621	SWISSPROT		PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
12447	24817		1.45	6.8E-02 AF165953.1	NT		Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1875	14613	27321	1.56	6.8E-02 AA498759.1	EST_HUMAN		ae30102.1 Gieseler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1875	14613	27322	1.56	6.8E-02 AA498759.1	EST_HUMAN		ae30102.1 Gieseler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02 AF155673.1	NT		ae30102.1 Gieseler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3097	15602	26503	1.19	6.8E-02 AA781696.1	EST_HUMAN		Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
3097	15602	26504	1.19	6.8E-02 AA781696.1	EST_HUMAN		ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
3097	15602	26505	1.19	6.8E-02 AA781696.1	EST_HUMAN		ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
4518	17251		0.86	6.8E-02 BE141076.1	EST_HUMAN		ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
6525	19291		0.6	6.8E-02 P20792	SWISSPROT		MRQ-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
6769	19460		1.09	6.8E-02 BE061890.1	EST_HUMAN		RC1-B10254-090300-017-409 BT0254 Homo sapiens cDNA
7180	19596	32939	8.73	6.8E-02 AL165268.2	NT		Homo sapiens chromosome 21 segment HS21C088
7584	20252	33558	0.63	6.8E-02 U16856.1	NT		Dicystidium discoidulum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8165	20680	34017	6.01	6.8E-02 AJ246287.1	NT		Pyrococcus abyssi complete genome, segment 516
8165	20680	34018	5.01	6.8E-02 AJ246287.1	NT		Pyrococcus abyssi complete genome, segment 516
11673	25379		2.3	6.8E-02 T03214.1	EST_HUMAN		FB4A8 Fetal brain, StrataGene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12001	24537		2.85	6.8E-02 AA768014.1	EST_HUMAN		ah67105.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
12551	24688		1.93	6.8E-02 AW975539.1	EST_HUMAN		EST1387948 MAGE resequencing, MAGN Homo sapiens cDNA
12613	24920		3.06	6.8E-02	NT		Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1519	14268		1.93	6.7E-02 AF115538.1	NT		Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1-101 allele, complete cds
1886	14623	27333	2.27	6.7E-02 AL20285.1	EST_HUMAN		hg79a04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3706	18459	25917	4.52	6.7E-02 P17278	SWISSPROT		HOMEOBOX PROTEIN HOXD4 (HOXD-4)
7749	20446	33567	0.55	6.7E-02 X62695.1	NT		H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7749	20446	33568	0.55	6.7E-02 X62695.1	NT		H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8337	21030	34167	0.47	6.7E-02 AW082888.1	EST_HUMAN		ad81611.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2880788 3'
8500	22153	35333	0.69	6.7E-02 AW137359.1	EST_HUMAN		LI-H-B1-4cr-g-01-Q-J1 s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
8500	22153	35334	0.69	6.7E-02 AW137359.1	EST_HUMAN		LI-H-B1-4cr-g-01-Q-J1 s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1348	14098	26771	1.07	6.6E-02 AF246116.1	NT		Drosophila melanogaster cadherin mRNA, complete cds
2180	14099	27841	3.31	6.6E-02 AJ289241.1	NT		Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3466	19212	29865	10.57	6.6E-02 R64306.1	EST_HUMAN		y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3471	19227	29881	2.69	6.6E-02	NT		Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3471	19227	29882	2.59	6.6E-02	NT		Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

Page 132 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4060	16805	29436	1.29	6.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4921	17649	30261	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17649	30262	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6469	19256	32258	3.44	6.6E-02	X09411.1	NT	P.vulgatus mRNA for chalcone synthase
6701	19283	32286	0.58	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.58	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20542	33970	1.81	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21065	34206	0.84	6.6E-02	AF050553.1	NT	Dictyostellium discoideum dafin (darA) gene, complete cds
8678	21370	34654	0.63	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8819	21511	34654	0.58	6.6E-02	9829168	NT	Human respiratory syncytial virus, complete genome
8819	21511	34655	0.58	6.6E-02	9829168	NT	Human respiratory syncytial virus, complete genome
8951	22501	35701	0.65	6.6E-02	A1458752.1	EST_HUMAN	I97506.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2146408 3'
8987	22635	35846	1.66	6.6E-02	Y07648.1	EST	Homo sapiens EWS, gap22, rp22 and bam22 genes
10022	22670		0.63	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL) mRNA
10383	23563	36811	5.88	6.6E-02	BF374246.1	EST_HUMAN	MR1-SIN064-01060-008-612 SIN064 Homo sapiens cDNA
11987	24461	37793	1.46	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.60	6.6E-02		NT	Mus musculus DIPB gene (Dipb), mRNA
12740	25006		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cyclochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	26977	2.49	6.6E-02	BF027339.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:39564178 5'
868	13732	26598	1.32	6.6E-02	7706088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26793	3.08	6.6E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27189	1.77	6.6E-02	AE000784.1	NT	Aquifex acidicus section 88 of 109 of the complete genome
5471	18270	31142	2.03	6.6E-02	A4443991.1	EST_HUMAN	zw6h12.a1 Soares ovary tumor NoHOT Homo sapiens cDNA clone IMAGE:766743 3' similar to gp-M26038
6877	17653	30549	0.95	6.6E-02	U22661.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-5 BETA CHAIN (HUMAN);
6942	22493	35693	0.55	6.6E-02	BE663200.2	EST_HUMAN	Azobacter vinelandii ATCC 9046 negative regulator NucB (nucB) gene, partial cds
9842	22493	35694	0.55	6.6E-02	BE663200.2	EST_HUMAN	601659817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3856537 3'
10363	23010	36225	0.49	6.6E-02	BF106300.1	EST_HUMAN	601659817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3856537 3'
10363	23010	36225	0.49	6.6E-02	BF106300.1	EST_HUMAN	601623511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
10363	23010	36225	0.49	6.6E-02	BF106300.1	EST_HUMAN	601623511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
10363	23010	36225	0.49	6.6E-02	BF106300.1	EST_HUMAN	601623511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11894	24463		3.73	6.6E-02	M21496.1	NT	z32305.a1 Soares NIH/MPU_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12240	24691		4.66	6.6E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	13743	25970	2.09	6.6E-02	X94549.1	NT	Rabbit haematopoietic kinase related protein 2 (KRP2) gene, complete cds
3014	15380	29429	0.66	6.6E-02		NT	A. carotene precursor of peridinin-chlorophyll-protein (PCP) gene
4839	15780	28428	1.18	6.6E-02	6956523	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5993	19195	30850	1.97	6.4E-02	AI191886.1	EST_HUMAN	q07b01.x1 Scores_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR.b3 LTR repetitive element;
5791	18582	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31763	4.21	6.4E-02	AF032733.1	NT	Holoferin glycinase beta-1, 4-endoglucanase-1 precursor (HG-snp-1) gene, complete cds
6022	18802	31764	4.21	6.4E-02	AF032733.1	NT	Holoferin glycinase beta-1, 4-endoglucanase-1 precursor (HG-snp-1) gene, complete cds
6008	19080	32065	0.82	6.4E-02	AF072895.1	EST_HUMAN	wf3g12.x1 Scores_Dickkopf, caten_NKCD Homo sapiens cDNA clone IMAGE:2345780 3'
6719	19634	32677	6.43	6.4E-02	BE974448.1	EST_HUMAN	601768042R02 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950503 3'
7360	20041	33119	0.84	6.4E-02	AL162757.2	NT	Nesheria meningitidis serogroup A strain Z2491 complete genome; segment 617
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeit) (Cct6a), mRNA
8563	21265	34392	3.42	6.4E-02	AA03305.1	EST_HUMAN	kl419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21715	34688	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from c634+ stem cells Homo sapiens cDNA clone CBDAIA10
9498	22139		0.59	6.4E-02	BE634083.1	EST_HUMAN	RC1-OT0083-150600-014-p08 OT0083 Homo sapiens cDNA
9817	22270	35457	1.73	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF037150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF037150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37628	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12188	24659	31055	2.47	6.4E-02	AJ27174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF106905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MUS hsc70, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
3590	16344		2.38	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6945	18825	31766	1.18	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4097489 5'
7142	18829		0.82	6.3E-02	X97659.1	NT	H. sapiens gene encoding La autoantigen
9191	21861	35028	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exon 1-3
9913	22802	33768	2.94	6.3E-02	AB010162.1	NT	Hepatitis B virus RNA for polyprotein (NSA region), partial cds, strain: CMR-152
10171	22819		0.85	6.3E-02	AF698070.1	EST_HUMAN	AF698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10515	18825	31766	2.88	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4097489 5'
4224	16945	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4304	17043		1.02	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		6.31	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6998	19816	32658	0.65	6.2E-02	D4630.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7327	20188	33232	1.03	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8546	25529		0.6	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35082	0.52	6.2E-02	AA778450.1	EST_HUMAN	af20403.61 Soares_t041 deus_Nb2HF8_3w Homo sapiens cDNA clone IMAGE:1032176 3'
9380	22042	35214	1.65	6.2E-02		6677898	Mus musculus atrial cell derived factor receptor 2 (Sdr2), mRNA
11095	23765	37039	1.56	6.2E-02	AF217490.1	NT	Homo sapiens fragile 160 oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	6.2E-02	AJ242735.1	NT	Melanizum antisense mRNA for Chymotrypsin (chyl gene)
11865	24449	37791	1.74	6.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uglp) mRNA, complete cds
11869	25405		13.39	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.2E-02	BF112039.1	EST_HUMAN	757708.x1 Soares_NSF_F9_PW_OT_PA_P_81 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR-097439 Q9Y458 HYPOTHETICAL 30.3 KD PROTEIN, [1];
249	13058	25697	5.59	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3972	16721		2.29	6.1E-02	U73525.1	NT	Arabidopsis thaliana K ⁺ inward rectifying channel protein (AKC1) gene, complete cds
6023	18803		1.4	6.1E-02	4507070	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33998	3.75	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8559	21251	34338	0.57	6.1E-02	BE971833.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
8559	21251	34389	0.57	6.1E-02	BE971833.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
10830	23323	36560	4.91	6.1E-02	BE170643.1	EST_HUMAN	IL3-H10818-110500-136-C08 H10818 Homo sapiens cDNA
11862	24446	37787	1.27	6.1E-02	AB025333.1	NT	Epatelurus burgeri mRNA for RNA polymerase III largest subunit, partial cds
11945	25323		2.27	6.1E-02	X70869.1	NT	S. japonicus mRNA for serine enzyme
12333	24933		5.61	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
96	12822	25559	0.76	6.0E-02	AA198730.1	EST_HUMAN	zp78604.r1 Stralagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
96	12922	25560	0.76	6.0E-02	AA198730.1	EST_HUMAN	zp78604.r1 Stralagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
1239	13988	26655	1.54	6.0E-02	AE001777.1	NT	Thermoga maritima section 89 of 136 of the complete genome
2682	15391	28130	1.09	6.0E-02	AW66848.1	EST_HUMAN	EST130924 MAGC resequencer, MAGJ Homo sapiens cDNA
2776	15490		1.62	6.0E-02	AB031289.1	NT	Mesocricetus crati mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gh, rRNA-Phe, rRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2937	12822	25559	0.8	6.0E-02	AA198730.1	EST_HUMAN	zp78604.r1 Stralagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2937	12822	25560	0.9	6.0E-02	AA198730.1	EST_HUMAN	zp78604.r1 Stralagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

Table 4.
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	15866	28639	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST142368 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15866	28640	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST142368 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE96443.2	EST_HUMAN	601681569R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3876060 3'
5037	17756	30370	0.69	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW37021.1	EST_HUMAN	RC3-B10253-011188-013-04 B10253 Homo sapiens cDNA
6122	18900	31868	0.77	6.0E-02	AI807637.1	EST_HUMAN	wf4803x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains 1.1x1 L1 L1 repetitive element;
6891	17687	30524	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6891	17687	30525	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7088	19777	32842	2.33	6.0E-02	BF382240.1	EST_HUMAN	601815274F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4046226 5'
7680	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf56003x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764199 3'
8321	21014		0.54	6.0E-02	11486495	NT	Rec1 homologues americana mitochondrion, complete genome
9172	21842	35007	1.17	6.0E-02	AI823167.1	EST_HUMAN	Is78a03x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	35008	1.17	6.0E-02	AI823167.1	EST_HUMAN	Is78a03x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2237362 3'
9308	21973	35147	1.68	6.0E-02	AJ243365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9308	21973	35148	1.68	6.0E-02	AJ243365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST1180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST1180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11306	23965		1.69	6.0E-02	AA126386.1	EST_HUMAN	znf508.1 Stradiene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gp-X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31064	2.16	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12564	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf5903x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
223	13036	26671	3.87	5.9E-02	AW634719.1	EST_HUMAN	RC1-D10001-260100-012-e10 D10001 Homo sapiens cDNA
2962	15748	28396	2.69	6.0E-02	AF160269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
4817	17548	30173	1	5.9E-02	AF066304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17641	30457	0.73	5.9E-02	AW026748.1	EST_HUMAN	wf34602x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
5123	17641	30458	0.73	5.9E-02	AW026748.1	EST_HUMAN	wf34602x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
8515	21207	34350	1.68	5.9E-02	9055246	NT	O65386 F12F1 20 PROTEIN. ;
9351	20422		0.8	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus trophoblast related homeobox 5 (Drosophila) (trbx), mRNA
							601817609F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4105694 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23378		3.2	5.8E-02	6079870	NT	Mus musculus follistatin-like (Fsl), mRNA
10944	23623	36872	1.44	5.8E-02	11433356	NT	Homo sapiens ninein (LOC51199), mRNA
11544	24144		1.59	6.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
912	13678		5.18	5.8E-02	D90110.1	NT	Thibacillus ferrooxidans merG, merA genes and URF-1
2884	15632		0.86	5.8E-02	AJ226291.1	NT	Populus trichocarpa COAOMT1 gene, exon 1 to exon 5
4322	17061	29887	4.9	5.8E-02	AJ0051927.1	EST_HUMAN	w242402.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17091	29888	4.9	5.8E-02	AJ0051927.1	EST_HUMAN	w242402.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	AJ247505.1	EST_HUMAN	q15601.x1 Soares, fetal, liver, spleen, 1NF.LS, S1 Homo sapiens cDNA clone IMAGE:1846897 3' similar to
4510	17245	29880	4.95	5.8E-02	AJ247505.1	EST_HUMAN	q15601.x1 Soares, fetal, liver, spleen, 1NF.LS, S1 Homo sapiens cDNA clone IMAGE:1846897 3' similar to
4535	17270		2.62	5.8E-02	AF066284.1	NT	gbM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
7578	20247	33362	2.69	6.8E-02	M99150.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33353	2.69	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8585	21257	34394	0.67	5.8E-02	AL163283.2	NT	Human polymorphic microsatellite DNA
12084	21580		1.79	6.8E-02	AF220177.1	NT	Homo sapiens chromosome 21 segment HS21C083
12373	25366		7.06	5.8E-02	AA804289.1	EST_HUMAN	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
3053	15819	29463	1.39	5.7E-02	AJ081644.1	EST_HUMAN	no75611.at NCI_CGAP_AAT1 Homo sapiens cDNA clone IMAGE:1112884 3'
3058	15824	29478	1.29	5.7E-02	AF119117.1	NT	ou5305.at NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632466 3' similar to WP-C37A2.2
3694	16448		0.97	5.7E-02	AF001292.1	NT	CE08611.1
3763	16535	29173	2.45	6.7E-02	AF069781.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
4637	17371		1.01	5.7E-02	N95098.1	NT	Chromosome humini thumini globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
7436	20115	33203	0.69	5.7E-02	D78003.1	NT	EST1378965 MAGE resequences, MAGE Homo sapiens cDNA
7438	20116	33204	0.69	5.7E-02	D78003.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
8055	20749	33860	1.42	6.7E-02	AJ286090.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8750	22401	35606	0.84	5.7E-02	6681260	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
11143	23810	37050	4.42	5.7E-02	AJ752685.1	EST_HUMAN	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
11143	23810	37051	4.42	5.7E-02	AJ752685.1	EST_HUMAN	Mus musculus ec2 oncogene (Ec2), mRNA
11321	24012		1.59	6.7E-02	AL163303.2	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC, cn18b09 random
12285	28213		7.24	5.7E-02	D50320.1	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC, cn18b09 random

Page 137 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12518	25283		3.18	5.7E-02	AF217480.1	NT	Homo sapiens fragile 18D oxide reductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	AF261280.1	NT	Pen troglodytes apolipoprotein-E gene, complete cds
1518	14265	26951	1.57	5.6E-02	AF064455.1	NT	Hydroxylase rotundifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4395	17330	29857	1.12	5.6E-02	AB013100.1	NT	Lyso-perlecan esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4848	17382	30014	1.46	6.6E-02	AA230399.1	EST_HUMAN	z024607.at NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700418 3'
6562	19327	32334	6.57	5.6E-02	AW172708.1	EST_HUMAN	y02c10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2658050 3' similar to TR:Q94879 Q94879 KIAA0905 PROTEIN.1
6791	19535	32563	1.25	5.6E-02	AA089182.1	EST_HUMAN	cd4712.c1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7051	19742	32804	3.05	6.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147:290400-214-g07 EN0147 Homo sapiens cDNA
7063	19764	32819	0.69	6.6E-02	AI093738.1	EST_HUMAN	w24f05.x1 NCL CGAP_Brn63 Homo sapiens cDNA clone IMAGE:2559689 3' similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20398	33502	0.69	5.6E-02	AI183583.1	EST_HUMAN	cd6401.L1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1734308 3'
8701	21393	34536	2.88	5.6E-02	BE542893.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8701	21393	34540	2.88	6.6E-02	BE542893.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9712	22363	35561	1.09	5.6E-02	AA482864.1	EST_HUMAN	nf49007.at NCL CGAP_A1M1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.1
11556	24165		2.35	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2863	16370	28108	0.8	5.5E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3208	15972	28625	3.93	6.5E-02	6755501	NT	Mus musculus SH3 domain protein TB (SH3d1B), mRNA
4191	16932	29561	1	5.5E-02	L41581.1	NT	Gallid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5535	18370	31281	3.58	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038	2	5.5E-02	6756602	NT	Mus musculus titin 1 (T1uT), mRNA
8019	20714	33846	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8019	20714	33846	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9565	22208	35392	0.6	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (AE-1), mRNA
9565	22208	35392	0.6	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (AE-1), mRNA
9650	22302	35497	1.32	5.5E-02	U08492.1	NT	Mus musculus second L1/T1 receptor alpha chain (L1/T1Ra2) gene, exons 1 and 2
10943	23622	36871	7.26	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cta) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhac), transcriptional activator (dhaf), 1,3-propanediol dehydrogenase (dhaf), glycerol dehydrogenase (dhac) >

Page 138 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12797	25349	30604	1.49	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SRRP-b2 (SRRP-b2), mRNA
3019	15765		0.91	5.4E-02	AJ277468.1	NT	Oryza sativa tdb33-1 gene for putative Bowman Birik tyrosin inhibitor
3416	17685		5.78	5.4E-02	BE073468.1	EST_HUMAN	RC6-BT0850-140200-012-C03 BT0850 Homo sapiens cDNA
3391	16641	20281	0.79	5.4E-02	U95905.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z09116.1	NT	Bacillus subtilis complete genome (section 13 of 21), from Z956281 to 2813730
8869	21698	34809	0.55	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	39497	1.82	5.4E-02	AU120889.1	EST_HUMAN	AU120888 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37076	1.32	5.4E-02	BE371289.1	EST_HUMAN	RC6-FN0112-160700-021-D06 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-160700-021-D06 FN0112 Homo sapiens cDNA
1031	13781	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1031	13781	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1495	14242	26929	14.72	5.3E-02	T94759.1	EST_HUMAN	y37712.1 Stragene lung (9937210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01509
2507	15218	27951	2.47	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2943	15709	28390	0.85	5.3E-02	M56417.1	NT	Pseudomonas putida tlgS gene
2943	15709	28391	0.95	5.3E-02	M56417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3150	15913	28558	5.61	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
6029	17749	30381	8.34	5.3E-02	M80463.1	NT	Pseudomonas putida tlgS gene
6236	18042	30670	1.88	5.3E-02	AE000327.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5238	18042	30671	1.88	5.3E-02	AE000327.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785	19529	32556	5.01	5.3E-02	AE000327.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6992	19683	32733	1	5.3E-02	U32832.1	NT	Lymphocytic disease virus 1, complete genome
7260	19944		2.06	5.3E-02	JG2822.1	NT	Haemophilus influenzae Rd section 147 of 183 of the complete genome
7777	20399	33574	0.85	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform (mice, mRNA, 4053 nt)
8304	20998		0.7	5.3E-02	U10068.1	NT	HYPOHETICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
9023	21713	34867	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/SvEv crystalin C (cs3) gene, complete cds
10032	22680	35897	0.62	5.3E-02	AB022905.1	NT	Podopora anserina mitochondrial epsilon-sen DNA
10032	22680	35898	0.62	5.3E-02	AB022905.1	NT	Homo sapiens hCGMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10156	22804		0.63	5.3E-02	Y07807.1	NT	Homo sapiens hCGMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10230	22878	36090	0.7	5.3E-02	X88432.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (nourila, 9-18 hpf and postmitogenesis, 20-28 hpf)
							B. rerio poic1 mRNA for transcription factor

Page 139 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1276	25030	30894	1.43	5.3E-02	AF270815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		160.56	6.2E-02	5931908	NT	Homo sapiens mephrin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3112	19377	28516	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	19377	28517	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16689	29310	1.23	5.2E-02	AF226101.1	NT	Arabidopsis thaliana putative disaccharide diuron protein (Csd1) mRNA, complete cds
3921	16671		1.19	6.2E-02	6871757	NT	Homo sapiens cyclin inducible SH2-containing protein 3 (Cish3), mRNA
4249	16988	28609	3.02	5.2E-02	U07132.1	NT	Homo sapiens steroid hormone receptor Nsr-1 mRNA, complete cds
5053	17772		0.9	5.2E-02	AA287940.1	EST_HUMAN	EST T11552 Uterus Homo sapiens cDNA 5' end
5628	18817	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AI830685.1	EST_HUMAN	W80904.X1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.B1
7174	18880	32932	3.13	5.2E-02	P49322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8065	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8929	22282	36472	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9029	22282	35473	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24795		1.89	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2364	15086		1.17	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 547 (pyrimin: hbr1) Homo sapiens cDNA clone DKFZp547D073.5
4179	16918	29547	1.03	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4960	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6676	16339	32360	0.72	5.1E-02	AF280369.1	NT	HIV-1 patient cd from Italy protease (pol) gene, complete cds
6760	17929	30594	1.44	5.1E-02	BF378625.1	EST_HUMAN	QYU00051-250800-350-508 UM0051 Homo sapiens cDNA
8151	20845	33975	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (hprt) gene, complete cds
8151	20845	33976	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (hprt) gene, complete cds
8245	20939	34076	1.48	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydroxyphenyl 3beta-reductase
8783	21475	34622	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
8783	21475	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
9709	22300	35556	6.89	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.69	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APQ (PROTEIN CEX)
10733	23420	35691	2.44	5.1E-02	AF083920.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	35692	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/6
12421	24797		2.56	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12079	24988		1.47	5.1E-02	AA334104.1	EST_HUMAN	nt3602.s1 NCL CGAP_P10 Homo sapiens cDNA clone IMAGE:598139
470	13256	28894	1.84	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	28599	6.54	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1883	14719	27438	3.91	5.0E-02	P02810	SWISSPROT	4) (PIF-F/PIF-S) (PROTEIN APPOIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	28397	1.28	5.0E-02	U77242.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305810	NT	Mus musculus Uro-S1 like kinase 2 (C. elegans) (ULK2), mRNA
3592	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3672	16425	29066	5.83	5.0E-02	U12769.2	NT	Anthrax toxin period clock protein homolog mRNA, complete cds
4170	17502		0.99	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18819	31780	0.95	5.0E-02	AF080264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-8
7437	20114	33202	12.49	5.0E-02	P35516	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
10100	22748	35963	1.28	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fas3) mRNA, complete cds
10521	23187		0.48	5.0E-02	BF213260.1	EST_HUMAN	801844753FT NIH_MGC_155 Homo sapiens cDNA clone IMAGE:4670101 5'
11473	24074	37383	2.5	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11956	25248		3.5	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13168	25800	2.69	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13168	25800	2.68	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	10043	28892	2.53	4.9E-02	P44258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3556	16311		0.89	4.9E-02	AA188940.1	EST_HUMAN	z448412.s1 Striatagene NNT neuron (993723) Homo sapiens cDNA clone IMAGE:532926 3' similar to
3579	16334	28978	0.89	4.9E-02	AA400814.1	EST_HUMAN	contains Alu repetitive element; contains element MSR1 repetitive element ;
3579	16334	28978	0.89	4.9E-02	AA400814.1	EST_HUMAN	z77803.s1 Soares, Iselis, NHT Homo sapiens cDNA clone IMAGE:729428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	z77803.s1 Soares, Iselis, NHT Homo sapiens cDNA clone IMAGE:729428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	z77803.s1 Soares, Iselis, NHT Homo sapiens cDNA clone IMAGE:729428 3'
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Ret elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Ret elastase II gene, exon 6
7042	19733	32793	0.91	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8552	21344	34489	0.71	4.9E-02	AL11559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191	22839	33054	0.48	4.9E-02	P18532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	33396	0.48	4.8E-02	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23085	37285	3.22	4.8E-02	AF008303.1	NT	Homo sapiens presso placental TGF-beta gene, complete cds
12345	24752		1.77	4.8E-02	8823880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12593	24912		3.41	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D18471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D18471.1	NT	Human mRNA, Xq terminal portion
476	13282	25896	9.98	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14697	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3203	15066	28620	2.1	4.8E-02	X1744.1	NT	Tetrahymena castralis histone H3II and histone H4II intergenic DNA
4523	17358		1.16	4.8E-02	Z84260.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5144	17863	30478	1.03	4.8E-02		NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
5144	17863	30479	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33894	1.32	4.8E-02	AJ388497.1	EST_HUMAN	MR2-ST0129-221099-012-502 ST0129 Homo sapiens cDNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes ps24 gene
9027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes ps24 gene
6731	19565	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	y95709.t1 Soares melanocyte 2NDHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains AU repetitive element
6919	19480	32503	2.02	4.7E-02	M82752.1	NT	Rat stathin-related protein (s1) gene, complete CDS
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	B. taurus mRNA for BF-36-DNA-binding protein
8852	21543	34690	0.90	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8875	21566		2.68	4.7E-02	AB026378.1	NT	Gallus gallus Wpich-8 gene, complete cds
9127	21815	34681	6.89	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9547	22200	33392	0.67	4.7E-02	BF305237.1	EST_HUMAN	601892992F1 NIH_JGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9635	22287		0.57	4.7E-02	A1873042.1	EST_HUMAN	w970c10.v1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23473143'
10854	23345	38582	1.4	4.7E-02	6754968	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11545	24148	37483	1.39	4.7E-02	U73921.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11545	24148	37484	1.39	4.7E-02	U73921.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
264	13072	25712	0.63	4.6E-02	BE163583.1	EST_HUMAN	PM0-H170339-25199-003-g05 H170339 Homo sapiens cDNA
722	1306	26149	2.91	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1269	14018		0.89	4.6E-02	A014295.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639879 3' similar to TR:P90633
1338	14088	28792	3.47	4.6E-02	AV727059.1	EST_HUMAN	P00533 LIMA, contains element LTR1 repetitive element ;
							AV727059 HTC Homo sapiens cDNA clone HTCSWC01 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2492	15209	27851	2.31	4.8E-02	AW236023.1	EST_HUMAN	nr2403.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2864653 3' similar to SW:GRF1_HUMAN
2811	13072	29712	1.9	4.6E-02	BE153593.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
3325	15774	28423	0.74	4.6E-02	BE153593.1	EST_HUMAN	PMO-HT0339-251195-003-g05 HT0339 Homo sapiens cDNA
3487	18744	28423	0.73	4.6E-02	BE153593.1	EST_HUMAN	PMO-HT0339-251195-003-g05 HT0339 Homo sapiens cDNA
4703	18848		1.35	4.6E-02	AF220395.1	NT	Mus musculus nuclear RNA helicase II/Gu (dsb2) gene, complete cds
5121	17839	30455	0.89	4.6E-02	AA079157.1	EST_HUMAN	zm95210.x1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERA1.N. TYPE II CYTOSKELETAL 7 (HUMAN);
5647	18442	31356	1.57	4.6E-02	AF075892.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6106	18914	31853	3.51	4.6E-02	X01624.1	NT	C.reinhardtii ap2 (apB) mRNA
6136	18914	31854	3.51	4.6E-02	X01624.1	NT	C.reinhardtii ap2 (apB) mRNA
8702	18917	32659	1.47	4.6E-02	A1149574.1	EST_HUMAN	qc60b06.x1 Scores, placenta, 80cweeks 2NBP80cW Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1, L3 L1 repetitive element;
8554	21246	34366	2.69	4.6E-02	BE154006.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11379	23986	37266	4.94	4.6E-02	AA073328.1	EST_HUMAN	627069.x1 Scores, NF, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12325	24744		1.86	4.6E-02	AV712871.1	EST_HUMAN	AV712871 DCA Homo sapiens cDNA clone DCAAZF07 5'
12705	24953		3.98	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
434	13220	25868	1.72	4.6E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1108	13945	28612	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1106	13945	28613	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2103	14634	27558	3.75	4.5E-02	AE003564.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3710	16403	29102	3.66	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6137	18915	31895	1.81	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
6415	19183	32162	0.77	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6779	19523	32550	0.61	4.5E-02	L26487.1	NT	Methanoscarcha frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
6779	19523	32551	0.61	4.5E-02	L26487.1	NT	Methanoscarcha frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8292	23088	34125	1.96	4.6E-02	AF036694.1	NT	Anabdoasis Italiana COAAT-box binding factor HAP3 homolog gene, complete cds
9549	22499	35659	4.57	4.5E-02	AA325216.1	EST_HUMAN	EST128187 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10000	22648	35850	0.48	4.5E-02	X95508.1	NT	A.europaeum mRNA for legum-like protein

Page 143 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10116	22764	36976	0.85	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12154	24640	31097	1.94	4.5E-02	11418013	NT	Homo sapiens rat finger protein-like 3 (RFPL3), mRNA
12337	25290	30733	6.91	4.5E-02	AA191097.1	EST_HUMAN	z43911.1 r1 Stragene INT neuron (9527233), Homo sapiens cDNA clone IMAGE:632493 5'
213	13025		5.52	4.4E-02	BE972738.1	EST_HUMAN	601652154F NIH_MGC 82 Homo sapiens cDNA clone IMAGE:3953588 5'
2088	14821		5.42	4.4E-02	P31556	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27833	2.4	4.4E-02	AF187476.1	EST_HUMAN	QV2P10012070000-070-g02 PT10072 Homo sapiens cDNA
3031	16384	28024	1.95	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkt10 (pkntD) gene, complete cds
4584	17319	20945	1.24	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4584	17319	20945	1.24	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4693	17427		2.28	4.4E-02	AJ222680.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7018	19710	32766	0.64	4.4E-02	AF065824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	19710	32767	0.64	4.4E-02	AF065824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8550	21342	34486	2.14	4.4E-02	AA179689.1	EST_HUMAN	rw13h03.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11007	23679	36936	2.62	4.4E-02	AF060869.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11157	23824	37104	2.78	4.4E-02	AA498739.1	EST_HUMAN	ae33704.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897831 5'
11890	24460		2.57	4.4E-02	AB040026.1	EST_HUMAN	Homo sapiens mRNA for KIAA1493 protein, partial cds
12087	25408		1.87	4.4E-02	BF241245.1	EST_HUMAN	601878748F NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4107418 5'
763	13536	26195	7.07	4.3E-02	AF003249.1	NT	Monone saxatilis myosin heavy chain FN3A (FN3A) mRNA, complete cds
2973	15287	28024	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3423	16180	28930	7.84	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3651	16404		1.37	4.3E-02	AF000468.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5152	17869	30482	0.95	4.3E-02	U11768.1	NT	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6404	19173	32172	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6833	19395	32410	0.73	4.3E-02	AA652266.1	EST_HUMAN	ns69512.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1198986
8411	21104	34245	0.73	4.3E-02	AF233369.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700	21392	34537	1.02	4.3E-02	X65322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8700	21392	34538	1.02	4.3E-02	X65322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
803	13576	26238	2.7	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
846	13616		2.32	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

Page 144 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
878	13845	28315	1.35	4.2E-02	AV003845.1	EST_HUMAN	w349p1.x1 NCL_OGAP_P101 Homo sapiens cDNA clone IMAGE:2645884 3' similar to TR:Q63291 Q63291
1714	14457		1.02	4.2E-02	AL445088.1	NT	L1 RETROPOSON, ORF2, MRNA, contains L1, L3, L1, L1 repetitive element;
1771	14517	27213	1.01	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3555	16408	29047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN NAF
4100	16843	26471	0.7	4.2E-02	BE262905.1	EST_HUMAN	601150033FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	28648	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4284	17023	28649	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4855	17429	30060	2.32	4.2E-02	BF342895.1	EST_HUMAN	602017105FT NCL_OGAP_Bm84 Homo sapiens cDNA clone IMAGE:4152972 5'
5530	18328	31231	0.88	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5530	18328	31232	0.88	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6885	17892	30517	0.59	4.2E-02	BE268285.1	EST_HUMAN	601124568FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5'
7428	20103	33190	4.7	4.2E-02	AF276762.1	NT	Legionella pneumophila cellulase-peroxidase (celA) gene, complete cds
8710	21402	34547	3.86	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10064	22712	38930	1.22	4.2E-02	Q16950	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-98)
10899	23645	36898	2.82	4.2E-02	AA976118.1	EST_HUMAN	on33b1.s1 NCL_OGAP_Luc Homo sapiens cDNA clone IMAGE:1559461 3' similar to gb:M65280
11278	23636	37231	2.54	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11278	23639	37252	2.54	4.2E-02	BE815822.1	EST_HUMAN	PN3-BN0774-260500-009-c10 BN0774 Homo sapiens cDNA
11489	24080	37402	1.68	4.2E-02	AF178458.1	NT	PN3-BN0774-260500-009-c10 BN0774 Homo sapiens cDNA
12415	25335		3.43	4.2E-02	AI953494.1	EST_HUMAN	PRRS isolate PRRS/38 envelope glycoprotein gene, complete cds
487	13281	25916	1.24	4.1E-02	AF200639.1	NT	w48910.x1 NCL_OGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2883	15392	28131	1.04	4.1E-02	AE002330.2	NT	Homo sapiens HP31 gene, intron 5
4438	17176		7.52	4.1E-02	AW893484.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5556	18353	31262	0.82	4.1E-02	BE251894.1	EST_HUMAN	QY1-NN0012-160400-164-008 NN0012 Homo sapiens cDNA
6566	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	PN3-BN0774-260500-009-c10 BN0774 Homo sapiens cDNA
6783	18527		0.67	4.1E-02	X75681.1	NT	601107535FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6899	18591	32742	1.25	4.1E-02	AE002132.1	NT	601107535FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7413	20090	33174	2.09	4.1E-02	7662347	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
							Uveasplasma uveasplasma section 33 of 59 of the complete genome
							Homo sapiens KIAA0867 protein (KIAA0867), mRNA

Page 145 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33285	0.66	4.1E-02	L02110.1	NT	Mus testis nuclear protein 1, with the proline insert encompassing the entire pseudogene (3' end) and 3' LTR
7565	20329	33439	3.12	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PU11) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and cadherin channel alpha-1 subunit
8541	21203	34376	0.68	4.1E-02	P34687	SWISSPROT	CTC10L COLLAGEN 34
9052	21741	34869	0.81	4.1E-02	AA372398.1	EST_HUMAN	EST184297 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25339	30715	4.07	4.1E-02	AJ271806.1	NT	Breast cancer protein 1 gene for pleckstrin homology domain, exons 1-12
3238	18000	28950	3.26	4.0E-02	AB040304.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3760	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5295	18100	30759	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18998	31866	0.63	4.0E-02	BF110434.1	EST_HUMAN	765207.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3668380 3' similar to TR:075296 O75296 R29124.1
7500	20258	33366	0.57	4.0E-02	L23898.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (subunit) mRNA, complete cds
7550	20314	33440	0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GP-anchored molecule-like protein, complete cds
7666	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GP-anchored molecule-like protein, complete cds
8617	21309	34451	2.22	4.0E-02	P06640	SWISSPROT	GLUCANAMYLASE S162 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197	35406	0.78	4.0E-02	BF979376.1	EST_HUMAN	802153847 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9597	22220	35406	4.01	4.0E-02	AJ000594.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thio: fumarate reductase subunit A
9884	22534	35406	1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24369	30868	1.54	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cat+ ATPase
12053	25169	30868	3.31	4.0E-02	AJ001066.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1068	13859	28516	2.76	3.9E-02	BF519149.1	EST_HUMAN	UHH-BW1-antix-08-Q1-51 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.8E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1054	14680	27402	2.4	3.8E-02	AJ403386.1	NT	Musculus DNA for desmin-binding fragment DesD7
2708	15415	28487	1.69	3.9E-02	4508862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118	18860	29487	0.63	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	18860	29488	0.63	3.8E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

Page 146 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
6544	18439	31353	1.04	3.9E-02	BE068841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833642 5'
6796	18557	31484	0.95	3.9E-02	BF075203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
6937	18439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049630 5'
7759	20435	33557	1.14	3.9E-02	BF238513.1	EST_HUMAN	601608848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4734779 5'
7859	20654	33778	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20554	33779	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11366	20396	33611	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25228		15.38	3.9E-02	AE042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24683		1.83	3.9E-02	U69051.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12688	28223		5.31	3.9E-02	AL048888.2	NT	Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, nmud28orf
1948	14680	27394	1.16	3.8E-02	BE865137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.9E-02	AJ251973.1	NT	Homo sapiens partial sizerin-1 gene
4876	17603	30226	1.1	3.8E-02	AJ124122.1	EST_HUMAN	AJ124122 NT2RN2 Homo sapiens cDNA clone NT2RM2001698 5'
5354	18157	30540	1	3.8E-02	M11228.1	NT	Human probin C gene, complete cds
5998	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
7218	19903	32978	1.66	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCAB8), mRNA
8502	21254		1.33	3.8E-02	M60075.1	NT	Human von Willebrand factor gene, exons 23 through 34
10549	23245	38481	2.82	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
971	13736	26401	4.84	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1387	14115	28760	0.91	3.7E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2230	14958	27698	3.84	3.7E-02	A984906.1	EST_HUMAN	wf8508X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2592	15286	28034	0.92	3.7E-02	AB019261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	15811	28457	0.99	3.7E-02	P78944	SWISSPROT	ECOMESEDERMIN
3047	13813	28458	2.99	3.7E-02	BF312983.1	EST_HUMAN	601688233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203		1.17	3.7E-02	6880541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Konmad), mRNA
6976	24422		0.83	3.7E-02	AF000063.1	NT	Aeropyrum pernix genome DNA, section 6/7

Page 147 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7592	20280	33368	0.58	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
9814	22563		1	3.7E-02	AA782516.1	EST_HUMAN	ad5509.st Soares_parenchyma_tumor_NDHPFA Homo sapiens cDNA clone IMAGE:1380912 3'
11664	24606	37811	3.86	3.7E-02	BF124974.1	EST_HUMAN	60176211YF1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024873 5'
12603	25193	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3646	16399	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare SstI gene for sucrose synthase
3654	19407	29046	0.89	3.6E-02	AL068806.1	NT	Homo sapiens genome region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5341	18144	30808	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X69403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30921	0.64	3.6E-02	AF181722.1	NT	Homo sapiens RUDAS (RUD2) mRNA, complete cds
6607	19370	32382	5.47	3.6E-02	AW645516.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6607	19370	32383	5.47	3.6E-02	AW645516.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6885	19678	32725	2.5	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (sgp2) gene, complete cds
7206	19861	32967	2.76	3.6E-02	AA714521.1	EST_HUMAN	hw20605.x1 NC1_CGAP CG80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gbJ00314 .rna2
7533	20203	33288	1.03	3.6E-02	BE1143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8291	21958	35130	1.72	3.6E-02	U20608.1	NT	Dicystostellium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dicystostellium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22165	35347	0.83	3.6E-02	BF347586.1	EST_HUMAN	602020463F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4166116 5'
11135	23803	37080	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820419F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11135	23803	37081	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820419F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11862	24456		1.46	3.6E-02	AI280965.1	EST_HUMAN	gk4800.x1 NC1_CGAP_C88 Homo sapiens cDNA clone IMAGE:1872188 3'
875	13644	20314	1.08	3.5E-02	U09508.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
988	13751	26413	1.39	3.5E-02	AF263417.1	NT	Homo sapiens microosomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14303	26961	1.55	3.5E-02	BF078085.1	EST_HUMAN	6020385136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1556	14303	26962	1.55	3.5E-02	BF078085.1	EST_HUMAN	6020385136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4188	16929	29558	1.83	3.5E-02	AE001773.1	NT	Thermoboga maritima section 85 of 136 of the complete genome
4281	17020	29647	1.27	3.5E-02	P93780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
8127	18805	31873	1.77	3.5E-02	J01238.1	NT	Maize actin 1 gene (Macl), complete cds

Page 148 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7677	20572		0.78	3.5E-02	H26951.1	EST_HUMAN	3p44a05.t1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8921	21213	34387	2.7	3.5E-02	BE989870.1	EST_HUMAN	807164470R12R NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3626737 3'
9917	22566	35762	1.45	3.5E-02	X70642.1	NT	Lacids MG1363 gpB end drak genes
9995	22613	35817	0.5	3.5E-02	BE591042.1	EST_HUMAN	801344991F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11477	24078	37388	1.82	3.5E-02	AY185164.1	EST_HUMAN	PM1-C10326-2917336-002-R03 C10326 Homo sapiens cDNA
11477	24078	37389	1.82	3.5E-02	AY185164.1	EST_HUMAN	PM1-C10326-2917336-002-R03 C10326 Homo sapiens cDNA
12590	26234		5.69	3.5E-02	BE276948.1	EST_HUMAN	80178766F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13789	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	3x26d07.xt Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2814283 3' similar to SW:0211. HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1184	13936		7.14	3.4E-02	11345450	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220). mRNA
2391	15112	27849	2.06	3.4E-02	T67160.1	EST_HUMAN	yc20a05.t1 Stratiogene lung (R937210) Homo sapiens cDNA clone IMAGE:91280 5' similar to contains MER29 repetitive element
3424	16181	28831	1.4	3.4E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	18509	29145	0.7	3.4E-02	BE339514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3900	18650	29281	3.19	3.4E-02	AW784952.1	EST_HUMAN	RC8-UJ0015-210200-021-A10 UM0015 Homo sapiens cDNA
4559	17284	26922	2.41	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5000	17723		3.59	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIGONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6019	17740	30349	1.2	3.4E-02	AJ012489.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
8764	17823	30658	4.73	3.4E-02	U24393.1	NT	Human yeyl oxidase-like protein gene, exon 3
8159	20853		3.25	3.4E-02	A696628.1	EST_HUMAN	w89d04.xt NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2433081 3'
8648	21358	34482	1.38	3.4E-02	AA064880.1	EST_HUMAN	nu7008.s1 NCL CGAP_A1T Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element;
					TR-G1017425 G1017425		zq04f11.s1 Stratiogene muscle 937200 Homo sapiens cDNA clone IMAGE:928749 3' similar to
8914	21509		5.97	3.4E-02	AA194306.1	EST_HUMAN	IPISCKPLKVTLSRDG/PKATATNFTEITENILNKESVTADAGRVEITAAANSQGTAKAFINIVLDRPG
9978	22300		0.83	3.4E-02	AIOB2718.1	EST_HUMAN	PPT GRVVISDITEESVTLKWEKPKYDGGSOVYNYLLKRETSJAVWTEVSATVARTMKV/MKL ...;
363	13161		9.61	3.4E-02	AA398735.1	EST_HUMAN	oz99r03.xt Soares_papillary_tumor_NHFA Homo sapiens cDNA clone IMAGE:1683519 3'
1143	13598	26559	17.85	3.3E-02	AB035967.1	NT	z175608.xt Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
							Cricetulus griseus GYP2A17 mRNA for cytochrome P450 2A17, complete cds

Page 149 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1469	14236	26923	1.16	3.3E-02	AF10703.1	NT	Homo sapiens cytochrome P450C18 (CYP2C18) gene, exons 2 and 3
1635	14381	27068	1.47	3.3E-02	AF10703.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.26	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2077	14909		2.46	3.3E-02	R09112.1	EST_HUMAN	Y25609.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27810	1.31	3.3E-02	6755892	NT	Mus musculus tumor rejection antigen gp98 (Trst1), mRNA
4156	14391	27068	2.44	3.3E-02	AF10703.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4495	17171	28800	1.78	3.3E-02	6756682	NT	Mus musculus tumor rejection antigen gp98 (Trst1), mRNA
6336	19108	32095	27.36	3.3E-02	BF245695.1	EST_HUMAN	80183910FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19106	32096	27.36	3.3E-02	BF245695.1	EST_HUMAN	601853910FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20065	33169	0.63	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia methylglutathione synthase sulphydrylase (mgs) gene, partial cds
9222	21801	35071	0.74	3.3E-02	BF116621.1	EST_HUMAN	7m62d04.x1 NGL CGAP_Brc23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21801	35072	0.74	3.3E-02	BF116621.1	EST_HUMAN	7m62d04.x1 NGL CGAP_Brc23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35162	0.66	3.3E-02	AA489202.1	EST_HUMAN	ad08109 at Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24-1D5 (HUMAN);
9324	21991	35163	0.66	3.3E-02	AA489202.1	EST_HUMAN	ad08109 at Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24-1D5 (HUMAN);
11065	23795	37008	3.93	3.3E-02	BF691107.1	EST_HUMAN	80224771F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:432497 5'
12142	24630		3.24	3.3E-02	T96545.1	EST_HUMAN	y649T1.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
12259	24704		1.52	3.3E-02	AF286695.1	NT	Mus musculus E1F4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12288	24718		2.92	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
128	12844	25588	0.74	3.2E-02	AJ02005.1	NT	Oryzopsis cuticular gene encoding ileal sodium-dependent bile acid transporter
1104	13681	26520	7.01	3.2E-02	AF06276.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
1104	13681	26521	7.01	3.2E-02	AF06276.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
2112	14843		3.01	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3131	15898	28540	10.06	3.2E-02	BE867353.1	EST_HUMAN	801442431F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE:3846727 5'
3701	16454	28094	0.82	3.2E-02	AL169203.2	NT	Homo sapiens chromosome 21 segment HS210203
3942	16692	28330	1.84	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3942	16692	28331	1.84	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4193	16624		14.21	3.2E-02	X94788.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	Sacchara nidifica malvase (malk) gene, chloroplast gene encoding chloroplast protein, partial cds
4894	17621		1.09	3.2E-02	AF108906.1	NT	Mus musculus MHC class II region RD gene, partial cds; B1, C2, GBA, NG22, Gb, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5448	18247	31135	1.83	3.2E-02	X68709.1	NT	S. griseocaudum wHG-Stv gene

Page 150 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6448	18247	31136	1.93	3.2E-02	X88708.1	NT	S. glaucocaneum whiG-Stv gene
6431	19189	32109	3.13	3.2E-02	M32437.1	NT	Rat polyomavirus left junction in cell line W88.14
6432	19200		33.46	3.2E-02	T89387.1	EST_HUMAN	Y433h12.81 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element;
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Sequius oedius tissue kallikrein gene, complete cds
7652	20328	33436	0.64	3.2E-02	11424048	NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8109	20863	34030	4.84	3.2E-02	6860565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
8839	21531		0.73	3.2E-02	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9125	21813	34878	1.21	3.2E-02	A1278971.1	EST_HUMAN	qm17504.X1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1882083 3'
9125	21813	34879	1.21	3.2E-02	A1278971.1	EST_HUMAN	qm17504.X1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1882083 3'
9657	22805		4.07	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.61 Soares_pineal_gland_X3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gbl.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10256	22904	36114	0.95	3.2E-02	U88762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	13566		2.14	3.1E-02	453341.6	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1282	14032	28702	1.72	3.1E-02	F18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14622	27532	1.09	3.1E-02	6871684	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (AP3d), mRNA
1997	14703		1.34	3.1E-02	Z50087.1	NT	Drosophila melanogaster mRNA for headcase protein
5182	17690	30506	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5276	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	zs81a05.11 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703558 5'
5591	18358	31289	0.74	3.1E-02	BF68742.1	EST_HUMAN	602068763.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
5628	25072	31336	0.59	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (theB- and theC-homologs, unknown genes) and flanking genes, strain FAM18
5940	21532	34677	0.46	3.1E-02	BE965092.2	EST_HUMAN	601658376.R1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3886291 3'
9831	22579	35778	2.93	3.1E-02	AF034778.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
11795	24358	37680	1.78	3.1E-02	8754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
1619	14368		1.88	3.0E-02	AF187125.1	NT	Phykolates minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2580	15304	28040	0.97	3.0E-02	AA402242.1	EST_HUMAN	z55h03.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3645	16338	28038	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	16480		0.74	3.0E-02	AY180223.1	EST_HUMAN	QV2-ST0286-150200-040-408 ST0286 Homo sapiens cDNA
3828	16878		1.42	3.0E-02	AA384003.1	EST_HUMAN	EST174680 Pineal gland II Homo sapiens cDNA 5' end
4991	17714	30318	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6160	19937	31605	1.4	3.0E-02	N98615.1	EST_HUMAN	2a39a10.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294909 5' similar to contains element TARY repetitive element;
6160	19937	31606	1.4	3.0E-02	N98615.1	EST_HUMAN	2a39a10.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294909 5' similar to contains element TARY repetitive element;
6692	19509	32048	3.32	3.0E-02	AJ242506.1	NT	Cytoplast carboxy terminal for inducible nitric oxide synthase (NOS gene)
6803	19497	32493	2.84	3.0E-02	BE889948.1	EST_HUMAN	801512206F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913848 5'
6805	19497	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	801512206F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913848 5'
6971	19453	32472	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6971	19453	32473	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19819	32885	1.4	3.0E-02	M86524.1	NT	Human dystrophin gene
7483	20155	32463	0.59	3.0E-02	BF246361.1	EST_HUMAN	801854981F1 NIH_MGC 37 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720	32705	0.48	3.0E-02	BF079705.1	EST_HUMAN	602154394F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295654 5'
8539	21231	34373	0.66	3.0E-02	BF353898.1	EST_HUMAN	IL5-HT0704-280600-108-004 HT0704 Homo sapiens cDNA
8692	21364	34373	1.8	3.0E-02	AF276654.1	NT	Omlthorhynchus andinus coagulation factor X mRNA, complete cds
10357	23004	36221	1.48	3.0E-02	AE001797.1	NT	Thermococcus maritima section 109 of 136 of the complete genome
10448	23092	36322	0.49	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23862	37148	2.73	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ne8704.81 NCJ CGAP_K01 Homo sapiens cDNA clone IMAGE:911263
12243	23389	30618	2	3.0E-02	R32019.1	EST_HUMAN	ph33304.81 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:134407 3'
12387	24609		2.46	3.0E-02	AW895953.1	EST_HUMAN	QV4-NN0038-270400-187-N05 NN0038 Homo sapiens cDNA
12628	25393		2.06	3.0E-02	AF048087.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2436	16594	27891	1.27	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2890	16768	28402	1.04	2.9E-02	BE66944.1	EST_HUMAN	801338428F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3600685 5'
2890	16768	28403	1.04	2.9E-02	BE66944.1	EST_HUMAN	801338428F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3600685 5'
3903	16658	28289	0.89	2.9E-02	H72805.1	EST_HUMAN	y07010.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18754	31715	0.97	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6199	18975	31683	7.39	2.9E-02	BF032233.1	EST_HUMAN	801432661F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3865598 5'
6855	19565	32585	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flacC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32904	12.03	2.8E-02	BE271437.1	EST_HUMAN	801140729F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3049830 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	20592	33723	0.87	2.8E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlichtendalla chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20592	33724	0.87	2.8E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlichtendalla chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
8568	22211	36394	2.49	2.8E-02	AF175979.1	EST_HUMAN	GN3-PT0014-071298-051-c04 PT0014 Homo sapiens cDNA
8568	22211	36397	2.49	2.8E-02	AF175979.1	EST_HUMAN	GN3-PT0014-071298-061-c04 PT0014 Homo sapiens cDNA
6724	22425	37425	0.76	2.8E-02	AF176697.1	EST_HUMAN	EST3388708 IMAGE resequences, MAGN Homo sapiens cDNA
10243	22891	39103	1.25	2.8E-02	AF0000084.1	NT	Aeropyrum pernix genomic DNA, section 777
10977	17902	30590	1.97	2.8E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
562	13335		0.66	2.8E-02	AF1970163.1	EST_HUMAN	EST382234 IMAGE resequences, MAGK Homo sapiens cDNA
3360	18119	28775	1.3	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
3360	18119	28776	1.3	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
5400	18200	30905	11.62	2.8E-02	BE741083.1	EST_HUMAN	607594078F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948067 5'
6711	19628	32670	1.15	2.8E-02	I78960.1	EST_HUMAN	Y21938.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8226	20920	34058	1.61	2.8E-02	AJ003820.1	NT	Orleatadigma plantagineum mRNA for homeodomain leucine zipper protein (bb-1)
8915	21608	34749	0.85	2.8E-02	AA280782.1	EST_HUMAN	zaf65c08.1 NCL_GGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5'
8109	21798	34680	1	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
8212	21891	35058	0.89	2.8E-02	AE001082.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R06986.1	EST_HUMAN	Y12H02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
12630	24876		1.48	2.8E-02	X06322.1	NT	Yeast GN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human geminin T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRCBV27S1P, TCRCBV22S1A2N1, TCRCBV6S1A1T, TCRCBV7S1A1N2T, TCRCBV6S2A2PT, TCRCBV7S2A1N4T, TCRCBV6S7P, TCRCBV7S3A2T, TCRCBV13S2A1T, TCRCBV6S2A2PT, TCRCBV7S2A1N4T, TCRCBV13S9/13S9
1472	14219	28905	1.23	2.7E-02	U68059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3425	18182	28632	1.74	2.7E-02	AL161404.2	NT	Y08H12.1T Soares_mullipla_polarisatc_2NHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	18918	28645	1.92	2.7E-02	N47268.1	EST_HUMAN	Y08H12.1T Soares_multiple_sclerotic_2NHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	18918	28646	1.92	2.7E-02	N47268.1	EST_HUMAN	Y08H12.1T Soares_multiple_sclerotic_2NHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	Y33408.1T Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS :
5912	18501	31529	0.86	2.7E-02	X51670.1	NT	T. aestivum p1T1420 mRNA for wheat type V thionin
5855	18571	31612	0.84	2.7E-02	AB004789.1	NT	Oniza salvia mRNA for ascorbate oxidase, partial cds
6505	19270		0.93	2.7E-02	X97690.1	NT	A. bisporus pgk4 gene
6967	19449	32487	2.29	2.7E-02	AA9693571.1	EST_HUMAN	AB06H03.at Soares_tetral_fetus_Nb2HFS_gw Homo sapiens cDNA clone IMAGE:1624691 3'

Page 153 of 538
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8252	20948		1.08	2.7E-02	A1377038.1	EST_HUMAN	tc25q08.x1 Soares_tadl_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:20655982 3' similar to contains Alu repetitive element
8514	21206	34349	0.49	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
558	13340	25089	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2368	15088	27525	3.29	2.8E-02	AA480021.1	EST_HUMAN	ac02b02.s1 StrataGene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2368	15090	27627	4.49	2.8E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2368	15090	27528	4.49	2.8E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2916	15682		1.88	2.8E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G8A, NG22, G9, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4947	17577	30200	2.25	2.8E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5005	17728	30332	1.56	2.8E-02	AE002014.1	NT	Delonococcus radiorum R1 section 151 of 229 of the complete chromosome 1
5032	17752	30384	2.35	2.8E-02	AW241154.1	EST_HUMAN	Xa52004.X1 NCL CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069
5754	18546		0.7	2.8E-02	AL161663.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
5900	18590		0.59	2.8E-02	AL161663.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6125	18603		7.34	2.8E-02	AL206030.1	EST_HUMAN	qg2711.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762217 3'
6331	18101	32089	1.9	2.8E-02	BE821748.1	EST_HUMAN	601483473.T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6728	18502	32583	0.9	2.8E-02	Z59004.1	NT	Vaccinia virus ORF1L, strain Wyeth
6728	18502	32584	0.9	2.8E-02	Z59004.1	NT	Vaccinia virus ORF1L, strain Wyeth
6810	19471	32494	7.11	2.8E-02	6891271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8403	21036	34232	0.71	2.8E-02	AA80946.1	EST_HUMAN	ac22004.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
9280	22014	35182	1.16	2.8E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9814	22267	35453	0.75	2.8E-02	AF114952.1	NT	Saccharomyces diereensis NRRL Y-12539(T) ATP synthase subunit 8 (ATP8) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9814	22267	35454	0.75	2.8E-02	AF114952.1	NT	Saccharomyces diereensis NRRL Y-12539(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10003	22950	38166	4.39	2.8E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11191	23556		1.87	2.8E-02	4806465	NT	Homo sapiens radixin (RDX) mRNA
11361	24049		2.33	2.8E-02	AA278351.1	EST_HUMAN	zsa3402.1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:704162 5'
11553	24152	37469	2.2	2.8E-02	AW500547.1	EST_HUMAN	UI-HF-BNG-ek-e-10-04.U1.N1H_MGC_60 Homo sapiens cDNA clone IMAGE:3077468 5'
12170	25378	30618	2.09	2.8E-02	BF34827.1	EST_HUMAN	602015501.F1 NCL CGAP_Bm04 Homo sapiens cDNA clone IMAGE:4150944 5'
619	13303	25835	1.75	2.8E-02	AI793130.1	EST_HUMAN	on2606.y5 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1557827 5'
519	13303	25836	1.75	2.8E-02	AI793130.1	EST_HUMAN	on2606.y5 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1557827 5'
791	13593	28224	15.9	2.8E-02	BE974314.1	EST_HUMAN	601480305.92 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'

Page 154 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
849	13619	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	60169035R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2768	14721		2.24	2.5E-02	U12571.1	NT	Rattus norvegicus rephosphatase mRNA, complete cds
2956	15722	28371	4.93	2.5E-02	X95897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2956	15722	28372	4.35	2.5E-02	X95897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17879	29399	1	2.5E-02	BE701195.1	EST_HUMAN	PM2-NN10128-060700-001-a12 NN10128 Homo sapiens cDNA
4023	17879	29400	1	2.5E-02	BE701195.1	EST_HUMAN	PM2-NN10128-060700-001-a12 NN10128 Homo sapiens cDNA
4182	16922	29550	4.23	2.5E-02	AW169214.1	EST_HUMAN	336G108.x1 Soares_NFL_T_OBC S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5923	18422	31035	0.61	2.5E-02	AI732776.1	EST_HUMAN	336G1010.x3 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:910354 3'
6100	18878		6.01	2.5E-02	BE670128.1	EST_HUMAN	7c30068.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1;11 L1 repetitive element;
8115	18993		4.1	2.5E-02	BE746898.1	EST_HUMAN	601576393FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
8244	19018	31692	1.04	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33337	1.7	2.5E-02	BF528722.1	EST_HUMAN	602070562FT NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
7563	20233	33337	1.7	2.5E-02	BF528722.1	EST_HUMAN	602070562FT NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34550	0.81	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8963	21554	34659	0.47	2.5E-02	AW025821.1	EST_HUMAN	346Bc10.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2516370 3'
9968	22614		0.55	2.5E-02	X71930.1	NT	D radicum 28S ribosomal RNA, D2 domain
10482	23128	36336	0.65	2.5E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NBRPU Homo sapiens cDNA clone IMAGE:1686982 3'
10712	23401	36840	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHEICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10712	23401	36841	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHEICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10773	23456	36700	2.32	2.5E-02	AJ231636.1	NT	Bac taurus perid. stat5b gene, exons 17-19
10795	23478						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ae1pha) and major histocompatibility protein class II beta chain (E1beta) genes, complete cds;
11770	24391		3.46	2.5E-02	AF060157.1	NT	butyrophilin-like (NG9), butyrophilin-like
12134	25311		2.65	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
12311	25162		2.89	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) LOC363634, mRNA
12432	24804	31043	1.94	2.5E-02	BE973327.1	EST_HUMAN	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
1593	14339	27028	1.7	2.5E-02	H66884.1	EST_HUMAN	601692365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935613 3'
2037	15594	27601	1.92	2.4E-02	P01901	SWISSPROT	y78f1.1r1 Soares fetal liver spleen cDNA clone IMAGE:211149 5'
2037	15594	27602	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4333	17074	26702	1.65	2.4E-02	J06110.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4465	17220	29847	1.56	2.4E-02	P01601	SWISSPROT	T. thermophila calcium-binding 28 kDa (TCBP 28) protein mRNA, complete cds
4465	17220	29848	1.56	2.4E-02	P01601	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

Page 155 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6068	17787	30403	0.65	2.4E-02	8922702	NT	Human epsilon hypothalamic protein FLJ10844 (FLJ10844), mRNA
6121	18899	31887	0.9	2.4E-02	W86980.1	EST_HUMAN	Z163304.s1 Soares_fetal_liver_spleen_TNFSF31 Homo sapiens cDNA clone IMAGE:416791 3'
6267	19040	32016	0.58	2.4E-02	M31650.1	NT	Chicken myotubular alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6267	19040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myotubular alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	19809	32875	0.8	2.4E-02	Z20373.1	EST_HUMAN	HSAAA0KXV.T_Human adult Fibrocytes/osteocoma cell-line Homo sapiens cDNA
7138	19825	32892	0.9	2.4E-02	X12825.1	NT	Rat gene for uncoupling protein (UCP)
7138	19825	32893	0.9	2.4E-02	X12825.1	NT	Rat gene for uncoupling protein (UCP)
7791	20489		0.72	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0198-230300-019-06 ST0180 Homo sapiens cDNA
7844	20539		0.6	2.4E-02	M16780.1	NT	Human retinotransposon 3' long terminal repeat
8340	21033		0.69	2.4E-02	H78376.1	EST_HUMAN	yt1205.s1 Soares_fetal_liver_spleen_TNFSF31 Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element/contains A3R repetitive element;
8429	21122	34260	0.78	2.4E-02	N69442.1	EST_HUMAN	z335g11.s1 Soares_fetal_liver_spleen_TNFSF31 Homo sapiens cDNA clone IMAGE:294568 3' similar to gb K02809 FAT5R7K Rat (RNA) contains A3R/b1 A3R repetitive element;
8995	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8907	21598	34740	0.78	2.4E-02	AA625660.1	EST_HUMAN	z301c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 SLET XTR repetitive element;
9391	22244	35427	0.92	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphuryase (crx5) gene, complete cds
9501	22244	35428	0.82	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphuryase (crx5) gene, complete cds
8708	22357	35553	2.38	2.4E-02	AV682854.1	EST_HUMAN	AV682854 GKC Homo sapiens cDNA clone GKCPD03 5'
9681	22531	35728	2.73	2.4E-02	AA493884.1	EST_HUMAN	inh7012.s1 NCL_GGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element/contains element PTRS repetitive element;
10512	23158		0.46	2.4E-02	BE387111.1	EST_HUMAN	601274862F1NH_MGC_20 Homo sapiens cDNA clone IMAGE:3871602 6'
11565	24164	37475	1.89	2.4E-02	AF106605.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown gene
11565	24164	37476	1.89	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11938	24495		2.28	2.4E-02	6827909	NT	Bacteriophage b14.67 complete genome
12061	24599	31424	1.91	2.4E-02	6759355	NT	Mus musculus Dmb homolog 1 (E_cdi) (Dmb1), mRNA
12136	24625	31094	2.37	2.4E-02	BE928859.1	EST_HUMAN	MRQ-F10176-310800-202-a08 F10176 Homo sapiens cDNA
12186	24637	31053	1.96	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor (cAMP-GEF1) mRNA, complete cds

Page 156 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12186	24657	31104	1.88	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12216	24678		1.34	2.4E-02	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12360	24764		3.88	2.4E-02	AB008589.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1865	14603		4.26	2.3E-02	W08340.1	EST_HUMAN	3x24q08.r1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:289284.5'
1880	14617		10.45	2.3E-02	U74165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2330	14672	27909	2.06	2.3E-02	U74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3970	16423	29084	6.16	2.3E-02	Z20377.1	EST_HUMAN	HSAAACACDH.P. Human foetal Brain Whole tissue Homo sapiens cDNA
3702	16455		0.8	2.3E-02	L23429.1	NT	Canis bala-galactoside-binding lectin (LGALS3) mRNA, 3'end
4129	16871	29469	1.06	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4129	16871	29500	1.06	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	29755	0.93	2.3E-02	AW889107.1	EST_HUMAN	GM4-NN0080-280-600-160-504 NN0080 Homo sapiens cDNA
4415	17152	29780	0.88	2.3E-02	BE935225.1	EST_HUMAN	GM3-MT0118-010600-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	BE935225.1	EST_HUMAN	GM3-MT0118-010600-318-g07 MT0118 Homo sapiens cDNA
4416	17680	29782	1.14	2.3E-02	AW693693.1	EST_HUMAN	3x26d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671.3'
4416	17680	29783	1.14	2.3E-02	AW693693.1	EST_HUMAN	3x26d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671.3'
4555	17290	28919	2.66	2.3E-02	BF026487.1	EST_HUMAN	6016727278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386.5'
4555	17290	29620	2.66	2.3E-02	BF026487.1	EST_HUMAN	6016727278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386.5'
5291	18069	30756	3.63	2.3E-02	U86303.1	NT	Caulethacter crescentius topoisomerase IV (PerE) subunit (perE) gene, complete cds, and propionyl-CoA carboxylase beta chain (ccbB) homolog gene, partial cds
6522	19288	32292	4.08	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 17
6883	17959	30613	0.68	2.3E-02	BE141476.1	EST_HUMAN	MRO-H0080-017099-002-609 HT0080 Homo sapiens cDNA
7776	20472	33595	0.28	2.3E-02	U03810.1	NT	Human plectin (PLECT) gene, exons 3-32, and complete cds
8370	21063	34204	0.84	2.3E-02	AL298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8370	21063	34205	0.84	2.3E-02	AL298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34429	0.68	2.3E-02	AI695360.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147.3'
8597	21289	34430	0.68	2.3E-02	AI695360.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147.3'
9036	21728	34880	0.98	2.3E-02	P41986	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9759	22410	35617	0.71	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9829	22577	35776	1.33	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9829	22577	35777	1.33	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Basillus licheniformis isolate N57N1 Kera gene, partial cds

Page 157 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10682	23373	36815	2.16	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE SUB2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12058	25168		5.07	2.3E-02	BE278331.1	EST_HUMAN	60117886FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12562	24832	30397	2.19	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12616	25408		2.42	2.3E-02	U11077.1	NT	Dicystellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12807	25280		1.62	2.3E-02	11428388	NT	Homo sapiens dead finger (Diaphophila)-like 1 (DRL1), mRNA
720	13494	29147	4.13	2.2E-02	AF018267.1	NT	Columbia lila nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1741	14483		1.38	2.2E-02	AF018267.1	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z82001.1	NT	S. pneumoniae popA gene and open reading frames
3423	16185		1.49	2.2E-02	AA577785.1	EST_HUMAN	mm24604.3T NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3537	16390		4.01	2.2E-02	AF083094.1	NT	Infectiousursal disease virus segment B strain IL4 VP1 gene, complete cds
3834	16585	29221	1.28	2.2E-02	AF060137.1	EST_HUMAN	PMO-BT0340-170100-024-653 BT0340 Homo sapiens cDNA
3899	16649	29290	0.76	2.2E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL245c
6006	17729	30333	1.05	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7146	19833	32902	3.63	2.2E-02	AF060721.1	EST_HUMAN	AV690721 GKB Homo sapiens cDNA clone GK8AND03 3'
8269	20663	34104	1.82	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8269	20663	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X70483.1	NT	P. vulgaris alpha tub 2 mRNA
9586	22239	35422	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORGTL4 gene region, section 1/2 (DLEC1, ORGTL3, ORGTL4 genes, complete cds)
9586	22239	35423	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORGTL4 gene region, section 1/2 (DLEC1, ORGTL3, ORGTL4 genes, complete cds)
10105	22763		0.89	2.2E-02	0678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11167	23634	37115	1.88	2.2E-02	BE797601.1	EST_HUMAN	601584309FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638571 5'
11841	24425	37766	1.64	2.2E-02	11428382	NT	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
12315	24737		4.07	2.2E-02	AA563563.1	EST_HUMAN	ne47107.1s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:300541 3' similar to contains Alu repetitive element
410	13195		6.11	2.1E-02	AF761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
436	13222		8.98	2.1E-02	AF028728.1	NT	Dicystellum discoideum histidine kinase C (dhcC) mRNA, complete cds

Page 158 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	13989	26855	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cdkLM cluster, CdkK (cdkK), CdkL (cdkL), and spore coat protein CdkM (cdkM) genes, complete cds
1366	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1366	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27492	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2028	14763	27493	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2591	15305	28041	1.32	2.1E-02	AA226095.1	EST_HUMAN	nc2103.11 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:1008920
2819	13534	26783	4.48	2.1E-02	N29266.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
3571	16328	26973	1	2.1E-02	AA461271.1	EST_HUMAN	Scars, total, fetus, N12Hfg, 9w Homo sapiens cDNA clone IMAGE:798121 5'
4110	18933	29480	0.81	2.1E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	26941	0.81	2.1E-02	BF343655.1	EST_HUMAN	60201506F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4410	17147	26775	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
4421	17157	26788	1.53	2.1E-02	A1768127.1	EST_HUMAN	wgB1d11.x1 Scars, NSF_Fg_9w_OT_PA_P_51 Homo sapiens cDNA clone IMAGE:2371509 3'
4481	17197		0.69	2.1E-02	Y18213.1	NT	Homo sapiens putative psitt-HbA pseudogene for hair keratin, exons 2 to 7
4882	17396	30031	4.51	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL165302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4769	17501	30124	0.76	2.1E-02	A1823432.1	EST_HUMAN	WH54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384828 3'
5553	18350	31259	1.13	2.1E-02	AW376529.1	EST_HUMAN	QV4-H70244-111186-040-H05 HT0244 Homo sapiens cDNA
6868	19448	32466	0.88	2.1E-02	BF086169.1	EST_HUMAN	DV3-GN0058-120600-323-a12 GN0058 Homo sapiens cDNA
8417	21110	34249	0.6	2.1E-02	9790238	NT	Mus musculus coding nonh T (Snx1), mRNA
9431	22065	35236	0.5	2.1E-02	AA984288.1	EST_HUMAN	AmB3907.a1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9503	22164	35368	0.61	2.1E-02	AJ24231.1	NT	Alu repetitive element, contains element MER11 repetitive element
9531	22194	35369	2.61	2.1E-02	AJ24231.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9683	22593	35790	1.15	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9961	22909	35814	0.69	2.1E-02	AA984288.1	EST_HUMAN	AmB3907.a1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
10522	23198	36395	0.45	2.1E-02	AP001619.1	NT	Alu repetitive element, contains element MER11 repetitive element

Page 159 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11479	24090	37391	1.38	2.1E-02	6764255	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp60a), mRNA
12298	17197		8.82	2.1E-02	U19213.1	NT	Homo sapiens putative psbHBA pseudogene for hair keratin, exons 2 to 7
12359	28163	30601	1.89	2.1E-02	U34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30989	5.71	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
16	12844	25457	1.1	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCI CGAP_P228 Homo sapiens cDNA clone IMAGE:3309908 3' similar to contains MER1.3
17	12845	25458	14.4	2.0E-02	AW895953.1	EST_HUMAN	MER1 repetitive element 1
282	13061	25999	3.76	2.0E-02	6753635	NT	QV4-NN0038-270400-187405 NN0038 Homo sapiens cDNA
288	13094	26736	2.72	2.0E-02	AA468638.1	EST_HUMAN	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
781	13553	28214	2.11	2.0E-02	6753635	NT	aa15510.1 Scores. NIHMPu_ST Homo sapiens cDNA clone IMAGE:813307 6'
1086	13923	28483	1.8	2.0E-02	AL068803.1	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1177	13930	28595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1177	13930	28596	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
1856	14604	27313	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1886	14604	27314	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15506		3.24	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3077	12844	25457	2.11	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCI CGAP_P228 Homo sapiens cDNA clone IMAGE:3309908 3' similar to contains MER1.3
3141	15805		1.4	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Semaph6B), mRNA
3221	15984		2.95	2.0E-02	AF065688.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3958	16736	29370	1.3	2.0E-02	M18095.1	NT	P. vulgaris hydroxytyrosine-rich glycoprotein (HRGP) mRNA, 3' end
5543	18345	31254	0.95	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6807	18568	31523	0.7	2.0E-02	U35321.2	NT	Dicostelium discoideum class VII unconventional myosin (myo1) gene, complete cds
7450	20126	33217	1.11	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (4/7)
7450	20128	33218	1.11	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (4/7)
9777	22428		2.21	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10259	22907	35117	1.62	2.0E-02	AF640342.1	EST_HUMAN	wa17502.X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2268315 3'
10539	23236	39469	1.78	2.0E-02	Z73968.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 83/182
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxysteroid 17,20-lyase, complete cds
11682	24277	37598	2.21	2.0E-02	10947055	NT	Equus caballus ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA

Page 160 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11880	17809	30595	1.9	2.0E-02	AA45538.1	EST_HUMAN	cat1b10.t1 Soares_NHMP_P1 Homo sapiens cDNA clone IMAGE:813307 5'
12358	15508		1.82	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	25038		6.4	2.0E-02	T80037.1	EST_HUMAN	y04c09.t1 Soares_infant brain T1NB Homo sapiens cDNA clone IMAGE:24675 5'
677	13452	26095	2.15	1.9E-02	AA52764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element:
1611	14358	27047	1.15	1.8E-02	P16488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27498	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2032	14767	27497	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27969	0.97	1.8E-02	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2906	15872	28320	7.48	1.9E-02	AA173856.1	EST_HUMAN	nv04105.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1288337 3'
2852	15718	28569	1.68	1.9E-02	AV948668.1	EST_HUMAN	AV948669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3588	18351		1.18	1.9E-02	NS2250.1	EST_HUMAN	y28b02.s1 Soares_multiple_sclerosis_ZNBMSP Homo sapiens cDNA clone IMAGE:284331 3'
3681	18444		8.68	1.9E-02	BE736088.1	EST_HUMAN	501572862.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839684 5'
3703	16466	29095	0.95	1.9E-02	AI301183.1	EST_HUMAN	gpd4c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1887260 3' similar to contains Alu repetitive element:
4028	18770	29402	1.49	1.9E-02	AF147040.1	NT	Myoplatina thaliana VthA1 precursor (vthA1) and VthA2 precursor (vthA2) genes, partial cds
4170	18910	29539	1.83	1.9E-02	P06081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4170	16810	29540	1.83	1.9E-02	P06081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	29872	3.21	1.9E-02	AI452959.1	EST_HUMAN	W46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element:
4651	15227	27868	4.09	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5233	18039	30687	0.99	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5382	18182	30872	1.41	1.9E-02	L47572.1	NT	Melagris_gallipavo paraxonase-2(PON2) mRNA, complete cds
6701	18495		0.88	1.9E-02	AB019507.1	NT	Drosophila kenelzi gene for glycerol-3-phosphate dehydrogenase, complete cds
7001	18693	32744	1.38	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7001	18693	32745	1.38	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8486	21161		1.23	1.9E-02	AL162754.2	NT	Nalaeeria meningitidis serogroup A strain Z2481 complete genome, segment 3/7
9230	21909	35082	1.03	1.9E-02	BF1316128.1	EST_HUMAN	60188130.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9613	22668	35452	0.8	1.9E-02	L10114.1	NT	Nicotiana tabacum type I phytochrome (phyA) gene, complete cds
8945	22503	35768	1.05	1.9E-02	BF88832.1	EST_HUMAN	50186236.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076253 5'
10152	22800	36017	0.54	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 293900-2644784
10681	23372	36814	1.44	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12090	25171	30903	2.82	1.9E-02	AF101053.1	NT	Hindoo medicinalis intermediate filament filerlin mRNA, complete cds
12848	25147		1.36	1.9E-02	L11088.1	NT	Candida albicans lambda C63/B fragment

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
336	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	h32008.x1 NCL_GCAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element:
670	13448	26088	0.83	1.8E-02	BF308122.1	EST_HUMAN	601804328FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1137	12853	26553	1.32	1.8E-02	X17664.1	NT	H.fransci mRNA for myelin basic protein (MBP)
1416	14194	26847	1.73	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encodes (enc) mRNA, complete cds
2685	15394	28133	1.71	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 829 of the complete genome
3205	15968		0.94	1.8E-02	AB003925.1	EST_HUMAN	h622609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
4055	16910		0.89	1.8E-02	AA861446.1	EST_HUMAN	h224004.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408833 3'
4396	17133	29764	1.17	1.8E-02	AW068683.1	EST_HUMAN	QV4-DT0021-301268-071-b11 DT0021 Homo sapiens cDNA
6712	19627	32671	5.02	1.8E-02	P14310	SWISSPROT	HYPOHETICAL 7.9 KD PROTEIN IN FXN 5'REGION
8026	20724	33857	0.69	1.8E-02	U37091.1	NT	Mus musculus carboxic anhydrase IV gene, complete cds
8367	21060	34200	0.91	1.8E-02	AW005327.1	EST_HUMAN	QV2-NN1073-220400-165-h09 NN1073 Homo sapiens cDNA
8410	21103	34242	0.8	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9392	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	60187026FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9392	22054	35226	0.49	1.8E-02	BF241924.1	EST_HUMAN	60187026FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9542	22195		2.41	1.8E-02	AA897543.1	EST_HUMAN	g02009.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb1.11872 ZINC FINGER PROTEIN 91 (HUMAN);
9683	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	601465345FT NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3865983 5'
10126	22774	35937	1.37	1.8E-02	X96933.1	NT	L.elagnalis mRNA for myomodulin neuropeptide precursor
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11673	24211	37636	1.69	1.8E-02	AF000006.1	NT	Pyrococcus horikoshii OTS genomic DNA, 1166001-1485000 nt, position (817)
11628	24223	37545	3.32	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
885	13935	26323	1.86	1.7E-02	BE394689.1	EST_HUMAN	601310628FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632160 5'
1793	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	h32403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2993740 3' similar to contains L1.1 L1 repetitive element:
1793	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	h32403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2993740 3' similar to contains L1.1 L1 repetitive element:
1854	14602		3.41	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2106	14837		10.5	1.7E-02	AB004816.1	NT	Oryzolaque cinctus mRNA for mitochondrion, complete cds
2291	15016	27152	0.89	1.7E-02	S74188.1	NT	(microsatellite INRA41) Ovis aries-a sheep, Genomic, 361 nt, segment 1 of 2
2648	16366		1.01	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
2696	15762	28411	1.44	1.7E-02	AI147616.1	EST_HUMAN	q022008.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'

Page 162 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3902	10288		4.67	1.7E-02	AW827398.1	EST_HUMAN	hm4504.x1 NCL CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015634 3' similar to contains
3614	16367		0.73	1.7E-02	P04920	SWISSPROT	MER19 b1 MER19 repetitive element ; HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	AA699618.1	EST_HUMAN	ac1904.x1 Stragene ovary (h937217) Homo sapiens cDNA clone IMAGE:866927 3' similar to contains Alu
4176	16919		2.04	1.7E-02	R02306.1	EST_HUMAN	repetitive element contains element MER24 repetitive element ; y68608.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4420	17159	29787	1.49	1.7E-02	A305279.1	EST_HUMAN	qm0807.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb-X62559 ZINC FINGER PROTEIN 30 (HUMAN);
4491	17227	20656	1.78	1.7E-02	AW673183.1	EST_HUMAN	h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2033740 3' similar to contains L1.11 L1 repetitive element ;
4686	17400	30034	1.61	1.7E-02	V00841.1	NT	Messenger RNA for angelfish (<i>Lophius americanus</i>) somatostatin II
4763	17495	584	5.84	1.7E-02	A015076.1	EST_HUMAN	o161602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5007	17730	30334	0.69	1.7E-02	6981289	NT	Rattus norvegicus N-arginine diasec convertase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 hg3509.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
5035	18815	31775	2.07	1.7E-02	A1780247.1	EST_HUMAN	contains Alu repetitive element;
8484	19251	32250	1.47	1.7E-02	A038280.1	EST_HUMAN	o161603.x1 Soares_fetal_liver_spleen_1NFL9_S1 Homo sapiens cDNA clone IMAGE:1672891 3'
8950	19432	32448	1.27	1.7E-02	AF190530.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19791	32859	2.44	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7267	19941	33016	1.06	1.7E-02	L07899.1	NT	Homo scdipoprotein (a) gene, exon 1
7257	19941	33017	1.05	1.7E-02	L07899.1	NT	Human scdipoprotein (a) gene, exon 1
7642	20307		1.78	1.7E-02	AJ010770.1	NT	Homo sapiens hyaluron gene, exons 1-50
8336	20407	33523	0.98	1.7E-02	U01854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9598	22251	35437	1.3	1.7E-02	AL040564.1	EST_HUMAN	DKFZp4340314.11.434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp4340314.15'
11801	24391	37724	1.38	1.7E-02	5802007	NT	Homo sapiens serum constituent protein (USE55), mRNA
12631	26337	30716	2.39	1.7E-02	AW963482.1	EST_HUMAN	GM4-NN1030-040400-130-106 NN1030 Homo sapiens cDNA
488	13282		3.19	1.6E-02	AL021828.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162
1653	14399	27088	1.04	1.6E-02	V18898.1	NT	Trepomonas mallophilum flae23, flae23 and flid genes for flagellin subunit proteins and CAP protein homologue
2246	14974	27711	0.9	1.6E-02	O64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.9	1.6E-02	O64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02	AJ008345.1	NT	Homo sapiens KVLQ11 gene
2649	16359	28102	1.48	1.6E-02	AA484872.1	EST_HUMAN	ne81006.s1 NCL CGAP_Ewt1 Homo sapiens cDNA clone IMAGE:910687
2699	15408		0.96	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0334 protein, partial cds

Page 163 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3016	16762	28431	0.71	1.6E-02	AF112282.1	NT	Lasaea sp. Isolate Bcl cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28029	5.9	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0218-160200-063-C07 CT0219 Homo sapiens cDNA
3830	16561	28215	1.32	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21G101
4164	16936		2.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, leucine, RAGOS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
4297	17007	29940	0.97	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
5536	18334	31241	1.25	1.6E-02	6671715	NT	Mus musculus CD8 antigen (Cd8), mRNA
6546	19311	32316	2.05	1.6E-02	AB015281.1	NT	Candida albicans CgOCR3 gene, complete cds
6832	19494	32517	1.76	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	0.86	1.6E-02	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33947	0.76	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8078	20772		1.68	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
8940	22588		2.72	1.6E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22966	36184	1.29	1.6E-02	AA572818.1	EST_HUMAN	n1f9q03 at NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE914260 similar to SW_TELO_RABIT
10319	22980	36185	1.29	1.6E-02	AA572818.1	EST_HUMAN	P22994 TELOKIN, [1];
10826	26132	36748	2.38	1.6E-02	Z94828.1	NT	P22994 TELOKIN, [1];
11174	23841	37124	2.54	1.6E-02	AL161508.2	NT	Gallus microsalinella DNA (LE0260) (T1616E11)
11174	23841	37125	2.64	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11485	24098	37407	1.54	1.6E-02	AL373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
734	13508		23.05	1.6E-02	8623734	NT	q28610.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE2042442 3'
2133	14968	27598	4.24	1.6E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130694), mRNA
2172	14901	27635	1.69	1.6E-02	AL161594.2	NT	Y27607 at Soares fetal liver spleen TINF5 Homo sapiens cDNA clone IMAGE:243825 3'
3057	15523	28467	1.6	1.6E-02	AJ008216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3057	15523	28468	1.6	1.6E-02	AJ008216.1	NT	Homo sapiens CA141F gene, exons 1 to 48
3711	19494	29103	0.86	1.6E-02	BF092942.1	EST_HUMAN	Homo sapiens CA141F gene, exons 1 to 48
6201	18977	31955	1.56	1.6E-02	Q09711	SWISSPROT	MR4-TN0115-060300-201-012 TN0115 Homo sapiens cDNA
7219	19504		1.63	1.6E-02	11467282	NT	HYPOPHYSAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7301	19984	33050	1.2	1.6E-02	11418713	NT	Cyanophora paradoxa cyanelle, complete genome
							Homo sapiens KIAA11009 protein (KIAA11009), mRNA

Page 164 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20469	33592	1.83	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20478	33602	3.59	1.5E-02	11417739	NT	Homo sapiens very-early RNA synthetase 2 (VARS2), mRNA
8729	21421	34552	0.9	1.5E-02	BF345554.1	EST_HUMAN	6020191935F1 NCI, CGAP, Brn87 Homo sapiens cDNA clone IMAGE:4164504 5'
9385	21943	34553	0.61	1.5E-02	AF066774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22079	35251	1.47	1.5E-02	D44609.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
8711	22362	35559	0.88	1.5E-02	R32667.1	EST_HUMAN	X154510.1 Scores placenta N23HP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.88	1.5E-02	R32667.1	EST_HUMAN	Y154470.1 Scores placenta N23HP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23760	37058	3.48	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11163	23830	37109	2.14	1.5E-02	AL111238.1	NT	Batylis chinensis strain T4 cDNA library under conditions of nitrogen deprivation
11856	24440	37761	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	25214		1.74	1.5E-02	AW793834.1	EST_HUMAN	RC4-ON0049-140100-071-c11 ON0049 Homo sapiens cDNA
12787	25039		1.46	1.5E-02	A1763127.1	EST_HUMAN	W06103.x1 NCI, CGAP, CLL1 Homo sapiens cDNA clone IMAGE:2380493 3' similar to contains Alu repetitive element; contains element MER25 MSF1 repetitive element.
408	13183	229	2.29	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 83 of 94 of the complete genome
1036	13854	25813	4.43	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13963		1.24	1.4E-02	U32600.1	NT	Haemophilus influenzae Rd section 116 of 163 of the complete genome
1276	14026		3.77	1.4E-02	U67778.1	NT	Xenopus laevis neurogranin related TB (XNGNR-1b) mRNA, complete cds
1376	14123		1.45	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1507	14263		1.25	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3207	15970	28622	2	1.4E-02	AF160669.2	NT	Bifidobacterium longum NewH+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agl1) genes, complete cds; and N-acetylglucosaminylxyle repressor protein (nagCxyR) gene, partial cds
3393	16152	28905	1.07	1.4E-02	AW074212.1	EST_HUMAN	X080406.x1 NCI, CGAP, GUT Homo sapiens cDNA clone IMAGE:2575793 3'
3478	16234	28988	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28989	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3948	16401	29041	8.63	1.4E-02	6990818	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29817	7.77	1.4E-02	AW662688.1	EST_HUMAN	EST1374761 MAGOE resequencing, MAGG Homo sapiens cDNA
4455	17191	29818	7.77	1.4E-02	AW662688.1	EST_HUMAN	EST1374761 MAGOE resequencing, MAGG Homo sapiens cDNA
4821	17552	30174	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403.F1 NIH, MGC, 21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403.F1 NIH, MGC, 21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	18391	32079	5.47	1.4E-02	AA559000.1	EST_HUMAN	m11c04.s1 NCI, CGAP, B12 Homo sapiens cDNA clone IMAGE:1028990 3' similar to contains Alu repetitive element

Page 165 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	18091	32080	5.47	1.4E-02	AA560300.1	EST_HUMAN	nt11c04.s1 ncl_CGAP_B2 Homo sapiens cDNA clone IMAGE:1029900 3' similar to contains Alu repetitive element;
9038	20733		1.94	1.4E-02	AL0022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8796	21488	34634	0.76	1.4E-02	M81702.1	NT	Cardilla bodilli methanol oxidase (ACD1) gene, complete cds
9053	21742	34900	0.84	1.4E-02	AL272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	BE544569.1	EST_HUMAN	601078259.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11955	24526	37267	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324665.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12601	24813		2.36	1.4E-02	11428668	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27935	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST_HUMAN	602128475.F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	BF697081.1	EST_HUMAN	602128475.F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF162268.1	NT	Mus musculus beta-actin/cytoskeleton gene, complete cds
4874	17001	30223	0.93	1.3E-02	U66091.1	NT	Human germline T-cell receptor beta chain TORBV17S1A1T, TORBV2S1, TORBV10S1P, TORBV29S1P, TORBV18S1P, TORBV15S1, TORBV11S1A1T, HVB relic, TORBV28S1P, TORBV34S1, TORBV14S1, TORBV35S1, TORBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
5166	17875	30532		1.3E-02	AL049888.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmeq28orf
5166	17975	30533	1.31	1.3E-02	AL049888.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmeq28orf
6072	18951	31816	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6105	18983	31851	0.88	1.3E-02	M62962.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6866	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6865	17942	30536	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7471	20150	33244	4.9	1.3E-02	AF031593.1	EST_HUMAN	aw06g05.x1 Soares_parallel hybrid, tumor_NHHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8390	21073	34212	1.85	1.3E-02	AF166951.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107	22795	35967	1.91	1.3E-02	M83707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22928	36040	0.88	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10813	23593	36538	3.97	1.3E-02	AW269593.1	EST_HUMAN	xy34603.x1 Soares_NFL1_QBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36539	3.97	1.3E-02	AW269593.1	EST_HUMAN	xy34603.x1 Soares_NFL1_QBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12337	25352		1.44	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2569451 to 2812870
12437	24607		2.41	1.3E-02	6633069	NT	Human herpesvirus 6B, complete genome
12307	25145		28.18	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	25783	3.48	1.2E-02	AA056259.1	EST_HUMAN	256501.1 Scores relina N264HR Homo sapiens cDNA clone IMAGE:361840 5' similar to contains element L1 repetitive element:
440	13226	25869	1.66	1.2E-02	P38898	SWISSPROT	HYPOPHOSPHATE 17.1 KD PROTEIN IN PURG3 REGION
721	13495	26148	2.02	1.2E-02	AI183522.1	EST_HUMAN	q88a1.2x1 Scores tests_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1 L1 L1 repetitive element:
2176	14904	27637	1.81	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2178	14907	27640	1.77	1.2E-02	AF1731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2444	15163	27801	1.39	1.2E-02	AW172350.1	EST_HUMAN	X37409.x1 Scores NFL_T_GBC-ST Homo sapiens cDNA clone IMAGE:2659432 3'
2642	15163	27801	1.07	1.2E-02	AW172350.1	EST_HUMAN	X37409.x1 Scores NFL_T_GBC-ST Homo sapiens cDNA clone IMAGE:2659432 3'
3098	15663		6.66	1.2E-02	AA075416.1	EST_HUMAN	2m88903.1 Stratagene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:246020 5'
3281	16042	26591	2.11	1.2E-02	R62805.1	EST_HUMAN	Y11508.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:138503 3'
3294	16045	26694	0.92	1.2E-02	AF689594.1	EST_HUMAN	2d56d07.x4 Scores fetal_lung_Nb19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element:
4676	17409	30045	0.91	1.2E-02	AB87378.1	EST_HUMAN	Wm3970.x1 NCL_CGAP_U04 Homo sapiens cDNA clone IMAGE:2438335 3'
4859	17588	30211	2.03	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NP13) gene, complete cds
4981	17704		1.13	1.2E-02	AB019786.1	NT	Oncoyl pyrophosphatase OPUB1 mRNA, partial cds
6025	17746	30358	1.41	1.2E-02	AF1731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5666	18461	31375	1.73	1.2E-02	D76589.1	NT	Rena rugosa mRNA for galactulin, complete cds
6028	18808	31787	0.72	1.2E-02	AF046555.1	NT	Homo sapiens wiser1 (WBSOR1) and wiser2 (WBSOR2) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
6907	18845	32891	8.46	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7182	18878	32852	1.36	1.2E-02	H02197.1	EST_HUMAN	X34112.x1 Scores placenta N62HP Homo sapiens cDNA clone IMAGE:156695 3'
7212	18937	32872	10.54	1.2E-02	AF1732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJ109 5'
7456	20130	33222	0.97	1.2E-02	BF276850.1	EST_HUMAN	601882849.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4962635 5'
							OMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAc6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
7886	20591	33722	2.18	1.2E-02	Q11205	SWISSPROT	Homo sapiens fringe protein mRNA, partial cds
8092	20769	33917	1.35	1.2E-02	AF169812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8092	20769	33918	1.36	1.2E-02	AF169812.1	NT	Homo sapiens fringe protein mRNA, partial cds

Page 167 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8788	21480		1.03	1.2E-02	T76987.1	EST_HUMAN	y47208.at Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35376	2.46	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9570	22223	35408	1.35	1.2E-02	ALJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (GIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
12615	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujijwara) Homo sapiens cDNA clone GEN-557505 5'
12468	13995	26682	1.49	1.1E-02	AA070384.1	EST_HUMAN	zmba81.1 st Stratiogene neuroepithelium (#637251) Homo sapiens cDNA clone IMAGE:530924 3'
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H. sapiens LPA gene, exon 4
2031	14766	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	ab57711.at Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:4153908 5'
2880	15647		4.05	1.1E-02	N98523.1	EST_HUMAN	z40405.1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4153908 5'
3513	16269	28624		1.1E-02	AI653508.1	EST_HUMAN	ig9850.x1 NCI CGAP OV23 Homo sapiens cDNA clone IMAGE:235040 5'
4086	16829		0.83	1.1E-02	AW813768.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30132	1.5	1.1E-02	ALC46383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZ598E0924_x1 598 (synonym: hua1) Homo sapiens cDNA clone DKFZ598E0924
6057	18537	31789	1	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (gha), YnaH (ynaH), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH)
7497	20169	33261	2.51	1.1E-02	BE149911.1	EST_HUMAN	RC1-HT0259-100300-018-j07 HT0259 Homo sapiens cDNA
8538	21230	34372	0.91	1.1E-02	AW068160.1	EST_HUMAN	QV3-BN0045-220300-128-t02 BN0045 Homo sapiens cDNA
8721	21413	34556	0.87	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynkamara) Homo sapiens cDNA clone 3NH4040
8800	21492	34639	6.43	1.1E-02	C01982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9829	22480	35682	2.03	1.1E-02	AA082678.1	EST_HUMAN	zn24a01.r1 Stratiogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9894	22642	35954	3.55	1.1E-02	AA314695.1	EST_HUMAN	EST198494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10800	23580	35630	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5' (TBX5), mRNA
11823	24494		4.16	1.1E-02	AA66239.1	EST_HUMAN	Alu repetitive element
12678	16829		1.62	1.1E-02	AW813768.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
6	12633	25448	9.18	1.0E-02	AW848120.1	EST_HUMAN	MR3-CT0176-111095-003-e10 CT0176 Homo sapiens cDNA
1513	14260	25646	1.55	1.0E-02	AV388128.1	EST_HUMAN	GM2-HT0177-041068-017-t12 HT0177 Homo sapiens cDNA
2577	15291		1.87	1.0E-02	AA800389.1	EST_HUMAN	cc2208.at NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1350465 3'
3087	15852	28494	2.7	1.0E-02	BE835566.1	EST_HUMAN	ROD-FN0025-250500-021-002 FN0025 Homo sapiens cDNA
3257	16018	28569	1.49	1.0E-02	BE968599.1	EST_HUMAN	601849587R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3861	16811	28250	0.79	1.0E-02	AI055086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA

Page 168 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3876	16828	28284	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
4728	17458	30094	4.24	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4793	17524	30146	5.16	1.0E-02	R6667.1	EST_HUMAN	Y54901.1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:166933 5'
5331	18134	30759	0.72	1.0E-02	H52681.1	EST_HUMAN	Y54901.1 Soares ovary tumor 1N1OT Homo sapiens cDNA clone IMAGE:236941 5'
5681	18456	31370	0.57	1.0E-02	AF305368.1	NT	Mus musculus transcription complex subunit NF-A1c4 (Nfatc4) gene, exons 1 and 2
6026	18805	31766	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (SY2) gene, complete cds
6088	18866	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-510365-070100-201-H01 BT0366 Homo sapiens cDNA
6088	18866	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-510365-070100-201-H01 BT0366 Homo sapiens cDNA
6654	19551	32616	1.92	1.0E-02	Z29642.1	NT	Z.mys U3snRNA pseudogene
9283	21590	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	60146570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9283	21590	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	60146570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11229	23892		1.97	1.0E-02	AF167659.1	NT	Citithia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11269	23925		1.48	1.0E-02	A417961.1	EST_HUMAN	ig55H07.X1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:U15183_cds1
11340	24030	37334	1.97	1.0E-02	AV760016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5
12003	25416		1.83	1.0E-02	Q62203	SWISSPROT	repetitive element;
12059	25189	30811	3.76	1.0E-02	AW635321.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12075	25243		5.63	1.0E-02	S70330.1	NT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12592	25289		3.74	1.0E-02	X62694.1	NT	RC2-DT0007-120200-076-H02 DT0007 Homo sapiens cDNA
12603	25505	30857	1.84	1.0E-02	AB038887.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
873	13642	28312	2.1	9.0E-03	AF061126.1	EST_HUMAN	H sapiens gene for Mx2/CD63 antigen
1241	13900		2.07	9.0E-03	BE781869.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
1463	14211	26869	1.1	9.0E-03	AE001270.1	NT	WH4206.X1 NCI_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2369433 3' similar to contains element MER22 MER22 repetitive element;
2394	15115	27852	2.48	9.0E-03	AF161559.2	NT	60147024F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873448 5'
2403	15124	27861	0.92	9.0E-03	AF068934.1	NT	Tropomyosin pallidum section 86 of 87 of the complete genome
3659	15412	29050	1.21	9.0E-03	U06184.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
4927	17655	30267	1.03	9.0E-03	BE047949.1	EST_HUMAN	Mus musculus MHC class III protein RPT1 (Rpt1) mRNA, partial cds
4964	17689	30297	0.95	9.0E-03	T70044.1	EST_HUMAN	S. acidocaldarius thermopain gene, complete cds
4984	17699	30268	0.95	9.0E-03	T70044.1	EST_HUMAN	ic44e10.Y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291489 5'
5720	18512		1.15	9.0E-03	AI609792.1	EST_HUMAN	yc177008.s1 Stratagene lung (8637210) Homo sapiens cDNA clone IMAGE:80919 3'
6533	19299		4.88	9.0E-03	BE749988.1	EST_HUMAN	yc177008.s1 Stratagene lung (8637210) Homo sapiens cDNA clone IMAGE:80919 3'

Page 169 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7362	20043	33122	0.57	9.0E-03	AJ242218.1	EST_HUMAN	qh87c12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7371	20051	33132	0.8	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7774	20470		1.05	9.0E-03	AL035691.1	EST_HUMAN	DKFZ49434.0412.J1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZ49434.0412.5'
8147	20841		0.65	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAGNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9745	22398	35501	0.47	9.0E-03	P28011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
9762	22413	35520	1.44	9.0E-03	P29008	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10907	23937		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10935	23615	36566	1.57	9.0E-03	BE395380.1	EST_HUMAN	601310881.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens progargalinin (GAL1) gene, exons 1, 2, and 3
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens progargalinin (GAL1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE246385.1	EST_HUMAN	hw7809.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.46	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
489	13274		4.08	8.0E-03	AAT23007.1	EST_HUMAN	ZK30603.e1 Scores_gland_N31PG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element
968	13734	26399	36.32	8.0E-03	AF105693.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2154	14884	27617	2.2	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HSZTC083
2950	15728		0.63	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mcbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3353	16113	28766	1.08	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3655	16418	29059	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BNH1 INTERGENIC REGION
3655	16418	29059	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BNH1 INTERGENIC REGION
4350	17089	29721	4.88	8.0E-03	BF393327.1	EST_HUMAN	OM4-KN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5053	17802	30420	1.09	8.0E-03	AU140281.1	EST_HUMAN	AU140281 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
5436	18235		2.82	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, kIFC1, Fas-binding protein, BING1, lipase, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6106	25085	31952	1.45	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-54400 nt, position (27)
6551	19413	32427	4.89	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6620	19481		0.93	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19795	32860	1.79	8.0E-03	MT1197.1	NT	A californica (marine gastropod mollusc) neuropeptide gene (bag celi), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8781	21473	34819	0.63	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)

Page 170 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8808	21500	34648	3.29	8.0E-03	AW60892.1	EST_HUMAN	MR1-ST0111-111109-011-H08 ST0111 Homo sapiens cDNA
8816	21508	34653	0.49	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
8878	21560	34713	0.58	8.0E-03	978959	NT	Mus musculus fucosyl 2 (human) (Fuc2), mRNA
8948	22498	34897	4.83	8.0E-03	BE088508.1	EST_HUMAN	QV1-BT087-040400-131-03 B10877 Homo sapiens cDNA
10668	23357	36597	1.36	8.0E-03	BE788441.1	EST_HUMAN	60147687R1 N1F_MGC_68 Homo sapiens cDNA clone IMAGE:3878406 6'
10688	23586	37632	3.58	8.0E-03	Z49652.1	NT	S cerevisiae chromosome X reading frame ORF YJR152w
11716	24309	37632	4.74	8.0E-03	AF094559.1	NT	Human melanoma-associated antigen (IMAGE-G1) gene, complete cds
11814	24402	37779	22.71	8.0E-03	AA016160.1	EST_HUMAN	z63241.1 r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360716 5'
11853	24437	37779	1.36	8.0E-03	BF342438.1	EST_HUMAN	602013941F1 NCI_CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4149418 5'
11933	24497		1.74	8.0E-03	M98033.1	NT	Oryctolagus cuniculus elf-2a kinase mRNA, complete cds
11980	24523		1.74	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13453	26098	18.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
678	13453	26097	18.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
958	13721	26387	3.57	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1094	13852	26511	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.67	7.0E-03	Q61060	SWISSPROT	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFN-2)
1374	14122	26707	6.71	7.0E-03	AA665298.1	EST_HUMAN	db79809.31 Staphylococcus aureus 837202 Homo sapiens cDNA clone IMAGE:853145 3'
1491	14238	26924	3.37	7.0E-03	AW303599.1	EST_HUMAN	XZ1602.1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27175	1.24	7.0E-03	AW605566.1	EST_HUMAN	EST362828 IMAGE resequences, MAGA Homo sapiens cDNA
1735	14477	27176	1.24	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2254	15589	27722	1.86	7.0E-03	AF160273.1	EST_HUMAN	q34402.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3549	16301	29951	0.71	7.0E-03	AF160273.1	EST_HUMAN	q34402.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3749	16502	29137	0.8	7.0E-03	AW444663.1	EST_HUMAN	U1H-B13-alc-b-10-UJ1 NCI_CGAP_S1b5 Homo sapiens cDNA clone IMAGE:2733691 3'
3782	16544	29179	1.32	7.0E-03	AF195344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4000	16502	29137	0.83	7.0E-03	AW444663.1	EST_HUMAN	U1H-B13-alc-b-10-UJ1 NCI_CGAP_S1b5 Homo sapiens cDNA clone IMAGE:2733691 3'
4560	17266		1.24	7.0E-03	AW603898.1	EST_HUMAN	h88ad05.1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:286936 5'
4929	17557		2.17	7.0E-03	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21G078
5729	18521		0.75	7.0E-03	H71106.1	EST_HUMAN	yf8201.1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:211624 5' similar to gb-X14723 CLUSTERIN PRECURSOR (HUMAN);
6021	25033		4.9	7.0E-03	AW881059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6222	18906	31972	1.47	7.0E-03	W69251.1	EST_HUMAN	z63310.1 Soares_testis_NHT_NHHT Homo sapiens cDNA clone IMAGE:342475 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8443	18211	32207	3.44	7.0E-03	AA327128.1	EST_HUMAN	EST336874 Cdon 1 Homo sapiens cDNA 5' end
8470	18237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	764310.X1 NCL CGAP Brn23 Homo sapiens cDNA clone IMAGE:3368347 3' similar to TR-Q13387
8978	19504	32529	1.87	7.0E-03	BE928133.1	EST_HUMAN	O13387 HYPOTHETICAL PROTEIN 39408_2, contains TARY12 TARY1 TARY1 repetitive element;
7420	20097	33184	5.48	7.0E-03	Z35583.1	NT	CM2-CT0476-230900-347-511 CT0478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35583.1	NT	S cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175687.1	EST_HUMAN	RC5-HT0582-160300-011-D02 H70832 Homo sapiens cDNA
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9297	21864		0.75	7.0E-03	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9495	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	Y49610.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9620	22273	35480	2.67	7.0E-03	P49882	SWISSPROT	Alu repetitive element
9620	22273	35481	2.57	7.0E-03	P49882	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10204	22852		1.32	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10394	23030		0.77	7.0E-03	AI706734.1	EST_HUMAN	AV687379 GNG Homo sapiens cDNA clone GKCAFC07 5'
10728	23417	36558	2.63	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP82, complete cds
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
10982	23657	36740	1.71	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12468	24833		1.29	7.0E-03	AJ242804.1	NT	Sporobolus stipularis mRNA for putative glycine and proline-rich protein
12553	24890		1.79	7.0E-03	BE265253.1	EST_HUMAN	601146164F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
12981	25400		1.81	7.0E-03	Y17465.1	NT	Homo sapiens LSF22 gene, penultimate exon
12981	25400		1.72	7.0E-03	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1218	13959	26637	12.34	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
1218	13959	26638	12.34	6.0E-03	AW511148.1	EST_HUMAN	SW-PXR_HUMAN OT5469 ORPHAN NUCLEAR RECEPTOR PXR;
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	h22a05.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2853	15560	29305	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW-PXR_HUMAN OT5469 ORPHAN NUCLEAR RECEPTOR PXR;
2853	15560	28306	3.36	6.0E-03	AA759135.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
3240	15002		2.22	6.0E-03	H75680.1	EST_HUMAN	h278e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1921772 3'
3298	16060		1.31	6.0E-03	AF190338.1	NT	h278e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1921772 3'
3377	18136	28793	1.18	6.0E-03	U00880.1	NT	Y777604.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
							Neobios sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
							Fugu rubripes zinc finger protein, Isobc1n, fatty acid binding protein, sepiapterin reductase and vasotocin
							genes, complete cds

Page 172 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3377	16138	28704	1.18	6.0E-03	U06880.1	NT	Fugu rubripes zinc finger protein, leucodin, fatty acid binding protein, sepiaplatin reductase and vasodilator genes, complete cds
3534	16280		1.19	6.0E-03	W37895.1	EST_HUMAN	zr13a1.1.1 Soares, parathyroid, tumor, NBHPA Homo sapiens cDNA clone IMAGE:322172 5'
3652	18405	29044	3.68	6.0E-03	BF610986.1	EST_HUMAN	UJH-B14-aptm-c-08-J1.01 NCI CGAP, SUB8 Homo sapiens cDNA clone IMAGE:3087754 3'
3682	16435	29078	1.08	6.0E-03	BE077358.1	EST_HUMAN	RC1-BT0608-260409-014-07 BT0608 Homo sapiens cDNA
3759	16511	29147	1.22	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
3902	16652	29294	0.78	6.0E-03	AW847284.1	EST_HUMAN	RC3-CT0204-240899-021-B10 CT0204 Homo sapiens cDNA
3936	16698		1.29	6.0E-03	BE290708.1	EST_HUMAN	605942504F1 NIH_MGC, 13 Homo sapiens cDNA clone IMAGE:2859513 5'
4331	17070		1.84	6.0E-03	A016833.1	EST_HUMAN	0433c1.1.X1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4847	17381	30013	8.67	6.0E-03	AA324242.1	EST_HUMAN	EST272118 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5073	17782	30407	2.88	6.0E-03	Q62209	SWISSPROT	SYNAPTONEURAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
6051	25084	31802	0.67	6.0E-03	9627521	NT	Varicella virus, complete genome
6718	19633	32876	1.16	6.0E-03	O14984	SWISSPROT	SYNAPSIN III
6755	17924	33059	0.97	6.0E-03	BE263748.1	EST_HUMAN	601112353F1 NIH_MGC, 16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	18536	32905	0.81	6.0E-03	AA289442.1	EST_HUMAN	EST11049 Uterus tumor Homo sapiens cDNA 5' end
7149	19636	32905	0.81	6.0E-03	AA299442.1	EST_HUMAN	EST11049 Uterus tumor Homo sapiens cDNA 5' end
7646	20216	33318	0.69	6.0E-03	AF126894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-10 and complete cds
7702	20365	33479	0.62	6.0E-03	P17894	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7757	20453	33578	6.9	6.0E-03	AI033980.1	EST_HUMAN	0w13a04.1 Soares, parathyroid, tumor, NBHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
7874	20569	33685	2.17	6.0E-03	AW796337.1	EST_HUMAN	RC3-U06081-210300-432-052 U06081 Homo sapiens cDNA
7845	20540		1.58	6.0E-03	BF038198.1	EST_HUMAN	601460915F1 NIH_MGC, 68 Homo sapiens cDNA clone IMAGE:3856526 5'
9454	22004	35176	7.26	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9843	22591		2.13	6.0E-03	AI432681.1	EST_HUMAN	122022.X1 NCI CGAP, Kdrl1 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10062	22710	35928	0.89	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A;
10164	22842		1.14	6.0E-03	AF084555.1	NT	Bacillus subtilis fndD gene
10304	22951	36166	0.69	6.0E-03	X68368.1	NT	Homo sapiens oleic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10845	23356	36576	1.75	6.0E-03	AW682164.1	EST_HUMAN	Mthermofornicum complete plasmid pEV1 DNA
10713	23402		2.64	6.0E-03	11545814	NT	EST374237 IMAGE rescues, MAG3 Homo sapiens cDNA
10750	23435	36880	1.28	6.0E-03	AI420786.1	EST_HUMAN	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
							1691612.X1 NCI CGAP, P28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519
							FATTY ACID AMIDE HYDROLASE;

Page 173 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23435	36681	1.26	6.0E-03	AI420786.1	EST_HUMAN	1661612.1 NCL CGAP P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.
10903	23593		4.6	6.0E-03	U14656.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10904	23594	36633	2.81	6.0E-03	BE737695.1	EST_HUMAN	601572748.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639747 5'
12042	24553		3.25	6.0E-03	AF010465.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12160	25174		6.69	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 423192 to 450298 (section 39 of 148) of the complete genome
12239	25235		3.17	6.0E-03	U30780.1	NT	Pneumocystis carinii f. sp. relli quinoline nucleotide binding protein alpha subunit (pgp1) gene, complete cds
12680	24808		1.64	6.0E-03	BE768019.1	EST_HUMAN	601462621.F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3685588 5'
12688	24810		1.68	6.0E-03	AI246480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
654	13432	25072	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	13432	25073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	25072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	25073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
10090	13848	25607	1.16	5.0E-03	AJ010467.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
2688	15397	28135	2.9	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1160 protein, partial cds
2938	15702	28351	0.88	5.0E-03	BE266057.1	EST_HUMAN	601194766.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538759 5'
3133	15898	28543	3.62	5.0E-03	T87623.1	EST_HUMAN	ycb1609.s1 Soares infant brain 1.N1B Homo sapiens cDNA clone IMAGE:22395 3'
3152	15915		2.83	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3164	15927	28575	1.3	5.0E-03	R77794.1	EST_HUMAN	y86902.s1 Soares breast 2.N1B8at Homo sapiens cDNA clone IMAGE:155666 3'
3272	16033		1.12	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3697	16440	25082	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3741	16494	28129	0.85	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3954	16704		1.17	5.0E-03	AA286675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' and
4272	16904	28129	0.82	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4589	17304	28931	0.73	5.0E-03	AI131016.1	NT	Homo sapiens SCL gene locus
4670	17404	30039	1.17	5.0E-03	AI752367.1	EST_HUMAN	en15002.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en15002 random
5707	18501	31422	5.5	5.0E-03	F36500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Page 174 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5953	18735	31894	2.97	5.0E-03	Q00507	SWISSPROT	PROBABLE UBQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBQUITIN THIOLESTERASE FAF-Y) (UBQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (AT FACETS PROTEIN RELATED, Y-LINKED) (UBQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5958	18769		0.81	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii ATCC 3699, section 62 of 94, of the complete genome
5959	19284		7.58	5.0E-03	BE300091.1	EST_HUMAN	60044584T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660871 3'
6746	17016	30578	7.48	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6940	19422		0.64	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7385	20065	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST103012 Fetal brain, Stratagene (cat#636206) Homo sapiens cDNA clone HFBOR63 similar to EST
7488	20170		1.21	5.0E-03	AW864327.1	EST_HUMAN	RC3-CT02655-031069-011-07 CT0255 Homo sapiens cDNA
7697	20331	33442	7.5	5.0E-03	AB018816.1	NT	Homo sapiens MASLT1 mRNA, complete cds
8119	20813	33948	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.49	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33965	3.29	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8599	21201		5.63	5.0E-03	M51132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D60723.1	NT	Escherichia coli genomic DNA, (18.1 - 19.4 min)
8838	21530	34876	0.71	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9432	22135	35315	0.45	5.0E-03	P33760	SWISSPROT	SOE1 PROTEIN
9739	22960	35595	0.89	5.0E-03	L21710.1	NT	Pleurodinium brightwellii 5S rDNA phosphoglycerin mRNA, partial cds
9871	23521	35716	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC0-CT0379-210100-032-cds ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA633143.1	EST_HUMAN	746h10.61 NC1 CGAP P19 Homo sapiens cDNA clone IMAGE:865587
10231	22879	36091	0.51	5.0E-03	7692557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10377	23023		0.48	5.0E-03	AA653291.1	EST_HUMAN	ay49c10.81 Gesler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10621	23314		4.99	5.0E-03	T10558.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC cervical tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC cervical tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
10971	23647	36900	1.89	5.0E-03	T46153.1	EST_HUMAN	x05904.r1 Stratagene placenta (#637225) Homo sapiens cDNA clone IMAGE:70680 5'
11021	23693	36958	1.47	5.0E-03	10946755	NT	Mus musculus hypodermal protein, MNC5-4760 (LOC58212), mRNA
11303	23962		3.64	5.0E-03	BE048035.1	EST_HUMAN	124604.y1 NC1 CGAP Brn52 Homo sapiens cDNA clone IMAGE:2391622 5'
11774	24365	37697	1.93	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24365	37699	1.93	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

Page 175 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12176	25367		0.28	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF057283.1	NT	Brugia malayi Y chromosome marker
12408	24792		2.62	5.0E-03	U10347.1	NT	Human pro- α 1 type I collagen (COL2A1) gene exons 1-54, complete cds
12441	24811		1.87	5.0E-03	AA456597.1	EST_HUMAN	XZ75d03.s1 Soares ovary tumor NIH/OT Homo sapiens cDNA clone IMAGE:806548 3' similar to SW-DXA2 MOUSE P14886 PROBABLE DIPHEOL OXIDASE A2 COMPONENT ;
12487	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	92027774.F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12643	24840	30980	4.2	5.0E-03	AW449109.1	EST_HUMAN	U1H-B3-and-408-0-01.s1 NCI_CGAP_S165 Homo sapiens cDNA clone IMAGE:2734215 3'
12662	26253		1.76	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA (VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN)
226	13038	25675	2.89	4.0E-03	AW500198.1	EST_HUMAN	U1-HF-BND-alc-T-04-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076931 5'
313	13117	25765	2.29	4.0E-03	R46482.1	EST_HUMAN	W516d04.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
589	13369	26697	2.89	4.0E-03	AA938339.1	EST_HUMAN	ca75g12.s1 Soares NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1682568 3'
857	13628	28298	2.03	4.0E-03	R49482.1	EST_HUMAN	W516d04.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
891	13660		4.84	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-001 BT0333 Homo sapiens cDNA
1128	13884	28544	29.46	4.0E-03	AA056977.1	EST_HUMAN	ZB17e08.r1 Stralagene cdont (#937204) Homo sapiens cDNA
1146	13801	28593	2.4	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1280	14030	28689	1.57	4.0E-03	AA284374.1	EST_HUMAN	2A59d01.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701736 5'
1581	14327		1.52	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1737	14479	27178	2.23	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory limbic associated protein AT1-46 mRNA, complete cds
2011	14746	27474	10.56	4.0E-03	AA098777.1	EST_HUMAN	ZB17e08.r1 Stralagene cdont (#937204) Homo sapiens cDNA clone IMAGE:510995 5'
2244	14972		2.49	4.0E-03	BE410555.1	EST_HUMAN	601304161.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3836510 5'
2276	15002	27742	1.64	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2576	15293	28030	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), G2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2578	15293	28031	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), G2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2696	15405	28140	3	4.0E-03	AJ27365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2696	15405	28141	3	4.0E-03	AJ27365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment H621C084
3219	15682	28634	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3219	15682	28635	1.16	4.0E-03	BE164134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3521	16277	28631	0.97	4.0E-03	AW198426.1	EST_HUMAN	X9804.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665279 3'

Page 176 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3521	16277	28932	0.97	4.0E-03	AW189428.1	EST_HUMAN	xp8904.x1 NCL_CGAP_G018 Homo sapiens cDNA clone IMAGE:2665279 3'
3612	16555	29008	0.73	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51T (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3909	16559	29300	0.73	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3977	16725		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5057	17776	30393	0.93	4.0E-03	AW103719.1	EST_HUMAN	xp83403.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1, L1 L1
5114	17832		0.97	4.0E-03	AA72898.1	EST_HUMAN	L1 repetitive element;
5194	18002	30625	1.8	4.0E-03	AF005859.1	EST_HUMAN	hs79d05.a1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:969176 3'
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Drosophila melanogaster aron2D7 (aron2D7) mRNA, complete cds
5705	18409	31421	2.48	4.0E-03	P04168	SWISSPROT	Rattus norvegicus beta-calactin binding protein mRNA, complete cds
5708	18502	31423	1.74	4.0E-03	P21649	SWISSPROT	(HPRC)
5792	18593	31510	0.98	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOZYTE ANTIGEN PRECURSOR
5993	18774		4.11	4.0E-03	U22180.1	NT	DKFZp791H1014.1 J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp/811014 5'
6140	18919	31688	0.95	4.0E-03	AW560572.1	EST_HUMAN	Rattus norvegicus cypin gene, complete cds
6217	18981	31987	1.6	4.0E-03	BE548453.1	EST_HUMAN	hp45d07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2948652 3'
6572	18938	32347	1.28	4.0E-03	AA613222.1	EST_HUMAN	601078015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6577	18994	32632	1.61	4.0E-03	U76408.1	NT	603211.a1 Soares_NHT Homo sapiens cDNA clone 1392045 3'
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	19767	32551	3.5	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
7331	20013	33061	1.23	4.0E-03	AI681483.1	EST_HUMAN	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7333	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	637G12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7424	20101		0.74	4.0E-03	X92106.1	NT	7a31b02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7843	20538	33686	0.7	4.0E-03	Q9T102	SWISSPROT	H sapiens hcgIX gene
7847	20542	33767	6.49	4.0E-03	AF111944.1	NT	ADAM-7S 6(A) DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8103	20797	33928	2.06	4.0E-03	7692067	NT	(ADAM-7S 5) (ADAM-7S6) (AGGRECANASE-2) (ADMP-2) (ADAM-7S 11)
8614	21306	34448	6.98	4.0E-03	AI553983.1	EST_HUMAN	Dicystotellum discoideum AX4 development protein DG11722 (DG11722) gene, partial cds
8767	21476		4.25	4.0E-03	AL163209.2	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	ter6b1.x1 Soares_NFL_T1_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9827	22478	35679	0.97	4.0E-03	AL163278.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
10275	22523	36135	1.3	4.0E-03	AL161555.2	NT	Homo sapiens chromosome 21 segment HS21C078
10466	23112		0.45	4.0E-03	AL163281.2	NT	yp-42712.1 Soares retina N2b-HR Homo sapiens cDNA clone IMAGE:180150 5'
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
						NT	Homo sapiens chromosome 21 segment HS21C081

Page 177 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11074	23744	37017	4.08	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21G008
11777	24358	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	23956		1.78	4.0E-03	BE816173.1	EST_HUMAN	PM4-BN0138-180900-002508 BN0138 Homo sapiens cDNA
12167	24649		2.38	4.0E-03	BE288290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12245	24694		2.27	4.0E-03	AW504273.1	EST_HUMAN	U4HF-BN0-alp5-044-04111 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	7q1406b.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12521	25283		2.08	4.0E-03	AW614596.1	EST_HUMAN	h020207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
12801	25048	30556	2.17	4.0E-03	11438955	NT	Homo sapiens Grib2-associated binder 2 (GUA0671), mRNA
302	13100	25903	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26269	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA408110.1	EST_HUMAN	nc73c05.e1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14892		1.38	3.0E-03	AF055038.1	NT	Homo sapiens MHC class 1 region
2292	15017		6.44	3.0E-03	Z32621.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2293	15018	27763	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2293	15018	27764	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3081	15946	28488	3.31	3.0E-03	BE376296.1	EST_HUMAN	601237892F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606923 5'
3149	15972	28557	2.52	3.0E-03	AW602837.1	EST_HUMAN	IL2-JM0076-240300-059-D03 UM0076 Homo sapiens cDNA
3412	16170	28819	1.72	3.0E-03	U34806.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3420	16177		5.97	3.0E-03	Y12600.1	NT	C.elegans same gene
3959	16708	28946	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3959	16708	29349	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4016	16782	29590	1.35	3.0E-03	AV792278.1	EST_HUMAN	8104109.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4130	16872		1	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4384	17102	29737	5.93	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4428	17164		0.73	3.0E-03	BE348739.1	EST_HUMAN	h189j08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3161934 3'
4482	17217	29844	4.97	3.0E-03	AF36141.1	EST_HUMAN	xu8.P10.H8 contig Homo sapiens cDNA 3'
4782	17514	30138	2.38	3.0E-03	AF32754.1	EST_HUMAN	ab18408.x5 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4802	17593	30155	7.94	3.0E-03	BE767945.1	EST_HUMAN	601482718F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5184	17982	30308	3.96	3.0E-03	8922459	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5468	18267	31159	1.98	3.0E-03	AL249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)

Page 178 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5539	18337	31244	0.99	3.0E-03	U38323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	19225	32225	11.75	3.0E-03	AA456701.1	EST_HUMAN	ant370.0.1 Soares. NIHMPU. S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19782	32857	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pop3 gene for purine-cytosine permease
7422	20039	33187	3.64	3.0E-03	AB021736.1	NT	Oriza sativa gene for bZIP protein, complete cds
7839	20534	33681	0.82	3.0E-03	BF333068.1	EST_HUMAN	RCO-BT0812-250900-032-007 BT0812 Homo sapiens cDNA
7839	20534	33682	0.82	3.0E-03	BF333068.1	EST_HUMAN	RCO-BT0812-250900-032-007 BT0812 Homo sapiens cDNA
8056	20750	33881	1.84	3.0E-03	NG2980.1	EST_HUMAN	2427b04.at Soares. parathyroid tumor. NIHHPA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20908		0.51	3.0E-03	M63498.1	NT	S. cerevisiae UGA35 gene, complete cds
8360	21053	34194	1.32	3.0E-03	P51689	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8381	21074	34213	1.47	3.0E-03	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
8485	21177		1.29	3.0E-03	Q0QIM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8590	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	h80R10.1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2889131 3' similar to contains L1.1 L1
8843	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8957	21657	34808	0.44	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.xt NCI CGAP Kd3 Homo sapiens cDNA clone IMAGE:4183638 5'
8971	21657	34817	0.73	3.0E-03	BF333078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9309	21978		0.83	3.0E-03	D00501.1	NT	Synchocytis sp. FOC8503 complete genome, 3/27, 271803-402289
9347	22418	33558	0.83	3.0E-03	BE154670.1	EST_HUMAN	PM3-HT0344-07139-003-007 HT0344 Homo sapiens cDNA
9536	22188		0.54	3.0E-03	PC3355	SWISSPROT	POL POLYPYRROLINE [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9606	22259		3.88	3.0E-03	P08672	SWISSPROT	CIRCUMSPORZITE PROTEIN PRECURSOR (CS)
9795	22446	35651	1.3	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9898	22546	35740	1.29	3.0E-03	P51689	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10040	22668	35606	3.97	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10762	23437		1.8	3.0E-03	5903028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11137	20059	33187	2.65	3.0E-03	AB021736.1	NT	Oriza sativa gene for bZIP protein, complete cds
11353	24043	37346	1.66	3.0E-03	AF003222.1	NT	Pneumocystis carinii teashirt-like serine endoprotease mRNA, partial cds
11424	23191	36422	2.92	3.0E-03	AF26285.1	NT	Homo sapiens p60-kinase protein (p60) gene, complete cds
11462	24065		2.72	3.0E-03	AF084481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11462	24065	37373	2.72	3.0E-03	AF084481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.58	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW294812.1	EST_HUMAN	U1H-B12-eh4-08-0-U1.1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:278642 3'
11927	25198		2.88	3.0E-03	AI828056.1	EST_HUMAN	promina-5.ED7.7 bvtumor Homo sapiens cDNA 5'
11982	24510	37258	1.88	3.0E-03	AA993154.1	EST_HUMAN	cd7b70.61 Scores. total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1922779 3' similar to contains L1.83 MER23 repetitive element;
12016	25321		2.28	3.0E-03	AB009688.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12180	24651	31058	2.71	3.0E-03	AI296282.1	NT	Rattus norvegicus mRNA for cornelin38 (cd38 gene)
5021	13288	29519	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
5021	13288	29520	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15532		12.31	2.0E-03	T70874.1	EST_HUMAN	Y11503.1 Scores fetal liver spleen 1NRLS Homo sapiens cDNA clone IMAGE:108341 5'
1342	14090	26768	2.07	2.0E-03	M20783.1	NT	Human dipeptidase-2-inhibitor gene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	AA681605.1	EST_HUMAN	nu8801.1 at NCI CGAP_AWT Homo sapiens cDNA clone IMAGE:1217583
1354	14102	26777	16.18	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26908	1.79	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1506	14252	26938	1.84	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1588	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1784	14508	27207	1.13	2.0E-03	AA450138.1	EST_HUMAN	2x42a10.1 Scores. total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144908.1	EST_HUMAN	CN2-T10183-061099-018-403 H10183 Homo sapiens cDNA
1888	14724	27445	1.87	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.18	2.0E-03	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15288		4.57	2.0E-03	AW137782.1	EST_HUMAN	U1H-B1-adi-g-10-U1.1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450139.1	EST_HUMAN	2x42a10.1 Scores. total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF66955.1	EST_HUMAN	602163960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3657	16410	29048	6.82	2.0E-03	X87344.1	NT	H sapiens DNA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP7, DOB2 and RIN08, 9, 13 and 14 genes
4093	16935	29461	1.86	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP32; COAT PROTEIN GP36]
4195	16938		11.03	2.0E-03	U68461.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4363	17130		1.12	2.0E-03	AW287380.1	EST_HUMAN	U1H-BW0-air-g-03-U1.1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4367	17134	29765	0.87	2.0E-03	A064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4509	17244	28877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4509	17244	28878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4653	17397		1.84	2.0E-03	R8773.1	EST_HUMAN	y64602.at Soares adult brain NZ44HB557 Homo sapiens cDNA clone IMAGE:180890 3'
4956	17682	30290	2.57	2.0E-03	AF005528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5062	17811	30427	1	2.0E-03	BE786380.1	EST_HUMAN	501853004.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937560 5'
5340	18169	30893	1.38	2.0E-03	BF241410.1	EST_HUMAN	601876385.F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4104692 5'
5596	20770	31245	2.06	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5623	18420	31333	1.88	2.0E-03	U63711.1	NT	Xenopus laevis xerillin mRNA, complete cds
6019	18800	31760	3.68	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.68	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6253	19027	32002	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6255	19029	32004	7.5	2.0E-03	BF308187.1	EST_HUMAN	601887434.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6291	19084	32048	2.44	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19085	32047	0.88	2.0E-03	AV709078.1	EST_HUMAN	AV709078 ADC Homo sapiens cDNA clone AACFE09 5'
6320	19090	32078	1.82	2.0E-03	X94481.1	NT	L-esculetum mRNA for l-tryptophan synthetase (LysRS)
6506	19271		1.16	2.0E-03	A1891089.1	EST_HUMAN	w436106.x1 Soares Dieckgrafe, codon, NHCD Homo sapiens cDNA clone IMAGE:2522177 3', similar to SW-R129 HUMAN P-47914 60S RIBOSOMAL PROTEIN L29 contains element MSR1 repetitive element;
8541	19306	32311	0.81	2.0E-03	AA677831.1	EST_HUMAN	L13at1.1.x1 Soares, fetal liver spleen, 1NFSL S1 Homo sapiens cDNA clone IMAGE:430952 3'
8882	19369	30675	1.52	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galactin LEC-11, complete cds
8939	19874	32720	0.6	2.0E-03	5031894	NT	Homo sapiens lipoma HMIC fusion partner (LHFP) mRNA
8939	19874	32721	0.6	2.0E-03	5031894	NT	Homo sapiens lipoma HMIC fusion partner (LHFP) mRNA
6981	19506	32531	3.65	2.0E-03	BE079983.1	EST_HUMAN	CM4-BT0386-051289-034-d01 BT0386 Homo sapiens cDNA
7044	19735	32785	0.98	2.0E-03	A1298883.1	EST_HUMAN	qm9941.1.x1 NCI_OGAP_Lu6 Homo sapiens cDNA clone IMAGE:1898885 3'
7193	19878	32953	0.8	2.0E-03	T86559.1	EST_HUMAN	yk77610.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:114306 5'
7517	20188	33281	1.18	2.0E-03	P07384	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7950	20645	33769	1.98	2.0E-03	AW592004.1	EST_HUMAN	h37606.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR-Q60979
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	yk42968.7 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:2844442 3' similar to contains L1.1b2 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	Y42906.s1 Soares melanocyte 2NB-HM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element:
8162	20856	33987	0.64	2.0E-03	O92350	SWISSPROT	HYPOHETICAL 32.8 KD PROTEIN CG9.05 IN CHROMOSOME 1
8164	20878	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20933	34069	0.81	2.0E-03	6005955	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	34070	0.81	2.0E-03	6005955	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8264	20958	34097	0.89	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone IMAGE:1004839 5'
8318	21011		0.91	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21262	34400	0.64	2.0E-03	AB033285.1	NT	Oryctolagus cuniculus mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AW766111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW766111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9139	21827	34692	0.64	2.0E-03	AF224689.1	NT	Homo sapiens menosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9426	21104	35278	0.89	2.0E-03	H50832.1	EST_HUMAN	Y86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194286 3'
9426	21104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	Y86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194286 3'
9458	22008	35176	3.46	2.0E-03	P24821	SWISSPROT	TEMASIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MITOCHONDRIAL ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9566	22218	35404	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9568	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35484	0.63	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9623	22276	35484	0.63	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22469	35668	0.81	2.0E-03	AW884269.1	EST_HUMAN	Q13A-OT0084-069400-144-401 OT0084 Homo sapiens cDNA
9842	22560		5.75	2.0E-03	AA351378.1	EST_HUMAN	251006.s1 NCI CGAP GC91 Homo sapiens cDNA clone IMAGE:694754 3'
10506	23152	36377	0.46	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0281-141099-012-401 CT0281 Homo sapiens cDNA
10508	23152	36376	0.49	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0281-141099-012-401 CT0281 Homo sapiens cDNA
10938	23618		2.07	2.0E-03	M86524.1	NT	Human dydrophlin gene
11470	20188	33281	2.56	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	BF330609.1	EST_HUMAN	RC3-BT0333-310800-115-004 BT0333 Homo sapiens cDNA
11538	24138	37446	9.1	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
11609	24473		3.23	2.0E-03	AB25745.1	EST_HUMAN	Q25H03.s1 NCI CGAP Kld11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW-VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G;
11926	24487	37507	2.41	2.0E-03	AF157518.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds

Page 182 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11948	24502	37810	2.41	2.0E-03	A084325.1	EST_HUMAN	q4y306.s1 Soares_papillary_thyroid_tumor_N8HPA Homo sapiens cDNA clone IMAGE:168634.3' similar to TR:P87833 P87833 PS-PLAT1 PRECURSOR. ;
11972	17007		0.37	2.0E-03	AJ245167.1	NT	Camelid dromedarius cyp19 gene for immunoglobulin heavy chain variable region
12172	25361		2.89	2.0E-03	AV987866.1	EST_HUMAN	AV987866 GKG Homo sapiens cDNA clone GKGX005.5'
12282	24707	31050	1.76	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12433	26224		1.48	2.0E-03	A375037.1	EST_HUMAN	h65072.x1 Soares_totai_fetus_N62HF8_gw Homo sapiens cDNA clone IMAGE:2049051.3' similar to contains Alu repetitive element;
12542	24882		1.64	2.0E-03	AF129788.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12713	25175		2.65	2.0E-03	AV987866.1	EST_HUMAN	AV987866 GKG Homo sapiens cDNA clone GKGX005.5'
429	13215	25860	1.28	1.0E-03	H96471.1	EST_HUMAN	Y68808.r1 Soares_pituitary_gland_N8HPG Homo sapiens cDNA clone IMAGE:232334.6'
810	13581	26248	2.31	1.0E-03	A1720263.1	EST_HUMAN	es70808.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039.3' similar to TR:Q13825 Q13825 AL-BINDING PROTEINENOVYL-COA HYDRATASE. ;
810	13581	26249	2.31	1.0E-03	A1720263.1	EST_HUMAN	es70808.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039.3' similar to TR:Q13825 Q13825 AL-BINDING PROTEINENOVYL-COA HYDRATASE. ;
1073	13931	29489	3.78	1.0E-03	A8665788.1	EST_HUMAN	w68606.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2422288.3'
1093	13951	29510	1.78	1.0E-03	A854572.1	EST_HUMAN	w68610.x1 NCI_CGAP_Met15 Homo sapiens cDNA clone IMAGE:2551242.3'
2021	14756	27486	3.38	1.0E-03	P47809	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN (HMMW)
2150	14890	27614	12.13	1.0E-03	AI131016.1	NT	Homo sapiens SCL gene locus
2979	15745	28593	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for K1A1261 protein, partial cds
3186	15949	28599	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3186	15949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3656	16409		1.65	1.0E-03	AB04400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4402	17139	29767	1.28	1.0E-03	BE826162.1	EST_HUMAN	TC1-TN0128-100800-021-g01 TN0128 Homo sapiens cDNA
4441	17177	29803	4.05	1.0E-03	BE246536.1	EST_HUMAN	sapiens cDNA clone TC8AP4609
4815	17350	29985	0.84	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4773	17505	30127	1.68	1.0E-03	A073485.1	EST_HUMAN	ov45204.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282.3'
4773	17505	30128	1.68	1.0E-03	A073485.1	EST_HUMAN	ov45204.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282.3'
4774	17506		4.29	1.0E-03	BE164067.1	EST_HUMAN	PMO-HT0399-200-000-010-D02 HT0399 Homo sapiens cDNA
5018	17739	30348	7.24	1.0E-03	Q46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5225	18032	30558	1.87	1.0E-03	AJ280851.1	EST_HUMAN	2x44f01.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5359	18170	30959	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5359	18170	30957	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5455	18284	31182	0.83	1.0E-03	BE76491.1	EST_HUMAN	001459841.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:384354 5'
5491	18280	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
							W07106.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270387 5' similar to contains element MER6 repetitive element;
5546	18343	31251	0.67	1.0E-03	N41974.1	EST_HUMAN	W07106.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270387 5' similar to contains element MER6 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41974.1	EST_HUMAN	Mouse nucleolin gene
5900	18714		2.75	1.0E-03	X07699.1	NT	001697518.RT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
5998	18760	31711	1.07	1.0E-03	BE69389.2	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6098	18877		8.76	1.0E-03	11528176	NT	X453a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6242	18016	31960	1.14	1.0E-03	T87761.1	EST_HUMAN	QV3.NN1024.260400-171-g05 NN1024 Homo sapiens cDNA
6315	18086		1.7	1.0E-03	AW602685.1	EST_HUMAN	Homo sapiens D'George syndrome critical region, centromere end
6557	18418	32432	1.37	1.0E-03	L77570.1	NT	Human gene for fourth somatostatin receptor subtype
7052	18743	32605	2.54	1.0E-03	D16826.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Cdk5/p34-dependent protein kinase I (CAMKI), creatine transporter (CRTF), CDM protein (CDM), extracellularly-located protein >
7599	20209	33308	1.8	1.0E-03	U52111.2	NT	Human TRPM2 protein gene, exons 1, 2 and 3
7608	20274	33382	3.37	1.0E-03	M63378.1	NT	001491081.F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 6'
7656	20320	33429	0.88	1.0E-03	BE680044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7759	20484	33608	0.93	1.0E-03	AF274581.1	NT	Homo sapiens partial stefin-1 gene
7850	20545	33673	5.18	1.0E-03	AJ251973.1	NT	2497009.at Soares_pregnant_uterus_NH-PU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.t1 repetitive element;
8043	20737	33870	1	1.0E-03	AA122270.1	EST_HUMAN	Homo sapiens exocyst-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8142	20836	33868	1.84	1.0E-03	AF159680.1	NT	Rattus norvegicus plasma membrane Ca2+-ATPase isoform 3 (PMCA3) gene, 5' flanking region
8328	21022	34158	0.68	1.0E-03	U29397.1	NT	2182208.at Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34326	0.81	1.0E-03	AA001613.1	EST_HUMAN	2182208.at Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.81	1.0E-03	AA001613.1	EST_HUMAN	V carrier gene encoding valoxopain
8642	21334		1.38	1.0E-03	Y11204.1	NT	OM8.L1T0078-170200-982-407 LT0078 Homo sapiens cDNA
8698	21560	34705	0.62	1.0E-03	AW840353.1	EST_HUMAN	

Page 184 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		0.68	1.0E-03	U52111.2	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34658	3.68	1.0E-03	M30471.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34659	3.68	1.0E-03	M30471.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9507	22160	35340	1.66	1.0E-03	AF014000.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9507	22160	35341	1.66	1.0E-03	AF014000.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9720	22371	35570	0.81	1.0E-03	Q01129	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10063	22711	35929	0.65	1.0E-03	AF005529.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10068	22716		0.75	1.0E-03	AF097495.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10214	22862	36075	1.72	1.0E-03	A024350.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10503	23149		0.49	1.0E-03	AA706202.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10583	23259	36495	1.78	1.0E-03	AW362393.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10583	23289	36498	1.79	1.0E-03	AW362393.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10651	23342	36580	2.78	1.0E-03	BE170659.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10725	23413		3.29	1.0E-03	AI683847.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
10808	23491	36727	1.38	1.0E-03	AW237482.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
11108	23778		3.05	1.0E-03	AW759949.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
11805	24470	37805	4.48	1.0E-03	BE894488.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
12124	24618		1.38	1.0E-03	AV731620.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
12371	25342		1.68	1.0E-03	AI047355.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
12478	25365	30612	7.05	1.0E-03	BE780572.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
12821	25187	30809	1.37	1.0E-03	AW847341.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
5130	17848	30465	0.7	9.0E-04	P08548	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
5508	18391		1.26	9.0E-04	P06727	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
8165	18942		0.6	9.0E-04	AJ008345.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
8395	19164	32185	0.96	9.0E-04	P02381	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9543	22166		1.42	9.0E-04	AB037203.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
1471	14218		1.02	8.0E-04	X98499.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc42/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4159	18999		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.93	8.0E-04	AA177084.1	EST_HUMAN	224c10.01 Scores: fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11268	23228		1.89	8.0E-04	AA177084.1	EST_HUMAN	165a08.01 NCL CGAP U28185.1
2398	15119	27896	0.97	7.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	16426	28104	1.19	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21Cp10
3274	19035	28695	1	7.0E-04	488570	NT	Homo sapiens chromosome X open reading frame 6 (XORF6) mRNA
6005	18786	31748	0.94	7.0E-04	AA16212.1	EST_HUMAN	rep591.2.s1 NCL CGAP Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.53 L1 L1
6420	19168		2.47	7.0E-04	AJ769331.1	EST_HUMAN	W53506.x1 Scores: NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387206 3'
7128	19818		0.78	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
9703	22354	35549	0.53	7.0E-04	PI3497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9703	22354	35550	0.53	7.0E-04	PI3497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24188		2.28	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
11686	24185	37500	4.04	7.0E-04	Z0591.1	EST_HUMAN	HSC2BA072 normalized infant brain cDNA Homo sapiens cDNA clone c-28407 3'
12642	24939		2.31	7.0E-04	R17338.1	EST_HUMAN	Y313505.1 Scores: infant brain IN1B Homo sapiens cDNA clone IMAGE:32298 5'
12698	24964		5.98	7.0E-04	6005955	NT	Homo sapiens RelA-derived POU-domain factor-1 (RPF-1), mRNA
3041	16591	29329	1.83	6.0E-04	AB62523.1	EST_HUMAN	Y17611.1 NCL CGAP Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4068	18812	29440	0.78	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (GHEP1) gene, 5' flanking region
4068	18812	29441	0.78	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (GHEP1) gene, 5' flanking region
4162	16902	29531	3.70	6.0E-04	U45983.1	NT	Homo sapiens OCA8 chemokine receptor (CXCR8) gene, complete cds
7478	20151	33245	0.81	6.0E-04	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIA0002
7765	20461		3.33	6.0E-04	P48408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7914	20809		0.82	6.0E-04	H92947.1	EST_HUMAN	Y94611.s1 Scores: pinned_dland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains
9880	22330		3.5	8.0E-04	AL048507.2	EST_HUMAN	LCR1 repetitive element
9880	22328	35837	2.28	6.0E-04	BE008950.1	EST_HUMAN	DKFZ-556M2024_1.586 (synonym: hube1) Homo sapiens cDNA clone DKFZ556M2024
10238	22886						RC2-8N0120-250400-012-111 BNG120 Homo sapiens cDNA
11487	24070	37378	0.71	6.0E-04	AF287478.1	NT	Lycodinus variegatus embryonic blastocellular matrix protein precursor (ECN3) mRNA, complete
11487	24070	37378	2.93	6.0E-04	AJ229042.1	NT	Homo sapiens 658 kb contig between AML1 and CBRT1 on chromosome 21q22, segment 2/3
11558	24157	37407	3.46	6.0E-04	AW013847.1	EST_HUMAN	U1-H-BD-sab-9-09-01.1 NCL CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11939	24233		2.17	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12082	25249		2.81	6.0E-04	AW380619.1	EST_HUMAN	RC1-H10269-281189-012-008 HT0269 Homo sapiens cDNA

Page 186 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12816	25058		1.34	6.0E-04	AI817088.1	EST_HUMAN	wf76g1.1x1 NCI_CGAP_Lut19 Homo sapiens cDNA clone IMAGE:249804 3' similar to contains element L1 repetitive element:
636	13415	26061	6.81	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATASE 2B3 KD PROTEIN (ORF52)
1480	14237		1.4	5.0E-04	AW851844.1	EST_HUMAN	Q100225-021099-330-a07 CT0223 Homo sapiens cDNA
3408	16166	26815	1.35	6.0E-04	AA548931.1	EST_HUMAN	nk2761.1x1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3704	18457	26906	2.32	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6386	18186	30877	2.99	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6532	18288	32303	7.89	5.0E-04	AA18080.1	EST_HUMAN	zo33b08.t1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:588653 5'
7276	19600	33037	3.75	5.0E-04	M23804.1	NT	Gonilla gonilla involucrin gene medium allele, complete cds
7856	20551	33677	5.2	5.0E-04	AI188382.1	EST_HUMAN	qt1306.x1 Soares_placenta_86cweeks_ZNBP8P809W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:551602_c051 VASCULECTIN ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Alu repetitive element;
8202	20886	34033	0.86	5.0E-04	AA814518.1	EST_HUMAN	cd96602.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element:
9177	21847	35013	1.39	5.0E-04	AA846545.1	EST_HUMAN	ai59403.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9271	22025	35195	0.68	5.0E-04	N83765.1	EST_HUMAN	KK2474F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9418	22066	35258	1.44	6.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
8598	22162	35344	4.1	5.0E-04	AW270938.1	EST_HUMAN	xs06602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768888 3'
10177	22826		0.48	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
10897	23577		2.38	5.0E-04	AL048607.2	EST_HUMAN	DKFZ:558612024_T1 988 (synonym: hulet1) Homo sapiens cDNA clone DKFZ:669M2024
11713	18186	30877	14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12020	25184		5.04	5.0E-04	AA668513.1	EST_HUMAN	nf1502.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:513876
668	13435	26076	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26267	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70208.x1 Barlested colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
827	13597	26268	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70208.x1 Barlested colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
1448	14198	26880	3.18	4.0E-04	AW753356.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE ;
2076	14807	27638	1.81	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-401 CT0254 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C078

Page 187 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2129	14600		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZ434D059.t1.434 (synonym: hhes) Homo sapiens cDNA clone DKFZ434D059.5'
2833	15345	28088	2.21	4.0E-04	O96915	SWISSPROT	SERPIN2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.95	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4288	17028	28953	3.18	4.0E-04	AA576331.1	EST_HUMAN	specific RANTES PROTEIN PRECURSOR (HUMAN);
4289	17028	28954	3.18	4.0E-04	AA576331.1	EST_HUMAN	nt04010.s1 NCL CGAP_Cot Homo sapiens cDNA clone IMAGE:951930.3' similar to gb:M21121 T-CELL
4500	17236	28959	1.76	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5028	17748	30360	3.1	4.0E-04	BE560660.1	EST_HUMAN	nt10810.s1 Stralagene muscle 837209 Homo sapiens cDNA clone IMAGE:592670.3'
							80134895.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3676910.5'
							EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7169	19855	32925	1.3	4.0E-04	P48442	SWISSPROT	CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	AL161566.2	NT	Arbidiopsis italiana DNA chitonosoma 4, contig fragment No. 85
7618	20284	33394	0.86	4.0E-04	AU122076.1	EST_HUMAN	AU122076 MAMMA1 Homo sapiens cDNA clone MAMMA1001620.5'
8434	21127	34264	1.07	4.0E-04	BF240712.1	EST_HUMAN	90187688.F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700.5'
8442	21134	34270	1.5	4.0E-04	N25507.1	EST_HUMAN	xd39012.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:264142.5'
9590	22243	35426	3.24	4.0E-04	AC028569.1	EST_HUMAN	xd67003.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644347.3'
8740	22391		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(af7) mRNA, alternatively spliced, complete cds
12390	25197		2.05	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
162	12967	25608	3.46	3.0E-04	AL119425.1	EST_HUMAN	DKFZ4761J221.t1.761 (synonym: harrv2) Homo sapiens cDNA clone DKFZ4761J221.5'
180	13003	25844	2.24	3.0E-04	P46250	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
860	13929	26500	1.32	3.0E-04	U85991.1	NT	Human short chain acyl CoA dehydrogenases gene, exons 1 and 2
1831	14570	27282	1.08	3.0E-04	AI087100.1	EST_HUMAN	g228003.yt NCL CGAP_K18T1 Homo sapiens cDNA clone IMAGE:2028197.5'
1846	14584		1.21	3.0E-04	AI368574.1	EST_HUMAN	g228002.yt NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2716082.3'
3303	16004	28712	3.43	3.0E-04	P25147	SWISSPROT	INTERALIN B PRECURSOR
3308	16008	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	xd6604.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478.5'
3946	16568	29335	4.07	3.0E-04	P46448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779		1.33	3.0E-04	AJ271795.1	NT	Homo sapiens Xq pseudoteleomeric region, segment 1/2
4072	18816		1.12	3.0E-04	BE146068.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
4768	17498		4.72	3.0E-04	BE153778.1	EST_HUMAN	PNG-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4827	17598	30180	0.96	3.0E-04	AY987725.1	EST_HUMAN	QV3-DT0045-221285-046-d08 DT0045 Homo sapiens cDNA
5063	17792	30399	0.86	3.0E-04	AA613145.1	EST_HUMAN	nt08008.s1 NCL CGAP_Lut Homo sapiens cDNA clone IMAGE:1143328.3'
8062	18832		7.86	3.0E-04	AL169281.2	NT	Homo sapiens chromosome 21 segment HS21C081
9722	19536	32599	2.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7491	20163	33256	0.84	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

Page 188 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20551	33983	3.23	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	z48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M92762
10078	22726	35543	0.85	3.0E-04	AJ892139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w75a11.x1 Soares_thymus_NHT.Homo sapiens cDNA clone IMAGE:2513276 3'
10398	23003	38220	3.73	3.0E-04	AA781201.1	EST_HUMAN	q24q05.s1 Soares_testis_NHT.Homo sapiens cDNA clone 1397288 3' similar to gb:M36072 60S
10495	23141	36597	0.54	3.0E-04	P13818	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN);
11555	24154	37468	1.38	3.0E-04	4801900	NT	GLUTAMIC ACID-RICH PROTEIN PRECURSOR Homo sapiens adrenegic, alpha-1A-, receptor (ADRA1A), mRNA
11976	25368	30617	4.81	3.0E-04	AA228301.1	EST_HUMAN	nc38a04.r1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12338	26230	30818	3.08	3.0E-04	AB018282.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
12730	29000	38814	2.76	3.0E-04	AL134489.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547L185 5'
171	12984	25624	2.85	2.0E-04	AF217796.1	NT	Homo sapiens SOG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
458	13251	25892	1.8	2.0E-04	AU145707.1	EST_HUMAN	AU145707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
887	13658	26524	10.71	2.0E-04	M86524.1	NT	Human dydrophlin gene
897	13658	26525	10.71	2.0E-04	M86524.1	NT	Human dydrophlin gene
1159	13911		3.93	2.0E-04	AL289021.1	EST_HUMAN	q08e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1183	13917		2.18	2.0E-04	AL165203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1824	14963		1.12	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Pib3 gene
2581	15295	28033	4.47	2.0E-04	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
2988	15752	28098	1.11	2.0E-04	A124529.1	EST_HUMAN	emb8009.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3328	16088	28740	1.1	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3429	16186	28834	1.99	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT00636-070600-194-b07 B10638 Homo sapiens cDNA
3892	16842	29282	0.79	2.0E-04	AW978441.1	EST_HUMAN	EST330350 MAGE sequences MAGEF Homo sapiens cDNA
4122	16884		4.83	2.0E-04	U01029.1	NT	Phaeosia vulgaris nitrate reductase (PNR2) gene, complete cds
4620	17355	29860	1.74	2.0E-04	H66265.1	EST_HUMAN	y07t611.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4620	17355	29861	1.74	2.0E-04	H66265.1	EST_HUMAN	y07t611.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4742	17474		1.63	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4998	17721	30324	1.1	2.0E-04	AB037987.1	NT	Danio rerio hagerorn gene, exons 1 to 6, partial cds

Page 189 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5089	17808	30424	1.04	2.0E-04	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMHHC)
5457	18298	31146	0.73	2.0E-04	AV954382.1	EST_HUMAN	AV954382 GLC Homo sapiens cDNA clone GICDUR10 3'
5489	18298	31160	1.75	2.0E-04	AI690862.1	EST_HUMAN	IQ03b11.x1 NC1 CGAP_U8 Homo sapiens cDNA clone IMAGE:2207709 3'
6664	18459	31373	0.98	2.0E-04	AA286552.1	EST_HUMAN	EST111191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
5857	18644	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNL3) mRNA
6144	18922	31892	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	18818		2.8	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
7225	18910		0.93	2.0E-04	AW860963.1	EST_HUMAN	QVQ-CT0387-180303-167-e10 CT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33285	1.42	2.0E-04	P64298	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (685 KD TITIN-ASSOCIATED PROTEIN) (685 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33676	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20878	34012	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20878	34013	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8463	21155	34298	1.99	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (F-HIT) gene, exon 5
8542	21334	34478	0.49	2.0E-04	X57931.1	NT	Human immunoglobulin (Cmu) and C(delta) heavy chain genes (constant regions)
9233	21912	35098	0.49	2.0E-04	AA725700.1	EST_HUMAN	AI22a12.s1 Soares Testis_NHT Homo sapiens cDNA clone 1343578 3'
9318	21986	35158	0.8	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOCF-26.1
9975	22525	35710	1.19	2.0E-04	BE149303.1	EST_HUMAN	RCS-HT0254-161099-011-b05 HT0254 Homo sapiens cDNA
9916	22593	35781	1.71	2.0E-04	AA405777.1	EST_HUMAN	zu06c11.1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:742984 5'
10755	23440	36084	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA001 5'
11128	23798		1.61	2.0E-04	AJ243213.1	NT	Homo sapiens partial GHT4 receptor gene, exons 2 to 5
11276	23937	37229	3.06	2.0E-04	AI440282.1	EST_HUMAN	U01111.x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11403	24052	37356	2.98	2.0E-04	AW138740.1	EST_HUMAN	UI-H-B11-actm-c-04-Q.U1.s1 NC1 CGAP_Su33 Homo sapiens cDNA clone IMAGE:2717190 3'
11887	24441	37782	2.71	2.0E-04	AI821304.1	EST_HUMAN	X770b10.35 Stragena ovary (#937217) Homo sapiens cDNA clone IMAGE:77371 3'
1033	13812	26472	3.3	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1092	13850	26508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BIG-abb-9-09-Q.U1.s1 NC1 CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708823 3'
1092	13850	26509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BIG-abb-9-09-Q.U1.s1 NC1 CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708823 3'

Page 190 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	U62318.1	NT	Angioma anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 88 gene, partial cds; and ORF 89, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GP, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 88 gene, partial cds; and ORF 89, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GP, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	AB048342.1	NT	Equine caballus DNA, chromosome 24q14, microsatellite TKY36
3276	19039	28889	1.06	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 82 (SAP 82) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A69)
3719	18472	29110	0.91	1.0E-04	AI440282.1	EST_HUMAN	h0111.1x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4037	18782	29412	2.11	1.0E-04	MT4042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4062	19807	29437	1.15	1.0E-04	AV847727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLOB004 3'
5036	17755	30368	1.28	1.0E-04	7862015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7862015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18500	31487	1.49	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31556	0.57	1.0E-04	T19815.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02a12.1 NCL CGAP_P33 Homo sapiens cDNA clone IMAGE:252
6738	19572	32805	0.92	1.0E-04	AA564581.1	EST_HUMAN	h02a04.1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:U97252
7086	19776	32841	15.36	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7470	19778	32841	17.82	1.0E-04	AI251980.1	EST_HUMAN	q97470.1 NCL CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
7894	20659	33719	0.96	1.0E-04	AA630453.1	EST_HUMAN	q97470.1 NCL CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
9236	21915	35098	2.27	1.0E-04	AI606220.1	EST_HUMAN	ab94908.1 Striatogene lung (H937210) Homo sapiens cDNA clone IMAGE:3854654 3'
9247	21928	35097	1.46	1.0E-04	D88589	SWISSPROT	W25a208.1 Soares NFL_T_OBG_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9326	21962		0.46	1.0E-04	T77183.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9546	22189	35381	1.86	1.0E-04	P08547	SWISSPROT	y072038.1 Soares fetal liver spleen INPLS Homo sapiens cDNA clone IMAGE:113774 5'
10079	22727		2.74	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04	M25387.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11567	24166	37478	2.05	1.0E-04	AW205336.1	EST_HUMAN	UHH-B11-aw-e-02-0-U1 st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720548 3'
11567	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	UHH-B11-aw-e-02-0-U1 st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720548 3'
11649	24246	37568	1.76	1.0E-04	AB032898.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds

Page 191 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11682	24287	37609	2.01	1.0E-04	AW286051.1	EST_HUMAN	x49412.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816618 3'
11725	24319	37643	2	1.0E-04	Q03698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11726	24319	37644	2	1.0E-04	Q03698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE576399.1	EST_HUMAN	7729a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3268058 3' similar to contains L1 L2 L1 repetitive element;
682	13457	26102	2.78	9.0E-05	AA719933.1	EST_HUMAN	ar45611.s1 Soares_testis_NHT Homo sapiens cDNA clone 1252468 3'
1897	14793	27465	1.14	9.0E-05	AW865218.1	EST_HUMAN	QV4-SN0023-070400-166-164 SN0023 Homo sapiens cDNA
5973	18660	31601	1.81	9.0E-05	Q00716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33242	0.6	9.0E-05	AW204958.1	EST_HUMAN	UJH-BIT-ear-4-05-0-J1.s1 NCI_CGAP_Su33 Homo sapiens cDNA clone IMAGE:2720285 3'
7476	20149	33243	0.8	9.0E-05	AW204958.1	EST_HUMAN	UJH-BIT-ear-4-05-0-J1.s1 NCI_CGAP_Su33 Homo sapiens cDNA clone IMAGE:2720285 3'
8376	21651		3.02	9.0E-05	D89605.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
8378	21653	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 1b5 repetitive element;
11082	23752	37027	2.68	9.0E-05	AW073078.1	EST_HUMAN	x34905.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1 L2 L1 repetitive element;
11207	23870	37156	1.75	9.0E-05	AI287978.1	EST_HUMAN	q12365.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982436 3' similar to contains element MIR repetitive element;
11617	16560	31601	3.3	9.0E-05	Q00716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12178	25259		6.63	9.0E-05	AF129753.1	NT	Homo sapiens MSH55 gene, partial cds; and CUC1, DDAH, G5b, G5c, G5d, G5e, G5f, G5g, G5h, G5i, G5j, G5k, G5l, G5m, G5n, G5o, G5p, G5q, G5r, G5s, G5t, G5u, G5v, G5w, G5x, G5y, G5z, G6a, G6b, G6c, G6d, G6e, G6f, G6g, G6h, G6i, G6j, G6k, G6l, G6m, G6n, G6o, G6p, G6q, G6r, G6s, G6t, G6u, G6v, G6w, G6x, G6y, G6z, G7a, G7b, G7c, G7d, G7e, G7f, G7g, G7h, G7i, G7j, G7k, G7l, G7m, G7n, G7o, G7p, G7q, G7r, G7s, G7t, G7u, G7v, G7w, G7x, G7y, G7z, G8a, G8b, G8c, G8d, G8e, G8f, G8g, G8h, G8i, G8j, G8k, G8l, G8m, G8n, G8o, G8p, G8q, G8r, G8s, G8t, G8u, G8v, G8w, G8x, G8y, G8z, G9a, G9b, G9c, G9d, G9e, G9f, G9g, G9h, G9i, G9j, G9k, G9l, G9m, G9n, G9o, G9p, G9q, G9r, G9s, G9t, G9u, G9v, G9w, G9x, G9y, G9z, G10a, G10b, G10c, G10d, G10e, G10f, G10g, G10h, G10i, G10j, G10k, G10l, G10m, G10n, G10o, G10p, G10q, G10r, G10s, G10t, G10u, G10v, G10w, G10x, G10y, G10z, G11a, G11b, G11c, G11d, G11e, G11f, G11g, G11h, G11i, G11j, G11k, G11l, G11m, G11n, G11o, G11p, G11q, G11r, G11s, G11t, G11u, G11v, G11w, G11x, G11y, G11z, G12a, G12b, G12c, G12d, G12e, G12f, G12g, G12h, G12i, G12j, G12k, G12l, G12m, G12n, G12o, G12p, G12q, G12r, G12s, G12t, G12u, G12v, G12w, G12x, G12y, G12z, G13a, G13b, G13c, G13d, G13e, G13f, G13g, G13h, G13i, G13j, G13k, G13l, G13m, G13n, G13o, G13p, G13q, G13r, G13s, G13t, G13u, G13v, G13w, G13x, G13y, G13z, G14a, G14b, G14c, G14d, G14e, G14f, G14g, G14h, G14i, G14j, G14k, G14l, G14m, G14n, G14o, G14p, G14q, G14r, G14s, G14t, G14u, G14v, G14w, G14x, G14y, G14z, G15a, G15b, G15c, G15d, G15e, G15f, G15g, G15h, G15i, G15j, G15k, G15l, G15m, G15n, G15o, G15p, G15q, G15r, G15s, G15t, G15u, G15v, G15w, G15x, G15y, G15z, G16a, G16b, G16c, G16d, G16e, G16f, G16g, G16h, G16i, G16j, G16k, G16l, G16m, G16n, G16o, G16p, G16q, G16r, G16s, G16t, G16u, G16v, G16w, G16x, G16y, G16z, G17a, G17b, G17c, G17d, G17e, G17f, G17g, G17h, G17i, G17j, G17k, G17l, G17m, G17n, G17o, G17p, G17q, G17r, G17s, G17t, G17u, G17v, G17w, G17x, G17y, G17z, G18a, G18b, G18c, G18d, G18e, G18f, G18g, G18h, G18i, G18j, G18k, G18l, G18m, G18n, G18o, G18p, G18q, G18r, G18s, G18t, G18u, G18v, G18w, G18x, G18y, G18z, G19a, G19b, G19c, G19d, G19e, G19f, G19g, G19h, G19i, G19j, G19k, G19l, G19m, G19n, G19o, G19p, G19q, G19r, G19s, G19t, G19u, G19v, G19w, G19x, G19y, G19z, G20a, G20b, G20c, G20d, G20e, G20f, G20g, G20h, G20i, G20j, G20k, G20l, G20m, G20n, G20o, G20p, G20q, G20r, G20s, G20t, G20u, G20v, G20w, G20x, G20y, G20z, G21a, G21b, G21c, G21d, G21e, G21f, G21g, G21h, G21i, G21j, G21k, G21l, G21m, G21n, G21o, G21p, G21q, G21r, G21s, G21t, G21u, G21v, G21w, G21x, G21y, G21z, G22a, G22b, G22c, G22d, G22e, G22f, G22g, G22h, G22i, G22j, G22k, G22l, G22m, G22n, G22o, G22p, G22q, G22r, G22s, G22t, G22u, G22v, G22w, G22x, G22y, G22z, G23a, G23b, G23c, G23d, G23e, G23f, G23g, G23h, G23i, G23j, G23k, G23l, G23m, G23n, G23o, G23p, G23q, G23r, G23s, G23t, G23u, G23v, G23w, G23x, G23y, G23z, G24a, G24b, G24c, G24d, G24e, G24f, G24g, G24h, G24i, G24j, G24k, G24l, G24m, G24n, G24o, G24p, G24q, G24r, G24s, G24t, G24u, G24v, G24w, G24x, G24y, G24z, G25a, G25b, G25c, G25d, G25e, G25f, G25g, G25h, G25i, G25j, G25k, G25l, G25m, G25n, G25o, G25p, G25q, G25r, G25s, G25t, G25u, G25v, G25w, G25x, G25y, G25z, G26a, G26b, G26c, G26d, G26e, G26f, G26g, G26h, G26i, G26j, G26k, G26l, G26m, G26n, G26o, G26p, G26q, G26r, G26s, G26t, G26u, G26v, G26w, G26x, G26y, G26z, G27a, G27b, G27c, G27d, G27e, G27f, G27g, G27h, G27i, G27j, G27k, G27l, G27m, G27n, G27o, G27p, G27q, G27r, G27s, G27t, G27u, G27v, G27w, G27x, G27y, G27z, G28a, G28b, G28c, G28d, G28e, G28f, G28g, G28h, G28i, G28j, G28k, G28l, G28m, G28n, G28o, G28p, G28q, G28r, G28s, G28t, G28u, G28v, G28w, G28x, G28y, G28z, G29a, G29b, G29c, G29d, G29e, G29f, G29g, G29h, G29i, G29j, G29k, G29l, G29m, G29n, G29o, G29p, G29q, G29r, G29s, G29t, G29u, G29v, G29w, G29x, G29y, G29z, G30a, G30b, G30c, G30d, G30e, G30f, G30g, G30h, G30i, G30j, G30k, G30l, G30m, G30n, G30o, G30p, G30q, G30r, G30s, G30t, G30u, G30v, G30w, G30x, G30y, G30z, G31a, G31b, G31c, G31d, G31e, G31f, G31g, G31h, G31i, G31j, G31k, G31l, G31m, G31n, G31o, G31p, G31q, G31r, G31s, G31t, G31u, G31v, G31w, G31x, G31y, G31z, G32a, G32b, G32c, G32d, G32e, G32f, G32g, G32h, G32i, G32j, G32k, G32l, G32m, G32n, G32o, G32p, G32q, G32r, G32s, G32t, G32u, G32v, G32w, G32x, G32y, G32z, G33a, G33b, G33c, G33d, G33e, G33f, G33g, G33h, G33i, G33j, G33k, G33l, G33m, G33n, G33o, G33p, G33q, G33r, G33s, G33t, G33u, G33v, G33w, G33x, G33y, G33z, G34a, G34b, G34c, G34d, G34e, G34f, G34g, G34h, G34i, G34j, G34k, G34l, G34m, G34n, G34o, G34p, G34q, G34r, G34s, G34t, G34u, G34v, G34w, G34x, G34y, G34z, G35a, G35b, G35c, G35d, G35e, G35f, G35g, G35h, G35i, G35j, G35k, G35l, G35m, G35n, G35o, G35p, G35q, G35r, G35s, G35t, G35u, G35v, G35w, G35x, G35y, G35z, G36a, G36b, G36c, G36d, G36e, G36f, G36g, G36h, G36i, G36j, G36k, G36l, G36m, G36n, G36o, G36p, G36q, G36r, G36s, G36t, G36u, G36v, G36w, G36x, G36y, G36z, G37a, G37b, G37c, G37d, G37e, G37f, G37g, G37h, G37i, G37j, G37k, G37l, G37m, G37n, G37o, G37p, G37q, G37r, G37s, G37t, G37u, G37v, G37w, G37x, G37y, G37z, G38a, G38b, G38c, G38d, G38e, G38f, G38g, G38h, G38i, G38j, G38k, G38l, G38m, G38n, G38o, G38p, G38q, G38r, G38s, G38t, G38u, G38v, G38w, G38x, G38y, G38z, G39a, G39b, G39c, G39d, G39e, G39f, G39g, G39h, G39i, G39j, G39k, G39l, G39m, G39n, G39o, G39p, G39q, G39r, G39s, G39t, G39u, G39v, G39w, G39x, G39y, G39z, G40a, G40b, G40c, G40d, G40e, G40f, G40g, G40h, G40i, G40j, G40k, G40l, G40m, G40n, G40o, G40p, G40q, G40r, G40s, G40t, G40u, G40v, G40w, G40x, G40y, G40z, G41a, G41b, G41c, G41d, G41e, G41f, G41g, G41h, G41i, G41j, G41k, G41l, G41m, G41n, G41o, G41p, G41q, G41r, G41s, G41t, G41u, G41v, G41w, G41x, G41y, G41z, G42a, G42b, G42c, G42d, G42e, G42f, G42g, G42h, G42i, G42j, G42k, G42l, G42m, G42n, G42o, G42p, G42q, G42r, G42s, G42t, G42u, G42v, G42w, G42x, G42y, G42z, G43a, G43b, G43c, G43d, G43e, G43f, G43g, G43h, G43i, G43j, G43k, G43l, G43m, G43n, G43o, G43p, G43q, G43r, G43s, G43t, G43u, G43v, G43w, G43x, G43y, G43z, G44a, G44b, G44c, G44d, G44e, G44f, G44g, G44h, G44i, G44j, G44k, G44l, G44m, G44n, G44o, G44p, G44q, G44r, G44s, G44t, G44u, G44v, G44w, G44x, G44y, G44z, G45a, G45b, G45c, G45d, G45e, G45f, G45g, G45h, G45i, G45j, G45k, G45l, G45m, G45n, G45o, G45p, G45q, G45r, G45s, G45t, G45u, G45v, G45w, G45x, G45y, G45z, G46a, G46b, G46c, G46d, G46e, G46f, G46g, G46h, G46i, G46j, G46k, G46l, G46m, G46n, G46o, G46p, G46q, G46r, G46s, G46t, G46u, G46v, G46w, G46x, G46y, G46z, G47a, G47b, G47c, G47d, G47e, G47f, G47g, G47h, G47i, G47j, G47k, G47l, G47m, G47n, G47o, G47p, G47q, G47r, G47s, G47t, G47u, G47v, G47w, G47x, G47y, G47z, G48a, G48b, G48c, G48d, G48e, G48f, G48g, G48h, G48i, G48j, G48k, G48l, G48m, G48n, G48o, G48p, G48q, G48r, G48s, G48t, G48u, G48v, G48w, G48x, G48y, G48z, G49a, G49b, G49c, G49d, G49e, G49f, G49g, G49h, G49i, G49j, G49k, G49l, G49m, G49n, G49o, G49p, G49q, G49r, G49s, G49t, G49u, G49v, G49w, G49x, G49y, G49z, G50a, G50b, G50c, G50d, G50e, G50f, G50g, G50h, G50i, G50j, G50k, G50l, G50m, G50n, G50o, G50p, G50q, G50r, G50s, G50t, G50u, G50v, G50w, G50x, G50y, G50z, G51a, G51b, G51c, G51d, G51e, G51f, G51g, G51h, G51i, G51j, G51k, G51l, G51m, G51n, G51o, G51p, G51q, G51r, G51s, G51t, G51u, G51v, G51w, G51x, G51y, G51z, G52a, G52b, G52c, G52d, G52e, G52f, G52g, G52h, G52i, G52j, G52k, G52l, G52m, G52n, G52o, G52p, G52q, G52r, G52s, G52t, G52u, G52v, G52w, G52x, G52y, G52z, G53a, G53b, G53c, G53d, G53e, G53f, G53g, G53h, G53i, G53j, G53k, G53l, G53m, G53n, G53o, G53p, G53q, G53r, G53s, G53t, G53u, G53v, G53w, G53x, G53y, G53z, G54a, G54b, G54c, G54d, G54e, G54f, G54g, G54h, G54i, G54j, G54k, G54l, G54m, G54n, G54o, G54p, G54q, G54r, G54s, G54t, G54u, G54v, G54w, G54x, G54y, G54z, G55a, G55b, G55c, G55d, G55e, G55f, G55g, G55h, G55i, G55j, G55k, G55l, G55m, G55n, G55o, G55p, G55q, G55r, G55s, G55t, G55u, G55v, G55w, G55x, G55y, G55z, G56a, G56b, G56c, G56d, G56e, G56f, G56g, G56h, G56i, G56j, G56k, G56l, G56m, G56n, G56o, G56p, G56q, G56r, G56s, G56t, G56u, G56v, G56w, G56x, G56y, G56z, G57a, G57b, G57c, G57d, G57e, G57f, G57g, G57h, G57i, G57j, G57k, G57l, G57m, G57n, G57o, G57p, G57q, G57r, G57s, G57t, G57u, G57v, G57w, G57x, G57y, G57z, G58a, G58b, G58c, G58d, G58e, G58f, G58g, G58h, G58i, G58j, G58k, G58l, G58m, G58n, G58o, G58p, G58q, G58r, G58s, G58t, G58u, G58v, G58w, G58x, G58y, G58z, G59a, G59b, G59c, G59d, G59e, G59f, G59g, G59h, G59i, G59j, G59k, G59l, G59m, G59n, G59o, G59p, G59q, G59r, G59s, G59t, G59u, G59v, G59w, G59x, G59y, G59z, G60a, G60b, G60c, G60d, G60e, G60f, G60g, G60h, G60i, G60j, G60k, G60l, G60m, G60n, G60o, G60p, G60q, G60r, G60s, G60t, G60u, G60v, G60w, G60x, G60y, G60z, G61a, G61b, G61c, G61d, G61e, G61f, G61g, G61h, G61i, G61j, G61k, G61l, G61m, G61n, G61o, G61p, G61q, G61r, G61s, G61t, G61u, G61v, G61w, G61x, G61y, G61z, G62a, G62b, G62c, G62d, G62e, G62f, G62g, G62h, G62i, G62j, G62k, G62l, G62m, G62n, G62o, G62p, G62q, G62r, G62s, G62t, G62u, G62v, G62w, G62x, G62y, G62z, G63a, G63b, G63c, G63d, G63e, G63f, G63g, G63h, G63i, G63j, G63k, G63l, G63m, G63n, G63o, G63p, G63q, G63r, G63s, G63t, G63u, G63v, G63w, G63x, G63y, G63z, G64a, G64b, G64c, G64d, G64e, G64f, G64g, G64h, G64i, G64j, G64k, G64l, G64m, G64n, G64o, G64p, G64q, G64r, G64s, G64t, G64u, G64v, G64w, G64x, G64y, G64z, G65a, G65b, G65c, G65d, G65e, G65f, G65g, G65h, G65i, G65j, G65k, G65l, G65m, G65n, G65o, G65p, G65q, G65r, G65s, G65t, G65u, G65v, G65w, G65x, G65y, G65z, G66a, G66b, G66c, G66d, G66e, G66f, G66g, G66h, G66i, G66j, G66k, G66l, G66m, G66n, G66o, G66p, G66q, G66r, G66s, G66t, G66u, G66v, G66w, G66x, G66y, G66z, G67a, G67b, G67c, G67d, G67e, G67f, G67g, G67h, G67i, G67j, G67k, G67l, G67m, G67n, G67o, G67p, G67q, G67r, G67s, G67t, G67u, G67v, G67w, G67x, G67y, G67z, G68a, G68b, G68c, G68d, G68e, G68f, G68g, G68h, G68i, G68j, G68k, G68l, G68m, G68n, G68o, G68p, G68q, G68r, G68s, G68t, G68u, G68v, G68w, G68x, G68y, G68z, G69a, G69b, G69c, G69d, G69e, G69f, G69g, G69h, G69i, G69j, G69k, G69l, G69m, G69n, G69o, G69p, G69q, G69r, G69s, G69t, G69u, G69v, G69w, G69x, G69y, G69z, G70a, G70b, G70c, G70d, G70e, G70f, G70g, G70h, G70i, G70j, G70k, G70l, G70m, G70n, G70o, G70p, G70q, G70r, G70s, G70t, G70u, G70v, G70w, G70x, G70y, G70z, G71a, G71b, G71c, G71d, G71e, G71f, G71g, G71h, G71i, G71j, G71k, G71l, G71m, G71n, G71o, G71p, G71q, G71r, G71s, G71t, G71u, G71v, G71w, G71x, G71y, G71z, G72a, G72b, G72c, G72d, G72e, G72f, G72g, G72h, G72i, G72j, G72k, G72l, G72m, G72n, G72o, G72p, G72q, G72r, G72s, G72t, G72u, G72v, G72w, G72x, G72y, G72z, G73a, G73b, G73c, G73d, G73e, G73f, G73g, G73h, G73i, G73j, G73k, G73l, G73m, G73n, G73o, G73p, G73q, G73r, G73s, G73t, G73u, G73v, G73w, G73x, G73y, G73z, G74a, G74b, G74c, G74d, G74e, G74f, G74g, G74h, G74i, G74j, G74k, G74l, G74m, G74n, G74o, G74p, G74q, G74r, G74s, G74t, G74u, G74v, G74w, G74x, G74y, G74z, G75a, G75b, G75c, G75d, G75e, G75f, G75g, G75h, G75i, G75j, G75k, G75l, G75m, G75n, G75o, G75p, G75q, G75r, G75s, G75t, G75u, G75v, G75w, G75x, G75y, G75z, G76a, G76b, G76c, G76d, G76e, G76f, G76g, G76h, G76i, G76j, G76k, G76l, G76m, G76n, G76o, G76p, G76q, G76r, G76s, G76t, G76u, G76v, G76w, G76x, G76y, G76z, G77a, G77b, G77c, G77d, G77e, G77f, G77g, G77h, G77i, G77j, G77k, G77l, G77m, G77n, G77o, G77p, G77q, G77r, G77s, G77t, G77u, G77v, G77w, G77x, G77y, G77z, G78a, G78b, G78c, G78d, G78e, G78f, G78g, G78h, G78i, G78j, G78k, G78l, G78m, G78n, G78o, G78p, G78q, G78r, G78s, G78t, G78u, G78v, G78w, G78x, G78y, G78z, G79a, G79b, G79c, G79d, G79e, G79f, G79g, G79h, G79i, G79j, G79k, G79l, G79m, G79n, G79o, G79p, G79q, G79r, G79s, G79t, G79u, G79v, G79w, G79x, G79y, G79z, G80a, G80b, G80c, G80d, G80e, G80f, G80g, G80h, G80i, G80j, G80k, G80l, G80m, G80n, G80o, G80p, G80q, G80r, G80s, G80t, G80u, G80v, G80w, G80x, G80y, G80z, G81a, G81b, G81c, G81d, G81e, G81f, G81g, G81h, G81i, G81j, G81k, G81l, G81m, G81n, G81o, G81p, G81q, G81r, G81s, G81t, G81u, G81v, G81w, G81x, G81y, G81z, G82a, G82b, G82c, G82d, G82e, G82f, G82g, G82h, G82i, G82j, G82k, G82l, G82m, G82n, G82o, G82p, G82q, G82r, G82s, G82t, G82u, G82v, G82w, G82x, G82y, G82z, G83a, G83b, G83c, G83d, G83e, G83f, G83g, G83h, G83i, G83j, G83k, G83l, G83m, G83n, G83o, G83p, G83q, G83r, G83s, G83t, G83u, G83v, G83w, G83x, G83y, G83z, G84a, G84b, G84c, G84d, G84e, G84f, G84g, G84h, G84i, G84j, G84k, G84l, G84m, G84n, G84o, G84p, G84q, G84r, G84s, G84t, G84u, G84v, G84w, G84x, G84y, G84z, G85a, G85b, G85c, G85d, G85e, G85f, G85g, G85h, G85i, G85j, G85k, G85l, G85m, G85n, G85o, G85p, G85q, G85r, G85s, G85t, G85u, G85v, G85w, G85x, G85y, G85z, G86a, G86b, G86c, G86d, G86e, G8

Page 192 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3156	15919	28565	5.72	7.0E-05	AB030800.1	NT	Dicystotellum discidium gene for TRFA, complete cds
4339	17076	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17140	29778	0.95	7.0E-05	U60890.1	NT	Caenorhabditis elegans Sxp1p homolog mRNA, complete cds
4871	17598	30221	0.71	7.0E-05	9846300	NT	Rat cytochrome P-450 2C19 mRNA, complete genome
8124	22013	33954	1.09	7.0E-05	AA058582.1	EST_HUMAN	h85090.1 nt1 CGAP_B7c Homo sapiens cDNA clone IMAGE:365088 3'
8453	22023	33175	2.97	7.0E-05	U07095.1	EST_HUMAN	BT024984 Fetal brain, Stratiogene (cat9265266) Homo sapiens cDNA clone HFBED80
11112	23782		3.09	7.0E-05	10835046	NT	Homo sapiens sacrocyticin, epsilon (SCGE), mRNA
2020	14755	27484	1.69	6.0E-05	4895170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2020	14755	27485	1.89	6.0E-05	4895170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2595	15309	28048	1.19	6.0E-05	AI055241.1	EST_HUMAN	w654h06.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03280 DNA TOPOISOMERASE I (HUMAN);
2590	15399	29137	1.1	6.0E-05	Z84508.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA.28B10
2660	15399	29138	1.1	6.0E-05	Z84508.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA.28B10
2817	13440	20080	3.07	6.0E-05	AF055630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5822	19811	31541	3.61	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5822	19811	31542	3.61	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6309	18081	32069	1.4	6.0E-05	N72829.1	EST_HUMAN	yf0601.1.1 Scores full length, infls Homo sapiens cDNA clone IMAGE:246212 5'
6834	19468	32520	0.95	6.0E-05	AA897680.1	EST_HUMAN	gc48h03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1604888 3'
7983	20678	33903	0.76	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0317-147169-011-H08 BT0311 Homo sapiens cDNA
7993	20678	33904	0.76	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0317-147169-011-H08 BT0311 Homo sapiens cDNA
8342	21035	34172	0.82	6.0E-05	AA150482.1	EST_HUMAN	contains element MER28 repetitive element;
8347	21040	34177	2.22	6.0E-05	AW086829.1	EST_HUMAN	PM4-NN050-310300-001-F40 NN050 Homo sapiens cDNA
8479	21171	34316	0.63	6.0E-05	G060401	SWISSPROT	COMPLEMENT DEACY-ACCELERATING FACTOR PRECURSOR
9151	21882	35950	1.21	6.0E-05	P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9151	21882	35951	1.21	6.0E-05	P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9421	22069	35271	0.85	6.0E-05	T64149.1	EST_HUMAN	y28c12.11 Stratiogene lung (8637210) Homo sapiens cDNA clone IMAGE:119052 5'
9521	22274	35462	0.59	6.0E-05	AW627985.1	EST_HUMAN	h37a03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
							yf0601.1.1 Scores_placenta NB2HP Homo sapiens cDNA clone IMAGE:143533 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
10649	23340	39578	3.06	6.0E-05	R76593.1	EST_HUMAN	485802.x1 Scores_pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:487035 5'
11502	24103	37415	3.38	6.0E-05	AA044015.1	EST_HUMAN	MRC-NT0038-250400-001-F09 NT0038 Homo sapiens cDNA
12887	25239	30822	14.34	6.0E-05	AW080110.1	EST_HUMAN	Tg28h03.x1 NC1 CGAP_B7c2 Homo sapiens cDNA clone IMAGE:3307768 3'
12810	25053		1.4	6.0E-05	BE058403.1	EST_HUMAN	QV4-ST0234-241169-040-H11 ST0234 Homo sapiens cDNA
1382	14128	26902	10.46	5.0E-05	AW392088.1	EST_HUMAN	QV4-ST0234-241169-040-H11 ST0234 Homo sapiens cDNA

Page 193 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1055	14583		1.2	5.0E-05	8923891	NT	Homo sapiens 220Da peroxisomal membrane protein-like (LOC55895), mRNA
2951	12566	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3961	16710	20350	2.41	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLG22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17763	30408	0.72	5.0E-05	Q26422	SWISSPROT	LIKULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17763	30408	0.72	5.0E-05	Q26422	SWISSPROT	LIKULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X68855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6003	19698	31639	3.75	5.0E-05	AF593544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA08 3'
6076	19855	31822	0.99	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19916		0.87	5.0E-05	AB037684.1	NT	Mus musculus gene for cadherin, exon 1
12176	24810		3.84	5.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4449	17185	28809	0.73	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	28810	0.73	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
8941	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9423	22101		7.67	4.0E-05	AF202635.1	NT	Homo sapiens PPI230 mRNA, complete cds
9901	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS; REVERSE TRANSCRIPTASE ;
10306	22953	36168	0.59	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10668	23359		4.16	4.0E-05	AW527945.1	EST_HUMAN	h39c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element :
12140	24928		1.48	4.0E-05	AW117580.1	EST_HUMAN	cd33c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element :
12789	25041		1.71	4.0E-05	AA417765.1	EST_HUMAN	q04c10.x1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains Alu repetitive element contains element KER repetitive element :
6965	13441	29082	1.6	3.0E-05	AI248061.1	EST_HUMAN	q04c10.x1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains Alu repetitive element contains element KER repetitive element :
1037	13797	29457	0.86	3.0E-05	AW273951.1	EST_HUMAN	X24903.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains Alu repetitive element contains element KER repetitive element :
1109	13865	26523	1.01	3.0E-05	BF037698.1	EST_HUMAN	60146163FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3685142 5'
1109	13866	26524	1.01	3.0E-05	BF037698.1	EST_HUMAN	60146163FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3685142 5'
9287	16048		0.73	3.0E-05	AI288919.1	EST_HUMAN	q04g11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:3685142 5'
4349	17058	29719	7.96	3.0E-05	BE169211.1	EST_HUMAN	CO8682 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4349	17058	29719	7.96	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-301-470 HT0521 Homo sapiens cDNA
4349	17058	29720	7.98	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-301-470 HT0521 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	26768	0.94	3.0E-05	AA368979.1	EST_HUMAN	EST76986 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4434	17170	26769	0.94	3.0E-05	AA368979.1	EST_HUMAN	EST76986 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4450	17285		0.99	3.0E-05	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21G102
4688	17420	30095	1	3.0E-05	P87468	SWISSPROT	CHEK2 KINASE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	25082	0.82	3.0E-05	AI248061.1	EST_HUMAN	q14c10.ct1 Soares_feld_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element contains element KER repetitive element ;
4791	17522	30144	0.97	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM44 Homo sapiens cDNA clone NT2RM4402075 5'
6470	18259	31161	1.06	3.0E-05	A1225782.1	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mye2p), mRNA
6659	19419	32433	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exon 6-8
6659	19419	32434	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exon 6-8
7709	20494	33616	2.33	3.0E-05	BE733157.1	EST_HUMAN	BD156743T1T1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8250	20944	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	z56005.x1 Stratigene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8761	21483	34630	1.58	3.0E-05	AW770982.1	EST_HUMAN	h64e08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006538 3'
8765	21487	34633	1.23	3.0E-05	AW770982.1	EST_HUMAN	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8769	21491	34638	0.61	3.0E-05	PA3381	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
8028	21719		0.56	3.0E-05	XG3273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21809	36068	1.22	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
9563	22216		2.92	3.0E-05	AJ769331.1	EST_HUMAN	w93608.x1 Soares_NSF_F8_9W_OT_PA.P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10433	23079	36303	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24595		1.77	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromere end
2323	18048	27784	1.09	2.0E-05	AI296021.1	EST_HUMAN	q19841.x1 Soares_NFL_T_05C_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2597	15301	28037	2.43	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element ;
2716	15425		7.45	2.0E-05	AA160592.1	EST_HUMAN	z476812.r1 Stratigene INT neuron (9637233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element contains element L1 repetitive element ;
3134	19899	28544	1.23	2.0E-05	BE060693.1	EST_HUMAN	RC3-BT0319-120200-074-H08 BT0319 Homo sapiens cDNA
3343	19102	28754	0.93	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3362	19121	28779	1.22	2.0E-05	X63211.1	NT	H. sapiens DNA for endogenous retroviral like element
3465	16242		0.71	2.0E-05	X85465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3767	16539		0.78	2.0E-05	AI039107.1	EST_HUMAN	DKFZp669064.r1 968 (synonym: hnf62) Homo sapiens cDNA clone DKFZp669064 5'
4643	17377		1.09	2.0E-05	BE378471.1	EST_HUMAN	601238455F1T1 MGC_44 Homo sapiens cDNA clone IMAGE:360863 5'
5672	18467	31382	1.92	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)

Page 196 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10489	23135	36893	1.98	2.0E-05	N41751.1	EST_HUMAN	yw91d06.11 Soares_pilocenta_Blo8weeks_2NBHFP8b9W Homo sapiens cDNA clone IMAGE:269570 5'
10541	19485		2.42	2.0E-05	A1691025.1	EST_HUMAN	wu3507.x1 Soares_Dickkopf2.colon_NHCD Homo sapiens cDNA clone IMAGE:252077 3'
11287	23948	37243	1.33	2.0E-05	A1463285.1	EST_HUMAN	130109.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR-Q13538 Q13538
11287	23948						ORF2: FUNCTION UNKNOWN.
11430	23197	36428	1.33	2.0E-05	A1463285.1	EST_HUMAN	130109.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR-Q13538 Q13538
11430	23197						ORF2: FUNCTION UNKNOWN.
12185	25168		4.86	2.0E-05	BE348228.1	EST_HUMAN	RC5-HT0582-280300-072E12 HT0582 Homo sapiens cDNA
12342	25168		2.27	2.0E-05	AF278948.1	NT	hw21d03.x1 NCL CGAP_Kd411 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR-Q12832
12674	25247		1.44	2.0E-05	D16583.1	NT	Q12832 GLYCOPHORIN HEP2;
2285	14691	27731	3.22	1.0E-05	P27448	SWISSPROT	Homo sapiens ABCAT (ABCA1) gene, complete cds
2700	15603	28143	1.6	1.0E-05	AL163282.2	NT	Human gene for L-Histidine decarboxylase, complete cds
3841	16304	28034	1.91	1.0E-05	AF088273.1	NT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
3793	16545		1.02	1.0E-05	AF223391.1	NT	Homo sapiens chromosome 21 segment HS21C082
3949	16699	28337	9.2	1.0E-05	P81274	SWISSPROT	Drosophila melanogaster strain Larnio 120 Suppressor of Hairless (Su(H)) gene, partial cds
4152	16904	29523	1.2	1.0E-05	AL163203.2	NT	Homo sapiens calcium channel alpha1E subunit (CA1NA1E) gene, exons 7-49, and partial cds, alternatively spliced
4244	16985	29003	2.52	1.0E-05	AA431118.1	EST_HUMAN	MOSAIC PROTEIN LGN
4789	17030	30152	1.81	1.0E-05	AW416134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6653	19415	32428	1.22	1.0E-05	AJ246003.1	NT	z689g04.11 Soares_leslie_NHT Homo sapiens cDNA clone IMAGE:781494 5'
6980	19505	32530	2.58	1.0E-05	AA641846.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2886548 3'
6982	19675	32722	3.28	1.0E-05	P19474	SWISSPROT	Homo sapiens Spast gene for spastin protein
7877	20341		1.18	1.0E-05	P19474	SWISSPROT	ns11902.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.L1 L1
8813	21505		2.24	1.0E-05	AL163227.2	NT	L1 repetitive element;
8958	21649	34769	3.02	1.0E-05	AA462578.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
9187	21857	35022	12.45	1.0E-05	AA238110.1	EST_HUMAN	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RQ(SS-A))
9266	22020	35180	0.62	1.0E-05	AV732190.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9738	22389	35583	0.74	1.0E-05	AW610802.1	EST_HUMAN	z3d3h12.s1 Soares_fetus_Ni2HFB_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to
							gblJ02382 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
							z3o5e11.1 NCL CGAP_GGB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu
							repetitive element/contains element TART repetitive element;
							AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
							hw41b02.x1 Soares_NFL_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OPR.11 OPR repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	22386	35594	0.74	1.0E-05	AW510602.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains
9816	22467	35680	1.16	1.0E-05	AW291521.1	EST_HUMAN	UHH-B12-3gk-a-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9818	22467	35670	1.16	1.0E-05	AW291521.1	EST_HUMAN	UHH-B12-3gk-a-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW466955.1	EST_HUMAN	hd07c10.x1 NCI_CGAP_Kd412 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element:
10836	23518	36760	1.07	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorAet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10836	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorAet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11854	24438	37760	1.39	1.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2678	15367	26129	4.9	9.0E-08	AI683811.1	EST_HUMAN	h73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3092	15857	28498	3.53	9.0E-06	AI218983.1	EST_HUMAN	gg11p08.x1 Soares_B15weeks_2N1b1P809W Homo sapiens cDNA clone IMAGE:1759191 3'
3597	16350		2.82	9.0E-06	M61755.1	NT	Human alanine glyoxylate aminotransferase (AGXT) gene, exon 1 and 2
9815	18504	31632	2.61	9.0E-08	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 6, 6
6765	19509	32534	0.9	9.0E-05	BE05042.1	EST_HUMAN	RC1-B10313-1T050-D17-a07 BT0313 Homo sapiens cDNA
7340	20021	33099	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7673	20337	33450	13.94	9.0E-06	AL034370.1	EST_HUMAN	ox20p01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655912 3' similar to contains Alu repetitive element;
8363	21056	34197	1.1	9.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment H6210009
8881	21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) [DOWN-REGULATED BY V-SRC]
8881	21572	34716	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) [DOWN-REGULATED BY V-SRC]
9122	21810	34976	4.3	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10838	23539	35784	3.46	9.0E-05	Q10354	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2522	15597	27886	1.27	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-111 CT0283 Homo sapiens cDNA
10430	23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASCIOLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36299	0.76	8.0E-06	P34083	SWISSPROT	FASCIOLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
859	13723		2.09	7.0E-06	AA069728.1	EST_HUMAN	ab06970.s1 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.1 MER20 repetitive element
1419	14167	26851	3.42	7.0E-06	7952177	NT	Homo sapiens KIA00555 gene product (KIA00555), mRNA
2876	15643		5.83	7.0E-06	A388952.1	EST_HUMAN	Y61605.x1 NCI_OGAP_U13 Homo sapiens cDNA clone IMAGE:1991266 3' similar to contains Alu repetitive element
3551	16309		0.92	7.0E-06	AA38542.1	EST_HUMAN	EST192205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5609	18408		5.68	7.0E-06	AW88341.1	EST_HUMAN	QV2-070082-200-00-173-R01 OT0082 Homo sapiens cDNA
5715	18508	31429	1.01	7.0E-06	N89846.1	EST_HUMAN	Y61507.r1 Scores_multiple_sclerosis_2NBH-MSP Homo sapiens cDNA clone IMAGE:278412 5'
8698	21380	34524	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probe (GS1 gene) (DXF68S1E), mRNA
8600	22451		0.45	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11830	25336	30608	2.32	7.0E-06	BF215972.1	EST_HUMAN	801881922FT NIH_MGC_S7 Homo sapiens cDNA clone IMAGE:4993972 5'
2918	15584	28329	1.28	6.0E-06	BE066189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3860	16433	29078	1.08	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4705	15708	28359	1.91	6.0E-06	Q01465	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAV PROTEIN)
4710	17442	30074	2.21	8.0E-06	A040099.1	EST_HUMAN	aa08402.x1 Scores_fetal_liver_spleen_INTLS_S1 Homo sapiens cDNA clone IMAGE:1855738 3' similar to contains MER8.12 MER8 repetitive element
5285	18071	30700	1.32	6.0E-06	AF167441.1	NT	Mus musculue E-cadherin binding protein E7 mRNA, complete cds
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9766	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	IL5JM0070-110400-063-002 UM0070 Homo sapiens cDNA
12765	25016	30979	2.27	8.0E-06	11418137	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5970	18782	31713	3.27	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS210048
6245	19019	31993	2.31	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M6004 Met protein (V8004 Met) gene, complete cds
7134	19821	32987	1.1	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8359	21052	34192	0.93	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
8359	21052	34193	0.93	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
10002	23562	35862	6.16	5.0E-06	AA313620.1	EST_HUMAN	EST188498 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10410	23036	36273	0.45	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C2/C3 CONVERTASE)
12640	24933	30987	2.83	5.0E-06	A065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	29048	6.1	4.0E-06	R16287.1	EST_HUMAN	yae6003.r1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element contains L1 repetitive element
829	13586	29266	7.07	4.0E-06	AW103354.1	EST_HUMAN	xc89g12.x1 NCI_OGAP_E502 Homo sapiens cDNA clone IMAGE:288574 3' similar to contains Alu repetitive element contains element MER21 repetitive element

Page 198 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1311	14059	26733	4.84	4.0E-06	AB34928.1	EST_HUMAN	h33a09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1311	14059	26734	4.84	4.0E-06	AB34928.1	EST_HUMAN	h33a09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1457	14204	26989	1.8	4.0E-06	BF366612.1	EST_HUMAN	QV2-NT0046-200600-250107 NT0046 Homo sapiens cDNA
2261	14968	27729	2.17	4.0E-06	AW015401.1	EST_HUMAN	UH4810-ea4-Q8-GU1.1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3090	15828	28471	0.9	4.0E-06	AF108349.1	NT	Gallus gallus Dactyl protein (Dactyl) mRNA, complete cds
3374	16824	29282	1.05	4.0E-06	AW848268.1	EST_HUMAN	IL3-CT0214-160200-074-B03 CT0214 Homo sapiens cDNA
4756	17488	30115	1.89	4.0E-06	AB896939.1	EST_HUMAN	WER22 repetitive element;
8397	21050	34225	0.56	4.0E-06	O16393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
8659	21351	34538	3.56	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9607	22280	35446	1.24	4.0E-06	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11427	23194	36425	4.21	4.0E-06	AB007855.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2160	14990	27824	1.75	3.0E-06	AA700582.1	EST_HUMAN	z3408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2160	14990	27825	1.75	3.0E-06	AA700582.1	EST_HUMAN	z3408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2283	14989		1.44	3.0E-06	AF202835.1	NT	Homo sapiens PPT200 mRNA, complete cds
2022	15698	28332	1.05	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.8 LTR1 repetitive element;
3259	16021		2.05	3.0E-06	AB85779.1	EST_HUMAN	M22a05.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:G00734 G00734 LINE-1 LIKE PROTEIN contains L1.12 L1 repetitive element;
3763	16315	29152	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg44d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3763	16315	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg44d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminals);
6036	18847	31811	0.93	3.0E-06	AU158412.1	EST_HUMAN	AU158412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7129	19817		2.43	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7891	20676	33801	0.83	3.0E-06	BE620694.1	EST_HUMAN	601336213.F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3690314 5'
8654	21276	34413	0.65	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12349	24755		3.84	3.0E-06	AW38282.1	EST_HUMAN	RC04-T0001-261159-011-A03 L10001 Homo sapiens cDNA
1597	13010		2.81	2.0E-06	F54358	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1591	14308		4.45	2.0E-06	P21414	SWISSPROT	POLY(POLY)PROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2376	15098	27839	4.8	2.0E-06	AB72138.1	EST_HUMAN	w64a03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2267088 3' similar to contains MER30.b1 MER30 repetitive element;

Page 200 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2480	15187	27826	2.37	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	15285	28023	1.88	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16265	28919	1.12	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLG Homo sapiens cDNA clone GLCFDB05.3'
3744	16467	29132	1.69	2.0E-06	AA173518.1	EST_HUMAN	ZP02405.11 Stragene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:495232.5'
3753	16505	29141	0.82	2.0E-06	AW450215.1	EST_HUMAN	U14-HB3-40y-95-D-U1.61 NCJ CGAP_S06 Homo sapiens cDNA clone IMAGE:2736176.3'
3798	16510	29146	1.82	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5998	18779		0.83	2.0E-06	AA974832.1	EST_HUMAN	on34H01.s1 NCJ CGAP_L05 Homo sapiens cDNA clone IMAGE:1658609.3' similar to contains Alu repetitive element;
6028	18808	31788	0.83	2.0E-06	AI59448.1	EST_HUMAN	165105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2060241.3' similar to TR:Q13637
6348	19118	32108	5.47	2.0E-06	AI810424.1	EST_HUMAN	Q13937 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7818	20513		1.63	2.0E-06	AW869223.1	EST_HUMAN	w90504.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063.3'
7888	20883	33809	0.57	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-102 SN0067 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H62051.1	EST_HUMAN	Z627c11.s1 Soares_pinea1_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300.3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9116	21804	34669	0.92	2.0E-06	AF03529.1	NT	Y37cd04.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235674.5' similar to gb-X74829
9116	21804	34970	0.82	2.0E-06	AF03529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 [HUMAN];
9135	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
9800	22253	35438	1	2.0E-06	N30676.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
9819	22170		0.83	2.0E-06	AV748909.1	EST_HUMAN	y16910.x1 NCJ CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730.3'
12251	23587	30609	2.1	2.0E-06	P23249	SWISSPROT	yw69e03.s1 Soares_placenta_bloodvessels_2NtHP899W Homo sapiens cDNA clone IMAGE:257212.3'
32	12860	26477	2.38	1.0E-06	O76082	SWISSPROT	AV748909 NPC Homo sapiens cDNA clone NPcAXD05.5'
842	13421	28060	2.62	1.0E-06	AF084364.1	NT	PROTEIN NOV-10
1434	14181	28886	1.61	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1514	14261	28947	1.67	1.0E-06	AL183276.2	NT	Mus musculus SURF6 protein (SURF6) mRNA, complete cds
1564	14311	26997	1.27	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CM2-9
1664	14311	26998	1.27	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	Z106412.s1 Soares_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982.3' similar to contains Alu repetitive element;
							Z106412.s1 Soares_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982.3' similar to contains Alu repetitive element;
							DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1987	14723	27443	5.09	1.0E-06	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1987	14723	27444	5.09	1.0E-06	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4396	17075	29703	12.81	1.0E-06	U07586.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M6804 Mol protein (M6804 Mol) gene, complete cds
5208	18016	30638	5.07	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5232	18038	30685	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-006500-001-e04 FN0004 Homo sapiens cDNA
5232	18038	30688	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-006500-001-e04 FN0004 Homo sapiens cDNA
5396	18169	30881	1.22	1.0E-06	OB0613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5703	18500		0.78	1.0E-06	BE063527.1	EST_HUMAN	CM00-BT0281-031199-087-R04 BT0281 Homo sapiens cDNA
6773	18617	32545	0.91	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHA1(ALPHA-E) CHAIN PRECURSOR
7644	20595		0.63	1.0E-06	BE186330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
7900	20595		0.77	1.0E-06	AA912623.1	EST_HUMAN	Q28c08.s1 Scavenging_NEL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:1524878.3
8171	20865	33997	1.2	1.0E-06	A1347010.1	EST_HUMAN	gp54602.xt NCL CGAP_Co88 Homo sapiens cDNA clone IMAGE:1926842.3
8387	21080	34215	1.31	1.0E-06	A1287878.1	EST_HUMAN	q123706.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435.3 similar to contains element
8204	22083	35255	0.94	1.0E-06	N74635.1	EST_HUMAN	z155601.s1 Sources fetal liver spleen 1NELS Homo sapiens cDNA clone IMAGE:286472.3
9278	22033	35205	0.85	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9581	22234	35417	4.28	1.0E-06	U82688.1	NT	Homo sapiens atox gene, alternatively spliced products, complete cds
9581	22234	35418	4.28	1.0E-06	U82688.1	NT	Homo sapiens atox gene, alternatively spliced products, complete cds
9627	22280	35470	4.76	1.0E-06	AA132811.1	EST_HUMAN	z17608.11 Stragene cdna (z17604) Homo sapiens cDNA clone IMAGE:597174.5
9688	22340		3.37	1.0E-06	AA449257.1	EST_HUMAN	z04471.s1 Sources fetal, fetus, N20H8.9w Homo sapiens cDNA clone IMAGE:597174.5
10385	23031		1.88	1.0E-06	AL163203.2	NT	g16-D28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN)
11848	24245		3.85	1.0E-06	AW860641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
11724	24318	37641	1.38	1.0E-06	AA164914.1	EST_HUMAN	RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA
11724	24318	37642	1.38	1.0E-06	AA164914.1	EST_HUMAN	z142c02.s1 Stragene hNT neuron (z142c03) Homo sapiens cDNA clone IMAGE:632354.3 similar to
12390	14723	27443	1.78	1.0E-06	AF184814.1	NT	SW-POL_SMSAV_P03359 POL POLYPHOSPHATE
12390	14723	27444	1.79	1.0E-06	AF184814.1	NT	SW-POL_SMSAV_P03359 POL POLYPHOSPHATE
351	13150	25760	2.24	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
351	13150	25761	2.24	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8306	21000		0.93	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11212	23875	37181	2.87	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080

Page 202 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24326	37650	1.3	9.0E-07	AF087613.1	NT	Human endogenous retrovirus HERV-P.147D
4719	17451	30084	3.26	8.0E-07	AI28598.1	EST_HUMAN	q82907.x1 Soares_NHHPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
4719	17451	30085	3.26	8.0E-07	AI28598.1	EST_HUMAN	q82907.x1 Soares_NHHPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
6796	18987		9.43	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7801	20598		9.73	8.0E-07	AF138416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		8.59	8.0E-07	T07770.1	EST_HUMAN	EST05560 Fetal brain, Striata (cat#33235) Homo sapiens cDNA clone HFEN88
11912	24478		8.22	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL-1RAP) gene, exons 10 and 11
5432	18231	30944	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	27352	2.98	8.0E-07	AW855558.1	EST_HUMAN	CM3-CT10277-221059-024-6T1 CT10277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2490	15213	27958	4.52	6.0E-07	AF019413.1	NT	
3955	16705		1.83	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4P33 INTERGENIC REGION
9040	21730	34685	1.52	6.0E-07	BF001897.1	EST_HUMAN	7g9407.x1 NCL_CGAP_C018 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 075920 4F5L ;
11836	24420	37761	1.3	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031198-087-ac3 BT0281 Homo sapiens cDNA
12168	23307		2.28	6.0E-07	AW503222.1	EST_HUMAN	CM4-NN1028-250300-121-h12 NN1028 Homo sapiens cDNA
318	13121		1.94	5.0E-07	AI831893.1	EST_HUMAN	h9410.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13795		4.25	5.0E-07	AA380650.1	EST_HUMAN	EST186818 Supr cells Homo sapiens cDNA 5' end
3028	16704		0.88	5.0E-07	AI831893.1	EST_HUMAN	h9410.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6028	18809	31769	0.9	5.0E-07	U65007.1	NT	Mus musculus OG-2 homeodomain protein (OG-2), partial cds
6864	19446	32463	1.89	5.0E-07	AI939981.1	EST_HUMAN	ig08005.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element/contains element ABR repetitive element ;
6864	19446	32464	1.89	5.0E-07	AI939981.1	EST_HUMAN	ig08005.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element/contains element ABR repetitive element ;
7248	19383	33008	17	5.0E-07	AW070985.1	EST_HUMAN	xa316a2.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to g5-X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33969	0.74	5.0E-07	Q8WUQ1	SWISSPROT	ADAMTS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS-1) (ADAMTS-1) (ADAMTS-1)
8388	21091		0.82	5.0E-07	P06593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10295	22913	35123	4.94	5.0E-07	AI808387.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23258	36493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11600	24101	37413	2.62	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		4.04	5.0E-07	AJ271735.1	NT	Human sapiens Xq pseudautosomal region, segment 1/2
12591	25211		3.48	5.0E-07	AW862337.1	EST_HUMAN	OV0-CT0383-2:0400-204-b12 CT0383 Homo sapiens cDNA
3361	16729	23684	2.02	4.0E-07	AW00602.1	EST_HUMAN	wa64n03.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7078	19769		0.83	4.0E-07	AJ272285.1	NT	Human sapiens SP22 gene for secreted phosphoprotein 24 precursor, exons 1-8
7167	19854	32823	1.74	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7823	20518	33644	0.6	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21G007
8949	21640	34787	5.41	4.0E-07	AW419134.1	EST_HUMAN	Xy46g11.x1 NCL CGAP_L0434.1 Homo sapiens cDNA clone IMAGE:2886648 3'
10027	22876	35890	0.47	4.0E-07	BE901976.1	EST_HUMAN	601678748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3359651 5'
10027	22875	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601678748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3359651 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10556	23336	36761	3.14	4.0E-07	AI766528.1	EST_HUMAN	wa81b08.x1 NCL CGAP_K1612 Homo sapiens cDNA clone IMAGE:2399703 3'
10855	23356	36782	3.14	4.0E-07	AI766528.1	EST_HUMAN	wa81b08.x1 NCL CGAP_K1612 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.66	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
431	13217	25952	9.84	3.0E-07	U19719.1	NT	Human microtubulin-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
569	13350	26378	2.12	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1353	14101	26776	2.67	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1822	14389		2.03	3.0E-07	M64857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2039	14773		1.42	3.0E-07	AA528763.1	EST_HUMAN	n150j09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:390825 similar to contains Alu repetitive element; contains L1 13 L1 repetitive element
2266	15011	27749	1.83	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2472	15190	27930	7.61	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-11T BN0115 Homo sapiens cDNA
2472	15190	27930	7.61	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-11T BN0115 Homo sapiens cDNA
3031	15797	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	W50T12.1 Scars fetal liver spleen TNLFS Homo sapiens cDNA
3157	15920	28566	1.45	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCC001 3'
4711	17443	30075	0.65	3.0E-07	AI197236.1	EST_HUMAN	wa66b12.x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5004	17727	30330	1.3	3.0E-07	T57650.1	EST_HUMAN	yc14h06.s1 Scars lung (8937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to
5004	17727	30331	1.3	3.0E-07	T57650.1	EST_HUMAN	yc14h09.s1 Scars lung (8937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to
5004	17727	30331	1.3	3.0E-07	T57650.1	EST_HUMAN	gpi-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5004	17727	30331	1.3	3.0E-07	T57650.1	EST_HUMAN	gpi-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

Page 204 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5980	18377	31280	12.43	3.0E-07	098807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5983	19699	31610	0.83	3.0E-07	042280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6603	19366		5.57	3.0E-07	AA815175.1	EST_HUMAN	cd04c10.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1339890.3'
7409	20086	33170	3.48	3.0E-07	AW757168.1	EST_HUMAN	QY41JN0036-200309-115-g02 UN0036 Homo sapiens cDNA
7561	20231		0.70	3.0E-07	AI691065.1	EST_HUMAN	tw2811.X1 NCI CGAP OV35 Homo sapiens cDNA clone IMAGE:2261037.3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9028	21718	34873	0.86	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439409.1	EST_HUMAN	HTMT-025F1 HTM1 Homo sapiens cDNA
11659	24253		1.75	3.0E-07	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
12791	25043		5.1	3.0E-07	AI132342.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12865	25471	4.15	2.0E-07	AF282688.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
160	12865	26608	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
150	12865	26807	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
171	12869	26929	44.15	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
731	13505	26160	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	26161	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
922	13889	28353	3.73	2.0E-07	AA223280.1	EST_HUMAN	z08807.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869.3' similar to gbL31860 GLYOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
923	13680	29354	2.15	2.0E-07	T63042.1	EST_HUMAN	yo15904.s1 Stralagene lung (4637210) Homo sapiens cDNA clone IMAGE:80790.3' similar to contains L1 repetitive element ;
1140	13885	26566	1.37	2.0E-07	Q28768	SWISSPROT	J6 AUTOANTIGEN
1596	14342	27032	2.98	2.0E-07	Q06701	SWISSPROT	HYPOPHYSAL 72.6 KD PROTEIN C27F.10 IN CHROMOSOME 1
3876	16429	29070	15.93	2.0E-07	AF126348.1	NT	Homo sapiens cavadin 1 (CAV1) gene, exon 3 and partial cds
5059	17778	30395	0.84	2.0E-07	AW070995.1	EST_HUMAN	xad5h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485.3' similar to WP:C38H2.1 CED00923 PROBABLE RABGAP DOMAINS ;

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5059	17778	30395	0.84	2.0E-07	AW070955.1	EST_HUMAN	xa05f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP_C3942.1
5290	19099	30694	1.21	2.0E-07	AW68066.1	EST_HUMAN	CE006923 PROBABLE RABGAP DOMAINS
6455	25000	32223	0.81	2.0E-07	AW448968.1	EST_HUMAN	RC3-NN00066-260400-021-g11 NN00066 Homo sapiens cDNA
6566	16330	32337	1.79	2.0E-07	AI208715.1	EST_HUMAN	UJH-B10-ake-b-01-0-UI et NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
7568	20238	33342	0.87	2.0E-07	X96159.1	NT	sp56403.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8368	21082		4.08	2.0E-07	AV728390.1	EST_HUMAN	h.sapiens broad gene exon 9
8695	21287	34428	0.97	2.0E-07	AA035198.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9651	22313		2.8	2.0E-07	AL163303.2	NT	2d27.g08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10187	22815	36033	5.41	2.0E-07	AV1862307.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10388	23032	36245	0.9	2.0E-07	P00751	SWISSPROT	CM4-NN0003-260300-124-406 NN0003 Homo sapiens cDNA
10388	23032	36246	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
11871	24945		2.44	2.0E-07	BE153717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11953	25212		2.39	2.0E-07	AI732462.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
1080	13938		1.97	1.0E-07	AL163282.2	NT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	PMO-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
2630	14259	26945	2.51	1.0E-07	P08259	SWISSPROT	2i85h11.x5 Stralagene lung carcinoma 957218 Homo sapiens cDNA clone IMAGE:565029 3' similar to
3727	13838		1.29	1.0E-07	AL163282.2	NT	contains THR.b2 THR repetitive element;
4260	17001	29631	2.76	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4260	17001	29632	2.76	1.0E-07	AV718662.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
4690	17424		0.93	1.0E-07	076820	SWISSPROT	GLYCOPROTEIN GPV
5072	17791	30408	0.83	1.0E-07	AA016181.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
6410	19178	32177	0.87	1.0E-07	U62871.2	NT	Homo sapiens chromosome 21 segment HS21C082
6768	19512	32537	5.24	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7382	20071	33160	8.06	1.0E-07	N55081.1	EST_HUMAN	2d5g.q02.r1 Soares retina N2d4HR Homo sapiens cDNA clone IMAGE:363026 5'
7548	20218	33320	0.87	1.0E-07	BF375909.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
7548	20218	33321	0.87	1.0E-07	BF375909.1	EST_HUMAN	2d5g.q02.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:2291339 5'
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
							PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081

Page 206 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385	33469	0.64	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33241	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33842	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8653	21544	34651	2.78	1.0E-07	AA93576.1	EST_HUMAN	Z51610.s1 Soares, field liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:434346 3'
9170	21840	35005	0.97	1.0E-07	P57110	SWISSPROT	ADAMTS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9517	22170	35353	0.45	1.0E-07	BE327943.1	EST_HUMAN	h228005.x1 NCI_OGAP_Mel15 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-O65722 O65722
9836	22487	35698	2.77	1.0E-07	BF874524.1	EST_HUMAN	MER18 repetitive element
9844	22465	35998	1.21	1.0E-07	AA386311.1	EST_HUMAN	602137174F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274420 5'
10392	23009		1.28	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12122	25188	30810	3.83	1.0E-07	BE5048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12514	24884		1.87	1.0E-07	XG1755.1	NT	h53611.x1 NCI_OGAP_Kd11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-O65722 O65722
7181	19887	32840	0.84	9.0E-08	AI539362.1	EST_HUMAN	Human lambda4-immunoglobulin constant region complex (germline)
9787	22438	35845	1.89	9.0E-08	AV734819.1	EST_HUMAN	h51106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080193 3'
11136	23804	37082	1.71	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cBABFB08 5'
11688	24263	37687	2.8	9.0E-08	AL163301.2	NT	wn30407.x1 NCI_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
12168	24648		4.44	9.0E-08	AJ251973.1	NT	OFR repetitive element
563	15548		3.7	8.0E-08	AB11352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1028	13788		0.72	8.0E-08	BE705469.1	EST_HUMAN	Homo sapiens partial cleist-2 gene
3532	16288		1.53	8.0E-08	BE705469.1	EST_HUMAN	hcd16305.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
							3071580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
							601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8838	21330	34474	3.05	8.0E-08	AI752367.1	EST_HUMAN	cn1502.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8838	21330	34475	3.05	8.0E-08	AI752367.1	EST_HUMAN	cn1502.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9527	21330	35384	2.93	8.0E-08	AI970683.1	EST_HUMAN	EST1332778 IMAGE resequences, MAGK Homo sapiens cDNA
10461	23107	35338	0.47	8.0E-08	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
11211	23874		2.1	8.0E-08	AF253417.1	NT	Homo sapiens microsomal lipodase hydrolase (EPHX1) gene, complete cds
78	12904	25542	2.86	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1340	14089	26784	13.91	7.0E-08	X04800.1	NT	Rat mRNA for ribosomal protein L31
3563	15318	28685	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)

Page 207 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3593	16318	28996	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	AI835743.1	EST_HUMAN	cong3.P11.A6 conrnm Homo sapiens cDNA 3'
11672	24287	37959	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24979		1.89	7.0E-08	AJ131018.1	NT	Homo sapiens SCL gene locus
798	13570	26230	2.88	6.0E-08	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C00-48
798	13570	26231	2.88	6.0E-08	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C00-48
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0168-181194-004-g09 HT0168 Homo sapiens cDNA
3058	15824	28469	0.81	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	10963	25998	0.98	6.0E-08	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C00-48
7651	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21908		0.56	6.0E-08	AA827075.1	EST_HUMAN	ob56635.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element;
11391	29897	37299	2.24	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE
11520	24120		1.33	6.0E-08	AL163209-2	NT	Homo sapiens chromosome 21 segment HS21C00-9
83	12809	25847	3.72	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2229	14957	27697	1.82	5.0E-08	AA463851.1	EST_HUMAN	h030309.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
11814	24477		8.36	5.0E-08	P06581	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12099	24590	31065	2.64	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-at2 CT0225 Homo sapiens cDNA
1754	14496	27165	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-TOID PROTEIN PRECURSOR
1754	14496	27166	0.97	4.0E-08	P23723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-TOID PROTEIN PRECURSOR
2888	15593		1.09	4.0E-08	AL079591.1	EST_HUMAN	DKFZ434J0428_r1 t34 (synonym: h3a3) Homo sapiens cDNA clone DKFZ434J0428 5'
3894	16644	28284	1.04	4.0E-08	U82695.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
8311	19082	32067	1.08	4.0E-08	P62624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8697	21369	34533	0.63	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEINASE, SERINE 2
9037	21727	34681	1.05	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9545	22188		0.71	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		0.68	4.0E-08	AI016342.1	EST_HUMAN	ar78d12.at Soares, Itoai, Teius, Nb2Hf9_gw Homo sapiens cDNA clone IMAGE:1622903 3'
10284	22932		3.87	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x7 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;

Page 208 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11009	23681	36839	1.71	4.0E-08	AA393627.1	EST_HUMAN	276808.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
							G505579 NA/Ca_K-EXCHANGER ;
11009	23681	36840	1.71	4.0E-08	AA393627.1	EST_HUMAN	276808.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11031	23702	36899	4.02	4.0E-08	BF692463.1	EST_HUMAN	832248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
11031	23702	36970	4.02	4.0E-08	BF692463.1	EST_HUMAN	832248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
							zsf5503.r1 Soares, fetal_hear_NIH-H19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element ;
11919	25334		4.31	4.0E-08	W76159.1	EST_HUMAN	164511.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
12549	24887		2.18	4.0E-08	A343353.1	EST_HUMAN	167940.YT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z188 Q9Z158
8523	18321	31222	2.22	3.0E-08	BE018348.1	EST_HUMAN	SYNTAXIN 17 ;
8879	17955	30552	4.24	3.0E-08	A1792737.1	EST_HUMAN	gs7611.y6 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1644045 5'
7439	20116	33205	1.66	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7649	20313		3.59	3.0E-08	AI458352.1	EST_HUMAN	166309.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
9789	22449		0.92	3.0E-08	AF055065.1	NT	Homo sapiens MHC class I region
10848	23526	36877	1.32	3.0E-08	AI218001.1	EST_HUMAN	gh21a04.x1 Soares_NFL_T_GBG_S1 Homo sapiens cDNA clone IMAGE:1846204 3'
11566	24165	37477	61.58	3.0E-08	R66279.1	EST_HUMAN	yp12h10.x1 Soares breast 3NH/Bst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);
11566	24165	37478	61.58	3.0E-08	R66279.1	EST_HUMAN	yp12h10.st Soares breast 3NH/Bst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);
11858	24459		2.27	3.0E-08	R16420.1	EST_HUMAN	yp2104.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Aliu repetitive element;
201	13014		9.03	2.0E-08	AW302906.1	EST_HUMAN	x87606.x1 NCI_CGAP_Luz8 Homo sapiens cDNA clone IMAGE:2787135 3'
221	13033		9.14	2.0E-08	AA425998.1	EST_HUMAN	zw4807.r1 Soares_fetal_tetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Aliu repetitive element/contains element MER15 repetitive element ;
484	13269	25905	1.01	2.0E-08	AF158349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
645	13424	26062	13.82	2.0E-08	AW86638.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
645	13424	26063	13.82	2.0E-08	AW86638.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
969	13735		24.4	2.0E-08	BE280477.1	EST_HUMAN	801155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138863 5'
1320	14069	26743	2.38	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1734	14476		12.18	2.0E-08	BE734871.1	EST_HUMAN	80157043F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:39845198 5'

Page 209 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14585		4.11	2.0E-08	AW270271.1	EST_HUMAN	xc43f11.x1 NCL CGAP_FHN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2545	15280		1.71	2.0E-08	K00216.1	NT	Sheep His-UbA-GUG
3202	15985	28618	7.84	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15985	28619	7.84	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16501		1.76	2.0E-08	AW613620.1	EST_HUMAN	RC3-ST0197-161098-012-003 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA459040.1	EST_HUMAN	aa2607.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814580 5' similar to contains L1, L2 L1 repetitive element;
4903	17630		2.36	2.0E-08	AW572881.1	EST_HUMAN	het17h08.x2 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains A1u repetitive element;
5549	18346	31255	1.19	2.0E-08	AA813204.1	EST_HUMAN	al60H11.x1 Soares, testis, NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.83	2.0E-08	AW08624.1	EST_HUMAN	xd3204.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.53 MER18 MER18 repetitive element;
7603	20508	33728	0.92	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8009	20704	33832	1.35	2.0E-08	AA490121.1	EST_HUMAN	es02p06.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:939674 3'
8983	21073		0.9	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23002	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	y17202.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12184	24666	36282	0.78	2.0E-08	N78097.1	EST_HUMAN	y17202.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
1469	15571	25931	1.16	1.0E-08	P31722	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
1768	14570	27211	1.43	1.0E-08	AF125348.1	NT	POL POLYPROTEIN[CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2044	14777		2.31	1.0E-08	BE141656.1	EST_HUMAN	Homo sapiens cavallin 1(CAV1) gene, exon 3 and partial cds
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	PM2-HT0190-100999-001-412-HT0130 Homo sapiens cDNA
7668	20332	33443	1.26	1.0E-08	P19474	SWISSPROT	Homo sapiens hyperion gene, exon 1-50
7834	20829	33756	0.52	1.0E-08	AL163022.2	NT	S2 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RQ(SS-A))
8028	20723	33855	0.64	1.0E-08	AF224699.1	NT	Homo sapiens chromosome 21 segment HS21C102
8028	20723	33856	0.64	1.0E-08	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21137	34275	1.94	1.0E-08	AU15304.1	EST_HUMAN	(UBE2D3) genes, complete cds
9104	21762		0.46	1.0E-08	P09563	SWISSPROT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9105	21763	34956	0.78	1.0E-08	BE072572.1	EST_HUMAN	SANTAGON PROTEIN PRECURSOR
							PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA

Page 210 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8966	22516	35712		1.0E-08	P78110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10453	23058	36330	0.77	1.0E-08	P68063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1
11265	23946	37241	4.14	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12282	24715		2.82	1.0E-08	X51735.1	NT	Homo sapiens immunoglobulin constant region complex (germline)
4278	16858	29583	4.65	9.0E-09	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
4278	16858	26594	4.65	9.0E-09	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
9692	22610		0.52	8.0E-09	T67950.1	EST_HUMAN	y88a12.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:121918.3
6390	19159		0.62	8.0E-09	A270615.1	EST_HUMAN	qu86a11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1976964.3 similar to contains L1.13 L1 repetitive element;
7164	19851	32620	7.66	8.0E-09	A183500.1	EST_HUMAN	gd2607.x1 Soares_fetal_heart_NH-H1GW Homo sapiens cDNA clone IMAGE:1732164.3 similar to contains MSR1.11 MSR1 repetitive element;
7699	20594	33728	2.65	8.0E-09	AW600159.1	EST_HUMAN	CX0-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
8887	21578		2.65	8.0E-09	AA938892.1	EST_HUMAN	cp74008.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575.3
3593	16346		1.79	7.0E-09	D68842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7602	20497		0.81	7.0E-09	BF108755.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443.3 similar to contains MER29.b2 MER29 repetitive element;
7046	20841		0.82	7.0E-09	AA256200.1	EST_HUMAN	zr60c05.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:881992.5 similar to contains L1.12 L1 repetitive element;
8159	21929	34993	2.91	7.0E-09	L05709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10093	22731	36948	1.42	7.0E-09	BE254850.1	EST_HUMAN	50111173.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834.5
10244	22892		0.5	7.0E-09	AA059026.1	EST_HUMAN	z55e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381159.3 similar to contains L1.12 L1 repetitive element;
10571	23268		1.49	7.0E-09	T07950.1	EST_HUMAN	y88a12.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:121918.3
2149	14879		0.69	6.0E-09	AL040439.1	EST_HUMAN	DKF2p43C0514.t1 434 (synonym: Ites3) Homo sapiens cDNA clone DKF2p43C0514.5
4922	17650	30263	3.12	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT05927-160200-001-H05 HT05927 Homo sapiens cDNA
5296	18101	30760	11.59	6.0E-09	AW195784.1	EST_HUMAN	y88a12.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311.3
8475	21167	34311	0.93	6.0E-09	BE161663.1	EST_HUMAN	MR3-HT0446-260300-01-H12 HT0446 Homo sapiens cDNA
9074	21703	34925	1.95	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echinodermic, thanatophoric dwarfism) (FGFR3) mRNA
10176	22824		3.76	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443.3 similar to contains MER29.b2 MER29 repetitive element;

Page 211 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11768	24386	37722	1.37	6.0E-09	CQ1803.1	EST_HUMAN	HUMIGS003762 Human adult (K.Ouibo) Homo sapiens cDNA
1394	14141	28818	3.27	5.0E-09	BE149264.1	EST_HUMAN	RC2-H270252-120200-014-H10 HTD252 Homo sapiens cDNA
1845	14583	27208	1.08	5.0E-09	AL163284.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
6316	19087	32071	1.73	5.0E-09	AA369454.1	EST_HUMAN	EST8746 Fetal lung L1 Homo sapiens cDNA 5' end
							Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV2S1P, TCRBV2S1A2N1T, TCRBV5A11T, TCRBV7S1A1N2T, TCRBV4S1A1T, TCRBV13S3, TCRBV6S3P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A3P1, TCRBV7S2A1N4T, TCRBV13S3P13S>
6748	17917	30581	0.76	5.0E-09	U66058.1	NT	
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
9895	22843	35855	2.22	5.0E-09	AW70667.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
508	13292		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
944	13710		2.5	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1463	14200	26884	2.82	4.0E-09	P558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2016	14761	27478	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2018	14761	27480	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2450	16151	27855	6.07	4.0E-09	AA350978.1	EST_HUMAN	EST183955 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
7746	20442	33555	0.59	4.0E-09	AA485747.1	EST_HUMAN	zxc0c08.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:769288 5'
8420	21113	34250	0.62	4.0E-09	T64942.1	EST_HUMAN	yf11407.at Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66804 3'
10776	23462	36704	2.08	4.0E-09	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
11011	25863	36943	1.47	4.0E-09	A1896401.1	EST_HUMAN	wms4f10.x1 NCL CGAP_LU2 Homo sapiens cDNA clone IMAGE:2443827 3'
11061	25731		1.53	4.0E-09	AA195142.1	EST_HUMAN	z3442.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2351	15073	27810	4.77	3.0E-09	BE222239.1	EST_HUMAN	h09060.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2557	18271	28008	1.2	3.0E-09	BE222239.1	EST_HUMAN	h09060.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2956	15366	28104	1.13	3.0E-09	P22249	SWISSPROT	PROTEIN MOY-10
3323	16038	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	h09060.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
3371	15130		1.08	3.0E-09	AA442272.1	EST_HUMAN	z3544d.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4076	16820		0.7	3.0E-09	X16674.1	NT	H sapiens PADPR2-1 gene for NAD(+) ADP-ribosyltransferase
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4476	17211	29839	1.65	3.0E-09	Q973P5	SWISSPROT	256.1 KDA PROTEIN C21ORF6 (KIAA0933)

Page 212 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7600	20495	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h0602.21 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR-O55091
10147	22795	36009	1.7	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN. ; Homo sapiens chromosome 21 segment HS21C047
10945	23624	36873	4.8	3.0E-09	BF109943.1	EST_HUMAN	717208.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3627030 3'
10945	23624	36874	4.8	3.0E-09	BF109943.1	EST_HUMAN	717208.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3627030 3'
794	13568		2.43	2.0E-09	X16874.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1235	13994	26653	7.89	2.0E-09	AL165284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1655	14401		7.46	2.0E-09	AL118573.1	EST_HUMAN	DKF7p781B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF7p781B1710 5'
2326	15051	27787	1.1	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3016	16656	29308	3.01	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5076	17795	30411	0.85	2.0E-09	M23161.1	EST_HUMAN	Human transcription-like element mRNA
5633	18428	31341	0.55	2.0E-09	AI004082.1	EST_HUMAN	pk47509.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6036	18838		0.57	2.0E-09	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6682	19598		0.83	2.0E-09	AA357407.1	EST_HUMAN	EST168142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	z63h06.11 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:795187 5' similar to contains Alu repetitive element
7423	20100	33188	0.68	2.0E-09	W28834.1	EST_HUMAN	52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7717	20381	33494	0.62	2.0E-09	AW682126.1	EST_HUMAN	NR1-CT0352-240200-105-b06 CT0352 Homo sapiens cDNA
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11233	23668	37183	1.62	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12428	13568		22.07	2.0E-09	X16874.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12495	25403		2.41	2.0E-09	AA228070.1	EST_HUMAN	nc11602.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
12634	24834		1.75	2.0E-09	U82688.1	NT	Homo sapiens allox gene, alternatively spliced products, complete cds
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	z176003.61 Soares_fetal_heart_NHH16W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1087	13845	26503	2.01	1.0E-09	5031624	NT	g5102932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	13845	26504	2.01	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17	1.0E-09	AJ229041.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2892	15659	26304	1.59	1.0E-09	U80047.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2926	15602	26336	3.25	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nab) and survival motor neuron protein (smn) genes, complete cds
2926	15602	26337	3.25	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3034	15800	28446	0.7	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
							801058092F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'

Page 213 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476			6.4	1.0E-09 AA719297.1	EST_HUMAN	2135003.x1 Soares_pituit_gland_N8HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5416	18216	30923	0.66	1.0E-09 AL163283.2	NT	EST_HUMAN	Alu repetitive element contains element MER22 repetitive element ;
6740	18532	31466	1.89	1.0E-09 U07000.1	NT	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
6853	18833	31785	3.13	1.0E-09 P26894	NT	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8289	20983	34124	0.85	1.0E-09 A1688474.1	EST_HUMAN	EST_HUMAN	CIRCUJMSPOROZOITE PROTEIN PRECURSOR (CS)
10212	22960		2.92	1.0E-09 AL163283.2	NT	EST_HUMAN	wd59055.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
11789	24359		1.09	1.0E-09 AL163283.2	NT	EST_HUMAN	MER25.11 MER25 repetitive element ;
12333	25344	30717	2.25	1.0E-09 11418127	NT	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
12503	24857		1.35	1.0E-09 T83176.1	EST_HUMAN	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1288	14038	26707	3.74	9.0E-10 AW887740.1	EST_HUMAN	EST_HUMAN	2c24c05.r1 Strabagene lung (8837210) Homo sapiens cDNA clone IMAGE:118688 5'
2038	15508	28258	4.41	9.0E-10 A1870071.1	EST_HUMAN	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
6735	18668	32601	4.76	9.0E-10 A4452682.1	EST_HUMAN	EST_HUMAN	we78n03.x1 Soares_Dieckgraeft colon_NHCD Homo sapiens cDNA clone IMAGE:2347293 3' similar to
142	12957	25589	13.27	8.0E-10 U63630.2	NT	EST_HUMAN	SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element ;
3337	19097	28748	0.88	8.0E-10 BE080748.1	EST_HUMAN	EST_HUMAN	TR-003372 000372 PUTATIVE P150. ;
4177	18917	29544	3.17	8.0E-10 AA376832.1	EST_HUMAN	EST_HUMAN	QV1-BT0031-1150200-071-01 BT0031 Homo sapiens cDNA
9855	22515		2.44	8.0E-10 U36308.2	NT	EST_HUMAN	EST18666A Small intestine I Homo sapiens cDNA 5' end
685	13460	28107	9.36	7.0E-10 7706226	NT	EST_HUMAN	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
685	13460	28108	9.36	7.0E-10 7706226	NT	EST_HUMAN	Homo sapiens TPA inducible protein (LOC51686), mRNA
1618	14365	27055	2.24	7.0E-10 Q13342	SWISSPROT	SWISSPROT	Homo sapiens TPA inducible protein (LOC51686), mRNA
2013	14748		3.17	7.0E-10 P08548	SWISSPROT	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2564	15278		24.23	7.0E-10 P08547	SWISSPROT	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3092	18590	28481	2.19	7.0E-10 X00856.1	NT	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6092	18398	31838	4.19	7.0E-10 AA345220.1	EST_HUMAN	EST_HUMAN	H. sapiens DHFR gene, exon 3
7316	19999	33078	1.08	7.0E-10 BF352883.1	EST_HUMAN	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7568	20226		1.48	7.0E-10 P36084	SWISSPROT	SWISSPROT	IL3-HT0819-110700-209-D12 HT0819 Homo sapiens cDNA
7875	20570	33688	1.9	7.0E-10 AF029701.2	NT	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7875	20570	33687	1.8	7.0E-10 AF029701.2	NT	EST_HUMAN	Homo sapiens preactin-1 gene, exons 1 and 2
10208	22657	36073	1.67	7.0E-10 L08895.1	NT	EST_HUMAN	Homo sapiens preactin-1 gene, exons 1 and 2
							Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds

Page 214 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8693	13662	28327	3.5	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2684	15303	28132	1.21	6.0E-10	AI424405.1	EST_HUMAN	102d07.x1 NC1 CGAP Pr28 Homo sapiens cDNA clone IMAGE:2065021.3'
4680	17423		2.7	6.0E-10	AW853718.1	EST_HUMAN	RC3-C10254C31089-012-g12 C10254 Homo sapiens cDNA
8682	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8682	21374	34519	1	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD68E)
9534	22187	36373	0.46	6.0E-10	P38073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
11950	24503		2.18	6.0E-10	AW971623.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD68E)
745	13518		7.27	6.0E-10	AL046804.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
3459	16224	28878	2.5	6.0E-10	Q01033	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD68E)
4931	17659	30269	1	6.0E-10	AF181887.1	NT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
7222	18907		1.51	5.0E-10	AF181887.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
8436	22114	35283	1.89	5.0E-10	BF105159.1	SWISSPROT	ESTERASE 12 (MAGE RESIDUES), MAGE1 Homo sapiens cDNA
8436	22114	36269	1.89	5.0E-10	P34678	SWISSPROT	DKFZp434N219.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219.5'
109	12930		1.17	4.0E-10	AL221083.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
597	13348	25976	0.74	4.0E-10	AA516260.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
1989	14725	27446	1.31	4.0E-10	AW594708.1	EST_HUMAN	80182218AFT NIH LMGCC 75 Homo sapiens cDNA clone IMAGE:404243.3'
2580	15294	28032	3.73	4.0E-10	AL163303.2	NT	HYPOTHETICAL 87.9 KD PROTEIN ZX688.8 IN CHROMOSOME III
7076	17167	32831	25.71	4.0E-10	AF224669.1	NT	HYPOTHETICAL 87.9 KD PROTEIN ZX688.8 IN CHROMOSOME III
10095	18743	35857	0.49	4.0E-10	AW283243.1	EST_HUMAN	gg0809.x1 Soares, placenta, 8105week, 2N8H-HP809W Homo sapiens cDNA clone IMAGE:1756049.3'
10343	22960	36208	0.89	4.0E-10	AI287342.1	EST_HUMAN	similar to contains LTRb.b2 LTR8 repetitive element
895	13693	26329	3.65	3.0E-10	N38113.1	EST_HUMAN	repetitive element
1329	14078		4.72	3.0E-10	AY005150.1	NT	repetitive element
4498	17234	28864	1.04	3.0E-10	AL163203.2	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4498	17234	29895	1.04	3.0E-10	AL163203.2	NT	(UBE2D3) genes, complete cds
5398	18169	30855	1.24	3.0E-10	N60106.1	EST_HUMAN	UHH-BIP-ah-a-07-Q-01.x1 NC1 CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727081.3'
6110	18897	31859	2.52	3.0E-10	P20350	SWISSPROT	eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
8258	18032	32007	3.43	3.0E-10	BE302970.1	EST_HUMAN	yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element
							Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003
							eq3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
							yg2709.s1 Soares, melanocyte 2N8HIM Homo sapiens cDNA clone IMAGE:272683.3' similar to contains L1.11 L1 repetitive element

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8629	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	Y974812 at Soares retina N264HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element
8647	21638	34784	1.58	3.0E-10	AW650731.1	EST_HUMAN	IL3-GT0218-160220-054-508 CT0219 Homo sapiens cDNA
8647	21638	34785	1.58	3.0E-10	AW650731.1	EST_HUMAN	IL3-GT0218-160220-054-508 CT0219 Homo sapiens cDNA
9240	21919		0.59	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10359	23006	23006	2.37	3.0E-10	T65891.1	EST_HUMAN	Y11012.11 Stragene lung (8637210) Homo sapiens cDNA clone IMAGE:80398 5'
10468	23139		1.34	3.0E-10	AA769294.1	EST_HUMAN	nc26603.61 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12984	24607	31003	2.65	3.0E-10	BE179517.1	EST_HUMAN	IL3-H10018-110500-136-507 HT0618 Homo sapiens cDNA
34	12862	25479	1.87	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12862	25480	1.87	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14627		1.96	2.0E-10	U80047.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
2086	15761		1.04	2.0E-10	BF676047.1	EST_HUMAN	602186640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5714	18507		2.54	2.0E-10	Q28640	SWISSPROT	(HPRG)
6156	18933	31900	1.37	2.0E-10	AF260107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	19693	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	607586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7612	20607	33737	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7612	20607	33738	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434585.1	EST_HUMAN	707808.X1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642203 3' similar to contains L1.19 L1 repetitive element 1
11297	23998		1.37	2.0E-10	AI892183.1	EST_HUMAN	lat0112.X1 Soares total testis Nb2HF6_gw Homo sapiens cDNA clone IMAGE:2043695 3'
1498	14245		1.87	1.0E-10	AW667767.1	EST_HUMAN	MFO-SN0035-290300-001-101 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2586	15300		3.16	1.0E-10	AW862001.1	EST_HUMAN	QV0-Q10225-181189-058-e08 CT0225 Homo sapiens cDNA
3481	16247	25801	0.89	1.0E-10	AW862291.1	EST_HUMAN	QV2-Q10003-181189-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.71	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3896	18744		6.19	1.0E-10	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Page 216 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4108	18851	28477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	18851	28478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4113	18856	28484	1.94	1.0E-10	AB031069.1	NT	Homo sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	18891		1.84	1.0E-10	M30623.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	AF07745.1	EST_HUMAN	W882104.x1 Soares, NFL, I, GRC, S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
9720	18935	32678	0.66	1.0E-10	AF083528.1	NT	Homo sapiens X-linked aniridic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7376	20055		0.85	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7683	20251	33357	0.59	1.0E-10	AI128584.1	EST_HUMAN	AI128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138	20632	33868	1.04	1.0E-10	AY408950.1	EST_HUMAN	FB_644 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	AI288340.1	EST_HUMAN	q10461.0.x1 NC1_COAP_Luc Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1, L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23405.t1 Stratiogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	35754	2.65	1.0E-10	AA038280.1	EST_HUMAN	y655103.x1 Soares, fetal, liver, spleen, LNFLS, S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11896	17913		1.71	1.0E-10	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING6, 9, 13 and 14 genes
255	13093	25702	1.59	9.0E-11	BE145600.1	EST_HUMAN	IL2-H10203-281099-018-C58 HT0203 Homo sapiens cDNA
2097	14828	27651	6.12	9.0E-11	AI134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	14828	27652	6.12	9.0E-11	AI134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28795	2.45	9.0E-11	AI134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796	2.45	9.0E-11	AI134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4465	17201	29827	1.03	9.0E-11	AA177585.1	EST_HUMAN	at7801.at1 Stratiogene scizto brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5487	18236		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-071-E06 BT0627 Homo sapiens cDNA
10054	22702	35919	1.19	9.0E-11	AA324600.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19	9.0E-11	AA324600.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16693.1	EST_HUMAN	C16693 Clontech human aorta polyA+ mRNA (H8572) Homo sapiens cDNA clone GEN-506908 5'
3114	15879		8.33	8.0E-11	HI16971.1	EST_HUMAN	y183111.at1 Soares adult brain N255HB557 Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;

Page 217 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3945	16695	28334	0.7	8.0E-11	A478617.1	EST_HUMAN	Bm54009.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4022	16768	28398	4.88	8.0E-11	N23712.1	EST_HUMAN	YW46968.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:295298 3'
6874	15338		0.85	8.0E-11	AW166188.1	EST_HUMAN	X49111.x1 NCL_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621081 3' similar to contains MER10.11 MER10 repetitive element.
1430	14177	26882	1.75	7.0E-11	AA330042.1	EST_HUMAN	EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
3852	16802	28240	1.03	7.0E-11	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8396	21059	34224	2.06	7.0E-11	AF163694.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22777		1.17	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE); ENDONUCLEASE
403	13188	25837	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
403	13188	26838	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6622	19384	32398	0.67	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7593	20291	33369	3.65	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8282	20958	34095	7.81	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCAS008 5'
8213	21892	36058	0.62	6.0E-11	BE063609.1	EST_HUMAN	GM0-810281-031196-087-403 B10281 Homo sapiens cDNA
11	12938	25451	1.49	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3359	12938	25451	1.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4203	16944	26571	1.36	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
8423	19191	32187	1.63	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7430	20107	33194	14.06	6.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1380	14127		1.94	4.0E-11	AA438042.1	EST_HUMAN	2a01512.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:730659 5'
2793	15498	28239	7.14	4.0E-11	BE885900.1	EST_HUMAN	901507331F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
2969	15735	28385	1.16	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4576	17311	28939	0.85	4.0E-11	DA4686.1	EST_HUMAN	HUMSUP1069 Human brain cDNA Homo sapiens cDNA clone 069
6364	16153	32153	3.2	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2 248970.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4.1
6903	19641	32886	0.82	4.0E-11	AA442630.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7274	19958		4.5	4.0E-11	AF224699.1	NT	(UBE2D3) genes, complete cds
9295	21992		1.79	4.0E-11	BE149423.1	EST_HUMAN	RC1-1T0256-2100-013-008 HT0256 Homo sapiens cDNA
9592	22215	35402	0.9	4.0E-11	AI009753.1	EST_HUMAN	982912.x1 NCL_CGAP_Bm29 Homo sapiens cDNA clone IMAGE:2105930 3' similar to WIP-ZK353.1 CE00385.1

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12482	24830	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH-3 domain binding protein 1 (SH3BP1), mRNA
1475	14222	26808	2.8	3.0E-11	6879077	EST	Mus musculus expressed in non-neuronal cells 2, protein (NM23B) (Nm2), mRNA
4243	16584		1.04	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	AH150502.1	EST_HUMAN	q33604.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.B
1162	13916	26880	3.99	2.0E-11	R24807.1	EST_HUMAN	yg34612.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:35144 5'
1162	13916	26881	3.89	2.0E-11	R24807.1	EST_HUMAN	yg34612.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:35144 5'
1808	14354	27042	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1808	14354	27043	4.86	2.0E-11	L17432.1	NT	COR3 beta (COR3 beta) genes, complete cds
1612	14359	27048	1.21	2.0E-11	AH26371.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
3101	15944	28607	7.58	2.0E-11	P10283	SWISSPROT	gp-L02892 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN) contains L1.11
3320	16080	28730	1.11	2.0E-11	AH78617.1	EST_HUMAN	L1 repetitive element:
						SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3356	18116	28771	0.83	2.0E-11	Q10473	SWISSPROT	IMP4606.x1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2161888 3'
							POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
							ACETYLGLACTOSAMINYLTRANSFERASE) [GALNAc-T1]
3488	18244		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4409	17146		0.69	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT10316-170200-014-e05 BT10316 Homo sapiens cDNA
4587	17302		0.72	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4882	17609		1.77	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT10258-281058-014-e01 BT10258 Homo sapiens cDNA
8044	18824	31785	1.02	2.0E-11	AW817808.1	EST_HUMAN	QV2-PT0073-280300-108-h08 PT0073 Homo sapiens cDNA
8218	18992	31968	1.87	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:767433 5' similar to SW/PR16_YEAST
7095	18784	32850	0.59	2.0E-11	BF592845.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	7/87603.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9123	21811		1.14	2.0E-11	AF020308.1	NT	Homo sapiens chromosome 8 duplication of the T cell receptor beta locus and tyrosinogen gene families
10184	22832	38046	5.44	2.0E-11	Q13806	SWISSPROT	OLFACTORY RECEPTOR 8T (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10413	23059	36277	1.12	2.0E-11	AW885974.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10413	23059	36278	1.12	2.0E-11	AW885974.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA

Page 219 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726	36997	1.48	2.0E-11	AA035369.1	EST_HUMAN	242702.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:471794 3'
11056	23728	36998	1.48	2.0E-11	AA035369.1	EST_HUMAN	242702.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:471794 3'
11090	23760	37035	1.57	2.0E-11	AA261956.1	EST_HUMAN	231804.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685619 5'
12017	26332		1.64	2.0E-11	AA704195.1	EST_HUMAN	277603.s1 Soares_fetal_liver_spleen_1NF.S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048	24567		3.54	2.0E-11	AW642143.1	EST_HUMAN	BC9-CN0027-210100-11-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377859.1	EST_HUMAN	GM2-TN0740-070900-372-g01 TN0740 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D28217.2	NT	Human spleen mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417668	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
681	13437	26078	1.34	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1195	13947	26811	3.35	1.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
1485	14232		2.36	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14765	27494	1.13	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14953	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
3460	16246	28500	1.2	1.0E-11	BE004315.1	EST_HUMAN	CM0-EN0105-170300-282-412 EN0105 Homo sapiens cDNA
5249	18055	30583	16.63	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18533	31456	0.63	1.0E-11	BF222640.1	EST_HUMAN	7p57401.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8101	20765	33026	3.16	1.0E-11	4885548	NT	MER10 repetitive element 1
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8948	21637	34782	1.89	1.0E-11	BF365118.1	EST_HUMAN	Q73408.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11257	23919	37212	1.62	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
8697	22348	35542	1.07	9.0E-12	AL163300.2	NT	602154807.F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4285977 5'
8697	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6237	21916		0.93	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12126	24517		3.91	8.0E-12	AJ271736.1	NT	IL6-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4613	17348	29982	1.16	7.0E-12	Q05604	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 2/2
11322	24013	37316	8.69	7.0E-12	AA704736.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3555	16291		0.71	6.0E-12	AV730554.1	EST_HUMAN	2323d01.s1 Soares_fetal_liver_spleen_1NF.S1 Homo sapiens cDNA clone IMAGE:45152 3'
4314	17053	29678	8.62	6.0E-12	AA732616.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW700 5'
6295	18068	32051	0.77	6.0E-12	AF020503.1	NT	m28811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21585	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
8374	21949		1.87	6.0E-12	AA847898.1	EST_HUMAN	cd10611.1 at NCL_GGAP CGOB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12 MER29 repetitive element;
1020	13780	28442	3.52	6.0E-12	T06573.1	EST_HUMAN	EST104462 Fetal brain, Stratagene (cat#33209) Homo sapiens cDNA clone HFBDV33
3395	16144	28801	1.61	5.0E-12	BE047778.1	EST_HUMAN	124205.y1 NCL_GGAP Bm52 Homo sapiens cDNA clone IMAGE:2281217 5'
3713	16466	28104	5.03	5.0E-12	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5931	18715	31871	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5931	18715	31872	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	19198	32167	11.33	5.0E-12	AW974760.1	EST_HUMAN	EST398950 IMAGE sequences, MAGN Homo sapiens cDNA
6933	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	DKF2p434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKF2p434B1615 3'
6942	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKF2p434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKF2p434B1615 3'
8128	20822	33959	1.33	5.0E-12	AA03745.1	EST_HUMAN	201912.st Scores_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.43 L1 repetitive element;
8556	21259		0.65	5.0E-12	AW867037.1	EST_HUMAN	RC1-OT0095-220300-011-007 OT0095 Homo sapiens cDNA
8893	21584		0.54	5.0E-12	AL079681.1	EST_HUMAN	DKF2p434J0428_t1 434 (synonym: hies3) Homo sapiens cDNA clone DKF2p434J0428 5'
9008	21688	34847	2.93	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9323	21990	35161	0.96	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR, TD2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGNP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10175	22823		4.45	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10282	22910	36120	0.76	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10468	23114	36344	0.44	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog (Dcc), mRNA 374911.st Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
237	13047	25688	4.2	4.0E-12	AA700326.1	EST_HUMAN	374911.st Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
238	13047	25688	4.03	4.0E-12	AA700326.1	EST_HUMAN	322805.x1 NCL_GGAP L024 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRQ13539 Q13539 MARINER TRANSPOSASE.;
4577	17312	28940	0.6	4.0E-12	A1689984.1	EST_HUMAN	nc021603.x1 NCL_GGAP L024 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MERY repetitive element;
7619	20180		0.72	4.0E-12	BF446140.1	EST_HUMAN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8141	20835		3.2	4.0E-12	AF109907.1	NT	Bos taurus Mib2 mRNA for mitochondrial carrier homolog 2, complete cds
8587	21270	34418	0.87	4.0E-12	AB042815.1	NT	Homo sapiens 999 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
11019	23691	36954	4.2	4.0E-12	AJ229043.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12376	24774		2.76	4.0E-12	U78027.1	NT	

Page 221 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	28011	4.27	3.0E-12	AW341883.1	EST_HUMAN	hfd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2903377 3' similar to TR:O14517
602	13380	28012	4.27	3.0E-12	AW341883.1	EST_HUMAN	hfd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2903377 3' similar to TR:O14517
5084	17603	30421	0.81	3.0E-12	AL163288.2	NT	O14517 SWRP. ;
5358	18167	30683	1.52	3.0E-12	AF111168.2	NT	Homo sapiens chromosome 21 segment HS21C088
7694	20318		0.63	3.0E-12	AW64328.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8273	20697	34109	0.51	3.0E-12	O35453	SWISSPROT	RC3-CT0235-031059-011-H02 CT02355 Homo sapiens cDNA
9004	21694	34844	0.52	3.0E-12	O35463	SWISSPROT	SERINE PROTEASE HEPSIN
10551	23247	36483	3.03	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSIN
10551	23247	36484	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1849	14395	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
4084	16838	29462	0.91	2.0E-12	J01894.1	NT	IL5-UM0071-120400-065-403 UM0071 Homo sapiens cDNA
4084	16838	29463	0.91	2.0E-12	J01894.1	NT	Rat U3a small nuclear RNA
4387	17124		2.03	2.0E-12	J01894.1	NT	Rat U3a small nuclear RNA
4840	17570	30192	1.18	2.0E-12	BE063509.1	EST_HUMAN	CNC-B10281-031189-087-403 B10281 Homo sapiens cDNA
4840	17570	30193	1.18	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5159	17978	30491	0.77	2.0E-12	P11369	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
8395	19154		2.9	2.0E-12	AW1971857.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
7075	19788	32830	3.74	2.0E-12	T08180.1	EST_HUMAN	ENDONUCLEASE]
7244	19929	33005	1.02	2.0E-12	BE173035.1	EST_HUMAN	EST183948 WAGE resequences, MAGL Homo sapiens cDNA
7558	20228	33331	2.2	2.0E-12	11422229	EST_HUMAN	EST183948 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBBA13 5' end
9208	22037		1.84	2.0E-12	AF108864.1	NT	MRC-H70559-200400-015-408 HT0559 Homo sapiens cDNA
9895	22535		11.12	2.0E-12	BE166960.1	EST_HUMAN	Homo sapiens Ac-like transposable element (ALTE), mRNA
10412	23058	39276	0.87	2.0E-12	A334130.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
12032	24557		2.81	2.0E-12	AL163283.2	NT	MR3-CT0487-160200-113-g01 HT0487 Homo sapiens cDNA
12223	24680		2.5	2.0E-12	11418248	NT	Q13538 ORF2: FUNCTION UNKNOWN. ;
119	12948	25379	2.21	1.0E-12	AW627674.1	EST_HUMAN	q00702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
1890	14716		1.39	1.0E-12	A871726.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
3097	15833	28476	1.29	1.0E-12	AF000091.1	NT	Homo sapiens sulfotransferase-related protein (SULT1X3), mRNA
							hhs00080.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
							W15107.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439483 3' similar to contains L1.83 L1
							repetitive element ;
							Homo sapiens testis-specific Testis Transcript Y2 (TTY2) mRNA, partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3067	16933	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	16905	29242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	16905	29243	28.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5977	16663		2.25	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5980	16732		1.93	1.0E-12	Q972G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIA0961
6438	18209	32202	0.62	1.0E-12	AF29843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
7016	19708	32764	2.07	1.0E-12	AF168964.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							qf66a04.x1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:U18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)/contains MER10.11 MER10 repetitive element;
7050	19741	32802	11.32	1.0E-12	AJ248533.1	EST_HUMAN	qf66a04.x1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:U18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)/contains MER10.11 MER10 repetitive element;
7050	19741	32803	11.32	1.0E-12	AJ248533.1	EST_HUMAN	qf66a04.x1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:U18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)/contains MER10.11 MER10 repetitive element;
8008	21298	34442	1.18	1.0E-12	AA782323.1	EST_HUMAN	ec26d05.t1 Stratiagene ovary (#937217) Homo sapiens cDNA clone IMAGE:2621317 3' similar to contains element LTR3 repetitive element;
11273	23934		1.72	1.0E-12	AW468478.1	EST_HUMAN	he39f07.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2621317 3' similar to contains element LTR3 repetitive element;
11942	24407	37609	4.54	1.0E-12	AW692164.1	EST_HUMAN	EST374237 MAGE sequences, MAGE Homo sapiens cDNA
12150	24637		1.82	1.0E-12	AJ738592.1	EST_HUMAN	w33n08.x1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:2392096 3'
12294	25308		2.92	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3618	16671		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3927	16877	29520	0.96	9.0E-13	AB029900.1	NT	Homo sapiens GST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
8001	22154		2.67	9.0E-13	N69653.1	EST_HUMAN	aa26b06.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:263651 3'
700	13476	28123	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	13476	28124	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1830	14659	27281	2.94	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nab) and survival motor neuron protein (smn) genes, complete cds
8011	20709	33934	0.76	8.0E-13	AJ884396.1	EST_HUMAN	wm31n09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8011	20709	33935	0.76	8.0E-13	AJ884396.1	EST_HUMAN	wm31n09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L-44-like ribosomal protein (L-44L) and F1P3 (F1P3) genes, complete cds
10046	22894		3.08	8.0E-13	U76027.1	NT	(L-44L) and F1P3 (F1P3) genes, complete cds

Page 223 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.87	8.0E-13	U6060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S9A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S9A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
7716	20362	33465	0.71	7.0E-13	AB94398.1	EST_HUMAN	hm31h9.x1 NCL CGAP_UK Homo sapiens cDNA clone IMAGE:2437601.3
7716	20362	33465	0.71	7.0E-13	AB94398.1	EST_HUMAN	hm31h9.x1 NCL CGAP_UK Homo sapiens cDNA clone IMAGE:2437601.3
8193	20827		0.58	7.0E-13	Q05165	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285FT NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866613.5
12817	24923		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
2094	14826	27658	6.76	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3316	16078		0.74	5.0E-13	R78336.1	EST_HUMAN	y8204.r1 Soares Placenta N52HP Homo sapiens cDNA clone IMAGE:145759.5
3392	16151		1.54	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:728350.5 similar to contains Alu repetitive element/contains element MER22 repetitive element;
8777	19521	32548	0.84	5.0E-13	P06983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10767	23461	36593	2.72	6.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1860	14598		2.23	4.0E-13	AW376914.1	EST_HUMAN	FM2-HT0224-221069-001-s11 HT0224 Homo sapiens cDNA
2462	15190		1.67	4.0E-13	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
5409	18207	31195	5.51	4.0E-13	BE169131.1	EST_HUMAN	FM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7105	19793	32958	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7512	20183	33277	0.94	4.0E-13	AA431626.1	EST_HUMAN	z177612.r1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:782182.5 similar to TR-G452763 G452763 COR1 MRNA;
7620	20286		1.07	4.0E-13	N44291.1	EST_HUMAN	Y93305.r1 Soares melanocyte 2NH1M Homo sapiens cDNA clone IMAGE:273080.5 similar to PIR-A32595 A32595.1 complex sterility protein - mouse;
8740	21432	34577	1.07	4.0E-13	AL049810.1	EST_HUMAN	DKF2p343A0128_r1 434 (synonym: Hae3) Homo sapiens cDNA clone DKF2p343A0128.5
9402	22084	35235	0.45	4.0E-13	AA076907.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
9819	22568	35764	4.94	4.0E-13	AI298931.1	EST_HUMAN	g1924005.x1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:189945.3 similar to contains Alu repetitive element;
11120	23789	37058	2.08	4.0E-13	AA435816.1	EST_HUMAN	z177610.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:728514.3
11120	23789	37057	2.09	4.0E-13	AA435816.1	EST_HUMAN	z177610.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:728514.3
175	12987		4.94	3.0E-13	AF009528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
845	13816		1.62	3.0E-13	AA430310.1	EST_HUMAN	z1788g08.r1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:781408.5

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15092	27831	1.26	3.0E-13	AI271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2463	15201		2.47	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2590	15379	28117	2.91	3.0E-13	BF372662.1	EST_HUMAN	CM3-FT100-140700-242-H08 FT100 Homo sapiens cDNA
3182	16945		2.97	3.0E-13	AA745844.1	EST_HUMAN	db18402.at NCL CGAP Kid5 Homo sapiens cDNA clone IMAGE:1324035.3
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	z18810.11 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315.5 similar to contains THR12 THR repetitive element;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	z18810.11 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315.5 similar to contains THR12 THR repetitive element;
5902	18687	31635	0.62	3.0E-13	AW005639.1	EST_HUMAN	w28802.at NCL CGAP Brm25 Homo sapiens cDNA clone IMAGE:2665890.3 similar to TR-O75139
7783	20478	33803	7.67	3.0E-13	U82111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), COM protein (COM), adrenoleukodystrophy protein >
7975	20570	33792	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
7975	20570	33793	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
10098	22746	35951	0.72	3.0E-13	AW695487.1	EST_HUMAN	RO2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10375	23270		3.61	3.0E-13	AI084788.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	35904	3.66	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031186-087-403 BT0281 Homo sapiens cDNA
11593	24197	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
145	12990	26502	3.42	2.0E-13	U82111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), COM protein (COM), adrenoleukodystrophy protein >
232	13043	25983	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1247	13998	26663	7.66	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	28419	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	28420	0.9	2.0E-13	8924118	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	18036	28668	1.13	2.0E-13	BF431696.1	EST_HUMAN	na37605.x1 Scores NS5_F8 SW OT PA P St Homo sapiens cDNA clone IMAGE:3
3498	18254	28908	1.11	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4088	18931		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 225 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	18812	31772	4.7	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.98	2.0E-13	X78477.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6717	16832	32875	7.15	2.0E-13	X16912.1	NT	Human PKL gene for liver-type B-phosphofructokinase (EC 2.7.1.11) exon 2
6954	19439	32461	0.65	2.0E-13	10835072	NT	Human sapiens N-myristoyltransferase 1 (NMT1), mRNA
6954	19438	32462	0.65	2.0E-13	10835072	NT	Human sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	38219	3.87	2.0E-13	5031898	NT	Human sapiens mab-21 (C. elegans)-like 1 (MAB2L1) mRNA
12106	24602		3.48	2.0E-13	AW892155.1	EST_HUMAN	CNO-NN0001-100305-274-st1 NN0001 Homo sapiens cDNA
235	13091	25732	1.52	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
888	13637	28307	5.64	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1313	14081	28739	1.08	1.0E-13	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nm21p02.st1 NCL CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.8
4553	17268	28917	1.64	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element;
7810	20505	33628	0.78	1.0E-13	AA677812.1	EST_HUMAN	602038009F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185666 5'
7810	20505	33627	0.78	1.0E-13	AA677812.1	EST_HUMAN	nm24401.st1 NCL CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
9590	22838		0.79	1.0E-13	O15481	SWISSPROT	repetitive element; contains element MER24 repetitive element;
10189	22847	36053	0.53	1.0E-13	AF300701.1	NT	repetitive element; contains element MER24 repetitive element;
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11824	24482		2.26	1.0E-13	AV716377.1	EST_HUMAN	Mus musculus osteocalcin protein [yocalin phosphatase mRNA, complete cds
12593	24893		2.12	1.0E-13	AJ271735.1	NT	745610.x1 Scores_NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
324	13129	25761	1.81	9.0E-14	AA781150.1	EST_HUMAN	AV716377 DOB Homo sapiens cDNA clone DOBAIE03 6'
325	13126	25762	3.05	9.0E-14	AA781150.1	EST_HUMAN	Homo sapiens Xq pseudocentromeric region, segment 1/2
2054	15221		3.66	9.0E-14	AA786157.1	EST_HUMAN	q24c01.st1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2589	15313	28050	1.18	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-009 CT0322 Homo sapiens cDNA
2589	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15463	28208	2.6	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
3109	15874	28513	3.96	9.0E-14	AW513286.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
							xc4-f405.xt NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'

Page 226 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3232	13125	25761	0.84	9.0E-14	AA781159.1	EST_HUMAN	sl24d0.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
3778	16530	29169	8.85	9.0E-14	D14647.1	NT	repetitive element;
4707	17439	30071	1.98	9.0E-14	AJ002163.1	NT	Human DNA, SINE repetitive element
3489	16245		1.27	8.0E-14	BE66263.1	EST_HUMAN	Saguinus oedipus gene for seminal vesicle secreted protein semiochogelin 1
3937	16597		2.97	8.0E-14	R76269.1	EST_HUMAN	h271cd03.x1 NCL CGAP LU24 Homo sapiens cDNA clone IMAGE:323424 3'
9348	20419	33539	15.04	8.0E-14	X89211.1	NT	h72903.11 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:144798 3'
9460	22010	35180	3.69	8.0E-14	A4218318.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
11410	24069		1.72	8.0E-14	BE002658.1	EST_HUMAN	Z017c10.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:623970 3'
12302	24727	31056	2.48	8.0E-14	AI688118.1	EST_HUMAN	QV2-BT0259-281089-014-01 BT0259 Homo sapiens cDNA clone IMAGE:623970 3'
1625	15574		4.77	7.0E-14	AW151873.1	EST_HUMAN	h67410.x1 NCL CGAP_Gac4 Homo sapiens cDNA clone IMAGE:2238143 3'
8818	21510		10.57	7.0E-14	AL183285.2	NT	MER10 repetitive element;
358	13156	25787				NT	Homo sapiens chromosome 21 segment HS21C085
8722	22373	35572	14.14	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9722	22373	35573	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
604	13362	28014	2.8	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4893	17716	30322	1.41	5.0E-14	AW073761.1	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5449	18245	31133	5.77	5.0E-14	P08547	EST_HUMAN	h03005.x1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1, L2, L3
1101	18560		2.18	4.0E-14	P04928	SWISSPROT	repetitive element;
1870	14608	27319	6.9	4.0E-14	AJ007673.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3735	16488		0.87	4.0E-14	AA046502.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
4259	17000	29530	1.05	4.0E-14	N46328.1	EST_HUMAN	Homo sapiens LGMD2B gene
7858	20553		0.59	4.0E-14	X87344.1	NT	h07008.11 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:497858 5'
12626	25414		7.02	4.0E-14	AI688224.1	EST_HUMAN	h73612.s1 Soares_multiple_sclerosis_ZNBMSP Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1, L8, L1 repetitive element;
930	13697	25361	1.88	3.0E-14	X95468.1	NT	H.sapiens DNA, DIMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, DOB, DOB2 and RIN68, 9, 13 and 14 genes
						EST_HUMAN	h080c03.x1 NCL CGAP_UK Homo sapiens cDNA clone IMAGE:2493332 3' similar to contains Alu repetitive element;
						NT	R.norvegicus mRNA for CPG2 protein

Page 227 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4870	17697	30220	0.82	3.0E-14	AW265354.1	EST_HUMAN	xp-61f2.1x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element/contains element MER9 repetitive element;
4873	17600	30222	0.97	3.0E-14	7659864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6835	18397	32411	1.48	3.0E-14	AL420786.1	EST_HUMAN	1691c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519 FATTY ACID AMIDE HYDROLASE...
6835	16397	32412	1.49	3.0E-14	AL420786.1	EST_HUMAN	1691c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519 FATTY ACID AMIDE HYDROLASE...
6744	25099		0.92	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8888	21378	34822	0.87	3.0E-14	N42165.1	EST_HUMAN	W07b10.1r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270523 5'
10914	23504	36840	1.28	3.0E-14	BE588018.1	EST_HUMAN	601f11503f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11201	17697	30220	7.19	3.0E-14	AW265354.1	EST_HUMAN	xp-61f2.1x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element/contains element MER9 repetitive element;
12539	25282		1.68	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
381	13168	25811	3.71	2.0E-14	AL271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 22
381	13168	25812	3.71	2.0E-14	AL271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 22
674	15548	25091	9.05	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2387	15108		1.49	2.0E-14	AW372888.1	EST_HUMAN	RC8-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2497	15185		2.15	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
2529	15245	27683	1.19	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2542	15258		1.14	2.0E-14	BE222432.1	EST_HUMAN	h60g10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element/contains OFR.11 OFR repetitive element;
2881	16390		0.95	2.0E-14	P08648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5437	18238	30850	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5437	18238	30850	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5533	18331	31238	0.92	2.0E-14	AL131235.1	EST_HUMAN	1678h01.x2 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5834	18429	31342	3.42	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6784	18528		0.91	2.0E-14	BE000650.1	EST_HUMAN	RC8-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
6984	19877	32724	0.82	2.0E-14	4595709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAMT1), mRNA
7195	19871	32945	1.25	2.0E-14	P36163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7407	20084	33167	22.12	2.0E-14	BE189761.1	EST_HUMAN	IL2-HT0397-071298-024-D04 HT0397 Homo sapiens cDNA
7407	20084	33168	22.12	2.0E-14	BE189761.1	EST_HUMAN	IL2-HT0397-071298-024-D04 HT0397 Homo sapiens cDNA
9817	22468		0.67	2.0E-14	AI978795.1	EST_HUMAN	wf69g10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2482034 3' similar to contains Alu repetitive element;
10317	22984	39181	0.53	2.0E-14	AV1741648.1	EST_HUMAN	AV1741648 CB Homo sapiens cDNA clone CBFB3F04 5'

Page 228 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10879	23370	36612	4.88	2.0E-14	AW139800.1	EST_HUMAN	U1H-BF1-ctw-a-(0-0.1).x1 NCL CGAP_S083 Homo sapiens cDNA clone IMAGE:2718234 3'
11691	24190	37507	1.28	2.0E-14	AW083989.1	EST_HUMAN	xc330102.x1 NCL CGAP_C020 Homo sapiens cDNA clone IMAGE:2886363 3' similar to contains MER1.13
12635	26284		2.29	2.0E-14	AF008191.1	NT	MER1 repetitive element
1045	13804	29463	1.98	1.0E-14	AL163248.2	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
1335	14132	28305	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C048
1385	14132	28306	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1984	14730	27452	12.44	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2182	14911	27643	4.55	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2409	15130	27868	3.56	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2946	15711	28393	1.79	1.0E-14	P08227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
3165	15928	28576	6.42	1.0E-14	BF33227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
3165	15928	28577	6.42	1.0E-14	BF33227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
3868	16616	29255	1.97	1.0E-14	AA62954.1	EST_HUMAN	ag89c12.x1 Stralegonne schizo brain S11 Homo sapiens cDNA clone IMAGE:371350 3'
4440	17178	28302	1.91	1.0E-14	AW275852.1	EST_HUMAN	xc38h10.x1 NCL CGAP_L028 Homo sapiens cDNA clone IMAGE:2753059 3'
5719	18511	31432	2.42	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6576	25095	32351	11.5	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6576	25095	32352	11.5	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
11878	15028	28576	3.05	1.0E-14	BF33227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
11878	15028	28577	3.05	1.0E-14	BF33227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
1570	14317	27002	2.06	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA
2170	14899		1.43	9.0E-15	AF166778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
7395	20374	33152	4.51	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7915	20610	33740	1.08	9.0E-15	BE603589.1	EST_HUMAN	601877750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960186 5'
12718	24991		0.91	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2814	13253		2.36	8.0E-15	BE261482.1	EST_HUMAN	501146532F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7081	19771	32536	1.14	7.0E-15	BF03527.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
10334	22991		3.07	7.0E-15	AW241958.1	EST_HUMAN	xc77402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element
973	13738	28403	8.84	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2

Page 229 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
5829	18618	31549	1.02	6.0E-15 X73462.1	NT	O-arif mRNA for hair keratin cysteine-rich protein
5829	18618	31550	1.02	6.0E-15 X73462.1	NT	O-arif mRNA for hair keratin cysteine-rich protein
401	13186	25634	6.63	5.0E-15 AL163208.2	NT	Human sapiens chromosome 21 segment HS21C008
2764	15469	26212	1.38	5.0E-15 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rfret gene, and sodium phosphate transporter (NPT3) gene, complete cds
3481	16217		1.03	5.0E-15 AW268817.1	EST_HUMAN	UI-H-BW-01-g10-Q11 NCI CGAP SubB Homo sapiens cDNA clone HTFAVE06 5'
10574	23269		2.4	5.0E-15 AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06 5'
418	12829	25442	2.95	4.0E-15 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8587	19332	32339	0.78	4.0E-15 AB001970.1	NT	Homo sapiens mRNA for transcription factor
10684	20392	33503	3.08	4.0E-15 AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10984	20392	33506	3.08	4.0E-15 AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4182	16933		7.06	3.0E-15 N98452.1	EST_HUMAN	LY1142F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIOLATIN)
4872	17569		0.79	3.0E-15 P22485	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 5
6716	19631		1.33	3.0E-15 Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7179	19865	32637	2.8	3.0E-15 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7179	19865	32638	2.8	3.0E-15 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9825	22478		2.51	3.0E-15 AA807128.1	EST_HUMAN	cc36a07 of NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element 1
10684	23385	36625	2.47	3.0E-15 ABO26898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12310	26316		1.81	3.0E-15 AJ271735.1	NT	Homo sapiens Xa pseudocautosomal region: segment 1/2
12814	25058		1.35	3.0E-15 AW87214.1	EST_HUMAN	GMA-PT0034-180200-506-d01 PT0034 Homo sapiens cDNA
243	13052	26892	3.8	2.0E-15 AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15 AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25799	3.99	2.0E-15 AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16258	28910	0.71	2.0E-15 AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16258	28911	0.71	2.0E-15 AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Page 230 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4049	16764	28423	1.08	2.0E-15	AW238499.1	EST_HUMAN	xp206101.x1 NCI CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1,18 L1 repetitive element ;
4580	17315		2.46	2.0E-15	AI80535.1	EST_HUMAN	w07706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN ;
6089	18887	31833	0.88	2.0E-15	BE662352.1	EST_HUMAN	601344253.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6089	18887	31834	0.88	2.0E-15	BE662352.1	EST_HUMAN	601344253.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7014	18708		1.5	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7171	19857	32226	2.82	2.0E-15	AA704165.1	EST_HUMAN	z17763.x1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7294	19877	33054	5.18	2.0E-15	W08064.1	EST_HUMAN	z176610.1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:298575 5' similar to WP:4474.8 CE02227 TRANSPOSASE ;
8804	21496	34642	2.86	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
8971	21561	34811	1	2.0E-15	AA397758.1	EST_HUMAN	z177608.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
8971	21561	34812	1	2.0E-15	AA397758.1	EST_HUMAN	z177608.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35145	1.23	2.0E-15	AW378465.1	EST_HUMAN	CAC-H10244-201099-078-412 H10244 Homo sapiens cDNA
9304	21971	35146	1.23	2.0E-15	AW378465.1	EST_HUMAN	CAC-H10244-201099-078-412 H10244 Homo sapiens cDNA
10742	23429		5.56	2.0E-15	AJ271735.1	NT	Homo sapiens Xai pseudocautosomal region; segment 1/2
12451	25338		2.04	2.0E-15	U82828.1	NT	Homo sapiens elaxia telangiectasia (ATM) gene, complete cds
12653	16256	28910	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12653	16256	28911	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2077	15482		2.39	1.0E-15	AI695984.1	EST_HUMAN	b228105.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3111	15777	28427	1.35	1.0E-15	BE043594.1	EST_HUMAN	ix40621.y1 NCI CGAP_Ox42 Homo sapiens cDNA clone IMAGE:2999162 5'
3139	15903	28548	1.29	1.0E-15	F08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5136	17856		0.97	1.0E-15	AW021431.1	EST_HUMAN	df23606.x1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2484202 5'
6279	19052	32030		1.0E-15	T66783.1	EST_HUMAN	yw40610.s1 Soares_fetal liver spleen_INFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER1 repetitive element ;
6909	19647		2.12	1.0E-15	BE074217.1	EST_HUMAN	Q153-B10569-270100-074-405 B10569 Homo sapiens cDNA
8131	20825	33681	0.88	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8319	21012	34149	4.56	1.0E-15	AI200976.1	EST_HUMAN	qf68106.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8319	21012	34150	4.56	1.0E-15	AI200976.1	EST_HUMAN	qf68106.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21828	34770	0.97	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007

Page 231 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8940	21631	34774	1.79	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9148	21877	35042	0.87	1.0E-19	Q38575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9532	22185	35370	0.94	1.0E-15	AA594553.1	EST_HUMAN	cl37c03.at NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459072 3' similar to contains L1.13 L1
10720	23409	36651	3.6	1.0E-15	AF044083.1	NT	repetitive element;
12722	25148	30896	4.72	1.0E-16	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
14899	17204	28930	0.98	9.0E-16	4503168	NT	cl37c03.at NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459072 3' similar to contains L1.13 L1
10915	23595	36841	3.04	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1459072 3' similar to contains L1.13 L1
11606	24291	37615	1.48	9.0E-16	A124341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1459072 3' similar to contains L1.13 L1
11696	24291	37616	1.46	9.0E-16	A124341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1459072 3' similar to contains L1.13 L1
5815	18411	31324	0.71	7.0E-16	4885120	NT	repetitive element;
7241	19928	33001	1.49	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7241	19928	33002	1.49	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12875	25237		1.98	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2137	14867		8.38	8.0E-16	AW972511.1	EST_HUMAN	PEPTIDYLARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
1476	14223	28309	1.08	5.0E-16	AJ251154.1	NT	EST1584702 MAGF resequences; MAGL Homo sapiens cDNA
2887	15396	28134	2.17	5.0E-16	AA92178.1	EST_HUMAN	mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
5854	22802	35906	0.64	5.0E-16	AL183248.2	NT	q680c04.x1 Sources: fetal, fetal, Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11504	24105	37418	3.6	5.0E-16	BF217968.1	EST_HUMAN	contains element L1 repetitive element;
12767	25018		14.19	5.0E-16	11418127	NT	Homo sapiens chromosome 21 segment HS21C046
2233	14891		1.81	4.0E-16	AB001523.1	NT	601885754.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2378	15100	27839	1.71	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2378	15100	27840	1.71	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
3460	15208	28856	3.59	4.0E-16	Q16653	SWISSPROT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4121	15953	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0038-200300-115-402 UM0036 Homo sapiens cDNA
4121	15953	29490	5.02	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0038-200300-115-402 UM0036 Homo sapiens cDNA
7812	20278	33380	49.62	4.0E-16	AL163284.2	NT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
							PMA-BT0650-010400-002-909 BT0650 Homo sapiens cDNA
							PMA-BT0650-010400-002-909 BT0650 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084

Page 232 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9195	21865	35529	1.04	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA.
11182	23847	37133	1.51	4.0E-16	AV730330.1	EST_HUMAN	AV730330 HTF Homo sapiens cDNA clone HTFAWA03 5'
11851	24435	37178	1.44	4.0E-16	Q62632	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24547		2.04	4.0E-16	P70548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24605	31087	2.51	4.0E-16	6912459	NT	Homo sapiens Gb2-associated binder 2 (GAB2), mRNA
1301	12945	25989	2.03	3.0E-16	AW022862.1	EST_HUMAN	af46501.Y1 Morton Fetal Cochlear Homo sapiens cDNA clone IMAGE:2466378 5'
130	12945	25590	2.03	3.0E-16	AW022862.1	EST_HUMAN	af46501.Y1 Morton Fetal Cochlear Homo sapiens cDNA clone IMAGE:2466378 5'
453	13239		1.5	3.0E-16	AL046445.1	EST_HUMAN	DKFZ-29454P037.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
463	13249		1.5	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	14182	28987	1.38	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2975	15741	28398	3.76	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3913	16983	29204	19.93	3.0E-16	T08169.1	EST_HUMAN	EST005030 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
3939	16989		0.95	3.0E-16	U03867.1	NT	Human BXP20 gene
5195	18004		0.99	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5529	18327	31230	1.79	3.0E-16	AF035526.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8556	21248	34397	4.26	3.0E-16	AI002836.1	EST_HUMAN	en89h05.s1 Striatum schizoid brain 311 Homo sapiens cDNA clone IMAGE:1694185 3' similar to contains THR.b2 THR repetitive element
9780	22441		0.99	3.0E-16	BF690017.1	EST_HUMAN	60224653B.F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10019	22667	35683	5.57	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
931	15717		1.2	2.0E-16	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2385	15108		0.91	2.0E-16	AA621761.1	EST_HUMAN	af06004.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2694	15403		1.05	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4157	16997	29526	1.16	2.0E-16	X69211.1	NT	H.sapiens DNA for endogenous retroviral like element
4447	17183	28607	0.96	2.0E-16	AI208733.1	EST_HUMAN	qs6803.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1691937 3' similar to contains MER28.13
5104	17622	30439	0.79	2.0E-16	BE091178.1	EST_HUMAN	MER29 repetitive element
6842	18404	32419	0.99	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-137189-203-H12 BT0046 Homo sapiens cDNA
							HISTIDINE-RICH PROTEIN KE4
7615	20261	33389	0.75	2.0E-16	AI470723.1	EST_HUMAN	ff16e11.x1 NCI_CGAP_G444 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element
7897	20562	33689	2.14	2.0E-16	AI723837.1	EST_HUMAN	ns4706.x5 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1280847 similar to TR-054849 054849
8038	20752	33983	0.57	2.0E-16	BE656026.1	EST_HUMAN	HYPOHETICAL 42.8 KDa COGAD P128 Homo sapiens cDNA clone IMAGE:1280847 similar to TR-054849 054849

Page 233 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8038	20752	33984	0.57	2.0E-16	BE686026.1	EST_HUMAN	7162909.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	AW877214.1	EST_HUMAN	GM4-P10034-180200-506-401 P10034 Homo sapiens cDNA
8425	21118	34257	0.81	2.0E-16	AW877214.1	EST_HUMAN	GM4-P10034-180200-506-401 P10034 Homo sapiens cDNA
180	12992	25630	1.84	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13188		29.68	1.0E-16	AA628582.1	EST_HUMAN	cd38g11.x1 Soares_t04a_fetus_N22Hf8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains ORF12 OFR repetitive element 1
1963	14659	27414	2.37	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-410 BN0148 Homo sapiens cDNA
5835	18430	31343	0.75	1.0E-16	AF163984.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6341	19111		27.85	1.0E-16	U46983.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
6479	19246	32246	3.39	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE M91)
7453	19111		7.15	1.0E-16	U46983.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
9183	21853	35018	1.07	1.0E-16	AW875831.1	EST_HUMAN	QV2-P10012-040400-124-405 P10012 Homo sapiens cDNA
3722	16475	29112	2.11	9.0E-17	AW800048.1	EST_HUMAN	GM4-NN1003-203000-153-401 NN1003 Homo sapiens cDNA
6624	18396		2.2	9.0E-17	AI32984.1	EST_HUMAN	1q22x11.x1 NCL CGAP_CLI1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.2
8007	20702		4.75	9.0E-17	AW150257.1	EST_HUMAN	MER28 repetitive element 1
10124	22772		2.47	9.0E-17	AF200719.1	NT	xq49g12.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR12 OFR repetitive element 1
897	13757		1.71	8.0E-17	AW680701.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
3872	16822		0.87	8.0E-17	AL163280.2	NT	QV6-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
5486	25059	31193	3.7	8.0E-17	BE172081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
7175	19851		1.94	8.0E-17	AV730759.1	EST_HUMAN	MRO-HT0569-060300-003-404 HT0559 Homo sapiens cDNA
1441	14188		3.44	7.0E-17	6763097	NT	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
5240	18046		3.3	7.0E-17	AF216650.1	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2) mRNA
6558	16351	32365	8.05	7.0E-17	AF229843.1	NT	Homo sapiens pituitary MTAP (MTAP) mRNA, partial cds, alternatively spliced
188	13011	25653	6	6.0E-17	AW683380.1	EST_HUMAN	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
6221	18995	31971	1.84	6.0E-17	AW662772.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10190	22038	36053	0.46	6.0E-17	P20138	SWISSPROT	h81.d04.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element 1
412	12823	25436	2.87	5.0E-17	T64110.1	EST_HUMAN	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
7486	20158	33250	2.09	5.0E-17	T81043.1	EST_HUMAN	yc05h03.r1 Stralsigne lung (#637210) Homo sapiens cDNA clone IMAGE:79839 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3626	16379	29020	0.89	4.0E-17	AA843697.1	EST_HUMAN	nt5600.5.c1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
9262	22016	35184	1.07	4.0E-17	AW129165.1	EST_HUMAN	Xt2600.5.c1 NCL_CGAP_K68 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element/contains MER19.b1 MER19 repetitive element ;
11475	24076	37386	2.64	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12027	24555		1.75	4.0E-17	AD073548.1	EST_HUMAN	ov45604.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR-Q16530
14771	14224		1.14	3.0E-17	DT14547.1	NT	Q16530 PNAS MRNA, contains MER10.12 MER10 repetitive element ;
2091	14822	27564	1.85	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3188	15951		1.18	3.0E-17	P35410	SWISSPROT	xb89c09.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3433	16366	29026	1.34	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633	16368	29027	1.34	3.0E-17	BE326522.1	EST_HUMAN	hw05004.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
4970	17695		1.89	3.0E-17	BF511266.1	EST_HUMAN	hw05004.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8166	20960	33992	6.16	3.0E-17	N68451.1	EST_HUMAN	U1-HB14-469-c06-00-01.1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3085043 3'
5801	22254	35439	6.88	3.0E-17	AB026868.1	NT	zaf14b02.x1 Soares fetal liver spleen, 1NfLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.3 PTR5 repetitive element ;
10278	22927	36140	0.64	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10278	22927	36141	0.64	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-412 BN0047 Homo sapiens cDNA
11584	24532		3.65	3.0E-17	11417968	NT	QV3-BN0047-270700-283-412 BN0047 Homo sapiens cDNA
12764	25023		1.44	3.0E-17	AV720204.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
343	13144	25782	3	2.0E-17	A1270080.1	EST_HUMAN	AV720204 GLG Homo sapiens cDNA clone GLCJF08 5'
344	13144	25782	2.17	2.0E-17	A1270080.1	EST_HUMAN	q363a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element ;
867	13733		1.94	2.0E-17	AA722932.1	EST_HUMAN	q363a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element ;
2448	15167	27904	2.21	2.0E-17	Q28983	SWISSPROT	zq81d04.x1 Soares, fetal, heart, NBHH19W Homo sapiens cDNA clone IMAGE:369751 3'
2448	15167	27905	2.21	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2930	15696	29343	6.64	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5282	18037	30745	1.88	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLE T H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5282	18037	30746	1.88	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5171	18648		2.04	2.0E-17	AF055068.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9398	19167		1.16	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class I region
7982	20677	33802	1.12	2.0E-17	Q95156	SWISSPROT	DKFZ67820610.J1 782 (synonym: hme2) Homo sapiens cDNA clone DKFZp682J0810 5'
							OLFATORY RECEPTOR-LIKE PROTEIN OLF3

Page 235 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8356	21049	34188	1	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
9769	22420	35528	2.81	2.0E-17	BE298683.1	EST_HUMAN	600948460.F1 NIH_XGCG_17 Homo sapiens cDNA clone IMAGE:2960615 5'
9804	22455	35657	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804	22455	35658	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10159	22807	36025	4.82	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	23228	36138	0.73	2.0E-17	P88063	SWISSPROT	BOONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	23228	36139	0.73	2.0E-17	P88063	SWISSPROT	BOONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10307	23954	36168	0.49	2.0E-17	A1798902.1	EST_HUMAN	wes4b04.x1 Scores: NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10307	23954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	wes4b04.x1 Scores: NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10307	23954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	wes4b04.x1 Scores: NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
733	13507	26164	3.06	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446	27204	1.26	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 22
1761	14503	27204	2.73	1.0E-17	AJ271736.1	NT	Homo sapiens chromosome 21 segment HS21C007
2109	14940	27571	2.35	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2335	15059	27795	2.06	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	16509		1.3	1.0E-17	AF224689.1	NT	Homo sapiens matrix metalloproteinase 2 (MMP2) gene, complete cds
4116	16558		7.37	1.0E-17	R08942.1	EST_HUMAN	YF30407.71 Scores: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128388 5'
6365	16136		0.69	1.0E-17	AW469468.1	EST_HUMAN	he33a05.x1 NC1 CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element: contains LTR8.1 LTR8 repetitive element:
6555	19320	32327	2.04	1.0E-17	A1185942.1	EST_HUMAN	q665b05.x1 Scores: fetal_lung_NbH1.19W Homo sapiens cDNA clone IMAGE:1743825 3'
6555	19320	32328	2.04	1.0E-17	A1185942.1	EST_HUMAN	q665b05.x1 Scores: fetal_lung_NbH1.19W Homo sapiens cDNA clone IMAGE:1743825 3'
6989	19592	32730	0.93	1.0E-17	Q116931	SWISSPROT	URIDINE PHOSPHORYLASE (UDPPASE)
8460	21182	34324	1.33	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0283-101269-072-407 BT0283 Homo sapiens cDNA
9607	22559	35751	0.88	1.0E-17	AW669538.1	EST_HUMAN	QV0-BT0283-101269-072-407 BT0283 Homo sapiens cDNA
11304	24000	37504	2.09	1.0E-17	Q28924	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
11732	24325	37649	2.47	1.0E-17	AA453647.1	EST_HUMAN	z44905.x1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:786469 3' similar to TR.G1263081
2474	15162	27632	0.95	9.0E-18	AA174078.1	EST_HUMAN	G1263081 MARINER TRANSPOSASE. ;
6308	22060		3.31	9.0E-18	AA172167.1	EST_HUMAN	zp18712.s71 Stratigene fetal retina G37202 Homo sapiens cDNA clone IMAGE:609962 3'
3765	16518	29156	1.62	8.0E-18	4758977	NT	1166405.x1 Scores: NSF_F8_PW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
							Homo sapiens protein tyrosine phosphatase, non-receptor type subfamily 1 (PTPNS1) mRNA
							xx11004.x1 NC1 CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
339	13140	25775	16.92	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);

Page 236 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20668.60S
7343	20024	33100	1.33	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0089-170300-011-403 OT0081 Homo sapiens cDNA
12402	13140	25776	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20668.60S
12492	13140	25777	3.41	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10604.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20668.60S
3289	16050	28808	1	6.0E-18	X71781.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived neurotrophase nexin 1, enhancer region
4898	17492		3.02	6.0E-18	P62181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8148	20342		2.84	6.0E-18	11428165	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H1. sapiens) (LOC63446), mRNA
8246	20340	34077	0.72	6.0E-18	AL193210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11079	23748	37024	1.61	6.0E-18	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
11300	23960	37280	1.74	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, PP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
12241	24692	31076	3.29	6.0E-18	U87629.1	NT	Human acetylcholinesterase (AChE) gene, exon 4
1125	13881	26541	21.7	5.0E-18	AL280214.1	EST_HUMAN	qmf5g11.x1 Soares_placenta_8168weeks_ZNHUP69W Homo sapiens cDNA clone IMAGE:1693668 3' similar to contains Alu repetitive element
5047	17766	30384	0.98	6.0E-18	D61517.1	EST_HUMAN	HM441F035 Clontech human fetal brain polyA+ mRNA (46635) Homo sapiens cDNA clone GEN-411F05 5'
5191	17999	30622	1.2	6.0E-18	AF087613.1	NT	Human endogenous retrovirus HERV-P-147D
8620	21312	34454	6.25	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
10899	23579	39828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein LOC51088, mRNA
10899	23579	39828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein LOC51088, mRNA
12958	24770		3.4	5.0E-18	AW887162.1	EST_HUMAN	MRI-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12955	24678		4.18	5.0E-18	AV680547.1	EST_HUMAN	AV680547 GLC Homo sapiens cDNA clone GLOC602 3'
121	12639	25590	1.37	4.0E-18	BE044076.1	EST_HUMAN	hs38h04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER28.b3 MER29 repetitive element;
121	12639	25581	1.37	4.0E-18	BE044076.1	EST_HUMAN	hs38h04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER28.b3 MER29 repetitive element;
1711	14454	27153	1.18	4.0E-18	AA621814.1	EST_HUMAN	mp24f1.x1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	14619		1.12	4.0E-18	A1736592.1	EST_HUMAN	w33h03.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2392085 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2168	14927	27862	1.33	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6N-ACETYLGLUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2168	14927	27863	1.33	4.0E-18	Q06430	SWISSPROT	ACETYLACTOSAMINIDE BETA-1,6N-ACETYLGLUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3772	16524	29162	0.68	4.0E-18	AJ581588.1	EST_HUMAN	ar38303.x1 Barstead colon HPLUB7 Homo sapiens cDNA clone IMAGE:1627139 3'
5279	18084	30740	2.24	4.0E-18	A017565.1	EST_HUMAN	ar23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627139 3'
5279	18084	30741	2.24	4.0E-18	A017565.1	EST_HUMAN	ar23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627139 3'
7745	20441		0.63	4.0E-18	AA74681.1	EST_HUMAN	nv64a08.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1265998 similar to contains L1 L2 L1
10927	23807	35859	8.78	4.0E-18	AA371807.1	EST_HUMAN	EST159533 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
829	13569	26270	1.69	3.0E-18	AA814198.1	EST_HUMAN	de23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
909	13570	26340	3.47	3.0E-18	BE08634.1	EST_HUMAN	P48782.40S RIBOSOMAL PROTEIN S5.1
3331	16581	28222	1.47	3.0E-18	AL103247.2	NT	Human sapina chromosome 21 segment HS21C047
6730	16584	32896	5.64	3.0E-18	BE001071.1	EST_HUMAN	PMD-BN0081-100300-001-008 BN0081 Homo sapiens cDNA
10944	23528	39769	1.61	3.0E-18	BF216550.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103662 5'
12497	24852		6.14	3.0E-18	AW022015.1	EST_HUMAN	d31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
244	13053	25693	4.42	2.0E-18	AW836820.1	EST_HUMAN	QV14-T0038-150200-070-07 L10038 Homo sapiens cDNA
1130	13883		82.93	2.0E-18	BE256097.1	EST_HUMAN	60114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
5326	18129		3.19	2.0E-18	AA686610.1	EST_HUMAN	ak63a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409632 3' similar to TR-O14577
5419	18219	30627	3.98	2.0E-18	D114547.1	NT	Human DNA, SINE repetitive element
5419	18218	30928	3.98	2.0E-18	D114547.1	NT	Human DNA, SINE repetitive element
5788	18579		1.68	2.0E-18	BF347229.1	EST_HUMAN	60202164F1 NCI_CGAP_Bln87 Homo sapiens cDNA clone IMAGE:4156670 5'
6073	18552	31817	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6073	18552	31818	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6185	18562	31835	1.04	2.0E-18	BF332940.1	EST_HUMAN	IL3-HT0618-220700-222-G12 HT0618 Homo sapiens cDNA
8226	19000	31977	5.18	2.0E-18	AW665863.1	EST_HUMAN	h94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2970684 3' similar to contains MER1B12 MER19 repetitive element
7335	20018	33066	0.81	2.0E-18	AA457619.1	EST_HUMAN	aas8d1.r1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR-G61634 G61634 POLYPEPTIDE PR77
8047	20741	33673	0.47	2.0E-18	BE439524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA

Page 238 of 538
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9947	22595	35798	1.66	2.0E-18	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2923146 3' similar to contains MER10.12
9947	22595	35799	1.66	2.0E-18	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2923146 3' similar to contains MER10.12
10884	23574	36824	2	2.0E-18	AW470791.1	EST_HUMAN	h333a06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875469 3' similar to contains THR.13
11739	24329	37653	3.91	2.0E-18	AW151299.1	EST_HUMAN	xq47e09.x1 NCI_CGAP_Uni Homo sapiens cDNA clone IMAGE:2830728 3' similar to contains MER18.b2
12174	13889		1.45	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element;
4382	17119		1.02	1.0E-18	T86408.1	EST_HUMAN	601114352F1 NH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5271	18077	30707	3.63	1.0E-18	AV653405.1	EST_HUMAN	y43g05.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
5483	18282	31180	2.64	1.0E-18	D00099.1	NT	AV653405 GLC Homo sapiens cDNA clone GLDKE11 3'
5483	18282	31181	2.64	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6363	19133	32128	1.53	1.0E-18	AL163280.2	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
8341	21034	34171	1.43	1.0E-18	AI148288.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
9799	22460	35653	4.22	1.0E-18	U91328.1	NT	cd36d09.x1 Soares_senescens_fibroblasts NIH/SEF Homo sapiens cDNA clone IMAGE:1880563 3' similar to contains L11 L1 repetitive element;
12130	24621	37092	4.23	1.0E-18	AF003529.1	NT	Human, hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA) gene, ROR1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
532	13316	25952	5.34	9.0E-19	AA281061.1	EST_HUMAN	Homo sapiens gipican 3 (GPC3) gene, partial cds and flanking repeat regions
533	13316	25952	3.24	9.0E-19	AA281061.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7747	20443		4.47	9.0E-19	P06888.1	EST_HUMAN	MER19 repetitive element;
8588	21280	34419	2.54	9.0E-19	AL163203.2	NT	MER19 repetitive element;
8588	21280	34420	2.54	9.0E-19	AL163203.2	NT	HSC2F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
11072	23742	37018	4.82	9.0E-19	AB032569.1	NT	Homo sapiens chromosome 21 segment HS21C003
11901	13316	25952	1.88	9.0E-19	AA281061.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1026	13785		1.25	8.0E-19	AW974902.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
4372	17110		1.04	8.0E-19	P08548	SWISSPROT	z111d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6046	20742	33874	0.92	8.0E-19	BE158938.1	EST_HUMAN	MER19 repetitive element;
							EST387007 MAGE resources, MAGE Homo sapiens cDNA
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOGY
							MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA

Page 239 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4798139	NT	Homo sapiens DEAD/HD (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6384	19134	32129	2.34	7.0E-19	AF092000.1	NT	Rattus norvegicus cpl51 mRNA, partial cds
7169	16985	32660	0.9	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
5911	22560	35765	0.51	7.0E-19	A344951.1	EST_HUMAN	U601c08.x1 NCL CGAP_L1028 Homo sapiens cDNA clone IMAGE:2052302 3'
12036	23597	-	2.05	7.0E-19	AJ709894.1	EST_HUMAN	z66001.s1 Scores: fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:436146 3'
3761	16513	28795	1.34	6.0E-19	AW852930.1	EST_HUMAN	PMA-CT0248-131089-001-001 CT0248 Homo sapiens cDNA
4430	17169	29706	1.39	6.0E-19	P34989	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4747	17479	29706	1.39	6.0E-19	P34989	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4967	17692	30301	1.04	6.0E-19	AJ271735.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
5767	18558	31485	5.36	5.0E-19	Q00193	SWISSPROT	DKFZ26762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZ62F192 5'
10324	22971	36191	1.03	5.0E-19	AJ287599.1	NT	Homo sapiens partial LL-125B1 gene for IL-12 receptor beta1 chain, exon 14
11525	24125	37431	7.45	5.0E-19	AW183725.1	EST_HUMAN	X87002.x1 Scores: NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element MSRT1 repetitive element
541	13324	26556	1.68	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2589	15398	28139	1.02	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4287674 5'
5311	18115	30773	0.97	4.0E-19	AF224569.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3833	16584	29219	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3833	16584	29220	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4253	16924	29622	0.89	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4263	16994	29623	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413	17150	29777	1.12	3.0E-19	AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADCANAL11 5'
5168	18008	-	0.64	3.0E-19	AF23487.1	NT	Homo sapiens NP0008 protein (NP0008) mRNA, complete cds
7283	16966	-	2.79	3.0E-19	11432214	NT	Homo sapiens similar to aldol-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC693222), mRNA
8359	20430	33548	1.15	3.0E-19	X86585.1	NT	Musculus mRNA for TPOR33 protein
12264	24709	-	23.34	3.0E-19	AF165520.1	NT	Homo sapiens photobin protein (PB) mRNA, complete cds
2565	15279	28017	21.33	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4411	17148	-	1.03	2.0E-19	AJ311783.1	EST_HUMAN	qq91e02.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915899 3' similar to TR-Q69386 Q69386 POLYOMY GENE
5993	18745	31706	0.97	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'

Page 240 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7298	19023	32088	0.93	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20922	34061	8.08	2.0E-19	AA012854.1	EST_HUMAN	OLF34c08.11 Soares retina N2bHR Homo sapiens cDNA clone IMAGE:360980 5'
9809	22460	35666	0.98	2.0E-19	Q96155	SWISSPROT	ZNF34c08.11 Soares retina N2bHR Homo sapiens cDNA clone IMAGE:360980 5'
11829	24413	31760	1.33	2.0E-19	BF330867.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11829	24413	31760	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
469	13255		1.87	1.0E-19	BE408611.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
2181	14891	27629	1.68	1.0E-19	H30795.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
2723	15430		2.37	1.0E-19	D33044.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
2831	15819		4.95	1.0E-19	4758977	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
3390	16154	28808	1.2	1.0E-19	AA834987.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
5983	18764	31726	2.38	1.0E-19	U12188.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
6114	25419		0.83	1.0E-19	AA595527.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
7528	20199	33293	0.86	1.0E-19	U09813.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
7528	20199	33294	0.88	1.0E-19	U09813.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
7695	25118		0.83	1.0E-19	AF20719.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
8349	21042	34176	1.75	1.0E-19	MB4657.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
8640	21632		2.64	1.0E-19	T9920.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
9649	22301		0.46	1.0E-19	U06822.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
10087	22735	35950	23.03	1.0E-19	AW812259.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
10097	22745	35960	1.46	1.0E-19	N44631.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
11700	24351	37983	1.55	1.0E-19	U03163.1	NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
6549	16314	32319	2.66	8.0E-20		NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
6549	16314	32320	2.66	8.0E-20		NT	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
7418	20095	33180	1.34	8.0E-20	A1221371.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
7418	20095	33181	1.34	8.0E-20	A1221371.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
3270	10031	28932	1.41	7.0E-20	BF326455.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
6898	17972	30529	8.29	7.0E-20	AL138120.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA
8394	21087	34222	12.46	7.0E-20	AA557657.1	EST_HUMAN	RC3-B1T0333-250900-114-04 BT0333 Homo sapiens cDNA

Page 241 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	AA557657.1	EST_HUMAN	m46c04.s1 NC1 CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
11714	24308		1.86	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3543	16298	28949	3.52	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4239	16980	29805	3.33	6.0E-20	BE822434.1	EST_HUMAN	601441231.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4556	17291		1.18	5.0E-20	AY725123.1	EST_HUMAN	AY725123 HTG Homo sapiens cDNA clone HTGTA01 5'
7015	19707	32763	1.07	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7846	20541	33669	5.29	5.0E-20	W00525.1	EST_HUMAN	z47808.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
7846	20541	33669	5.28	5.0E-20	W94525.1	EST_HUMAN	z47808.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8002	20687	33625	0.7	5.0E-20	BE165980.1	EST_HUMAN	MR3-H10487-150205-1T3-g01 HT0487 Homo sapiens cDNA
8734	21428	34572	2.84	6.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
8734	21428	34573	2.84	5.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
9345	20416		0.84	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1616	14363	27054	1.34	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5502	18339		0.8	4.0E-20	Q36980	SWISSPROT	HISTONE H2B C (H2B/C)
7826	20521		5.15	4.0E-20	AB74352.1	EST_HUMAN	z64g03.x1 NC1 CGAP_OV35 Homo sapiens cDNA clone IMAGE:2263396 3'
10396	23042	38259	1.33	4.0E-20	AW637469.1	EST_HUMAN	QV9-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2135	14655	27593	1.02	3.0E-20	U03888.1	NT	Human BPX21 gene
4168	16926	29557	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 14
4582	17317	28944	1.05	3.0E-20	AA037616.1	EST_HUMAN	z43b512.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484893 3' similar to contains L1.3 L1 repetitive element;
8933	21325		2.95	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10219	22667	36078	0.83	3.0E-20	BF185264.1	EST_HUMAN	601843561.F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10591	23257		1.87	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11466	24097	37408	1.5	3.0E-20	A284244.1	EST_HUMAN	q70d02.x1 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11496	24097	37409	1.5	3.0E-20	A284244.1	EST_HUMAN	q70d02.x1 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12051	24599	31118	2.95	3.0E-20	BE888422.1	EST_HUMAN	601614160.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
						EST_HUMAN	x24e10.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW_R35_MOUSE
811	13582		3.12	2.0E-20	AW303888.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6, ;

Page 242 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	AA516335.1	EST_HUMAN	ng8h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068
1089	13847	26506	3.37	2.0E-20	AA516335.1	EST_HUMAN	G1224068 ORF2: FUNCTION UNKNOWN ;
2820	13582		2.58	2.0E-20	AW303888.1	EST_HUMAN	ng8h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068
4893	17620	30238	4.97	2.0E-20	Q28983	SWISSPROT	G1224068 ORF2: FUNCTION UNKNOWN ;
4893	17620	30239	4.97	2.0E-20	Q28983	SWISSPROT	X224010.x1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:2761008 3' similar to SW:RS5_MOUSE
5097	17786		5.98	2.0E-20	5174538	NT	p97461.405 RIBOSOMAL PROTEIN S5 ;
8017	20712	33843	0.81	2.0E-20	AJ308457.1	EST_HUMAN	ZONADHESIN PRECURSOR
9089	21778	34942	8.6	2.0E-20	D10083.1	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9089	21778	34943	8.6	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
12426	25141	30895	2.03	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
12815	25057		1.39	2.0E-20	11437152	NT	Homo sapiens RGH1 gene, retrovirus-like element
2007	15525	27468	3.71	1.0E-20	AA281981.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4406	17143	29772	1	1.0E-20	BF115158.1	EST_HUMAN	Homo sapiens hepatitis-binding growth factor binding protein (HBP17) mRNA
6794	19539	32663	0.75	1.0E-20	AF048567.1	EST_HUMAN	Z11408.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
5051	21750	34309	2.04	1.0E-20	11418491	NT	MER19 repetitive element ;
11541	24141	37450	2.62	1.0E-20	AF223391.1	NT	repetitive element ;
12171	24951		1.73	1.0E-20	AA420453.1	EST_HUMAN	AF048567 Human activated dendritic cell mRNA Homo sapiens cDNA clone CA05
2913	15679		0.98	1.0E-20	AJ003514.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCIP) gene, exons 7-49, and partial cds, alternatively spliced
11904	24469		2.82	9.0E-21	AW698189.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8711	21403		2.15	8.0E-21	AW674891.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.03 L1
11526	24126	37432	3.52	8.0E-21	AA809411.1	EST_HUMAN	repetitive element ;
12064	24670		4.49	8.0E-21	Q24330	SWISSPROT	AJ003514 Saccid chromosome 21 cDNA library Homo sapiens cDNA clone MIP12.8J21
2081	14793	27518	1.82	7.0E-21	P15800	SWISSPROT	RC3-NN0085-090500-021-603 NN0088 Homo sapiens cDNA
2081	14793	27519	1.62	7.0E-21	P15800	SWISSPROT	b330a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN
3989	16442	28093	0.69	7.0E-21	AL163300.2	NT	O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
4228	16969		5.58	7.0E-21	AA046502.1	EST_HUMAN	aa71603.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
							ATP SYNTHASE A CHAIN (PROTEIN P)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							Z67408.r1 Soares_pregnantUterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'

Page 243 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6340	19110	32100	0.79	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287	20981	34121	1.53	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5576	21269	34407	10.76	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10013	22681	35877	0.86	7.0E-21	AW65922.1	EST_HUMAN	RC3-C10301-271199-031-1-03 C10301 Homo sapiens cDNA
10594	23268	36525	2.19	7.0E-21	AA723404.1	EST_HUMAN	z73703.61 Soares_fetalHeart_NBHH19W Homo sapiens cDNA clone IMAGE:398681 3' similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN) contains THR13 OFF repetitive element;
11234	23897	37184	1.75	7.0E-21	77069608	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4083	16827	28464	0.83	6.0E-21	BE08611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9034	21724	28464	0.83	6.0E-21	BE102737.1	EST_HUMAN	PM1-H10464-080100-002-H09 H10464 Homo sapiens cDNA
903	13670	28334	0.7	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330	17069	28697	2.91	6.0E-21	BE968839.1	EST_HUMAN	601849571F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4749	17481	30112	5.56	5.0E-21	4865474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6635	19582		0.9	5.0E-21	AW440884.1	EST_HUMAN	hs05610.X1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
6917	16654	32700	0.86	5.0E-21	BE956505.1	EST_HUMAN	783d11.X1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR11
10474	23120	36349	0.44	5.0E-21	Q91680	SWISSPROT	OFR repetitive element;
10474	23120	36350	0.44	5.0E-21	Q91680	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11986	24527		2.93	5.0E-21	AA393574.1	EST_HUMAN	Z17204.1 Soares_fetalHeart_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1727	14469	27168	1.81	4.0E-21	AA970713.1	EST_HUMAN	oa86968.61 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR-Q16530 Q16530
6772	16516	32544	3.27	4.0E-21	AB016578.1	NT	PMS3 MRNA contains OFR.H1 OFR repetitive element;
							Rattus norvegicus mRNA for R11M, complete cds
9680	22332	35527	0.83	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RORC gene, and sodium phosphate transporter (NP13) gene, complete cds
9705	22356	35552	0.7	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1829	14598	27280	0.94	3.0E-21	AA218891.1	EST_HUMAN	Z17606.51 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2272	14968	27736	1.24	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3078	15843	28465	4.31	3.0E-21	AJ07973.1	NT	Homo sapiens LOND2B gene
5412	18211	30919	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30920	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5

Page 244 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5652	18447		0.95	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLCG0A10.3
6095	18964		2.3	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4664945 5'
6959	18451	32469	7.69	3.0E-21	BF381063.1	EST_HUMAN	RC1-010083-100800-019-008 Q10083 Homo sapiens cDNA
9592	22245	35429	1.15	3.0E-21	AV687780.1	EST_HUMAN	CM1-NN0053-280400-203-108 NN0053 Homo sapiens cDNA
12333	32527	30714	2.98	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
141	12558		17.18	2.0E-21	BE163247.1	EST_HUMAN	QV5-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
914	13681	26342	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
914	13681	26343	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944		2.75	2.0E-21	BE094410.1	EST_HUMAN	RC4-BT0311-141199-011-106 BT0311 Homo sapiens cDNA
2844	15354	28098	1.99	2.0E-21	Q28893	SWISSPROT	ZONADHESIN PRECURSOR
2844	15354	28099	1.99	2.0E-21	Q28893	SWISSPROT	ZONADHESIN PRECURSOR
5396	18198	30890	1.64	2.0E-21	AI624652.1	EST_HUMAN	ts30703.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5489	18288	31184	0.68	2.0E-21	AA027211.1	EST_HUMAN	HYPOPHYSICAL 51.1 KD PROTEIN
5489	18288	31185	0.68	2.0E-21	AA027211.1	EST_HUMAN	zse97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8170	20684	33996	0.5	2.0E-21	AJ010770.1	NT	zse97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8261	20965	34094	0.16	2.0E-21	BE141783.1	EST_HUMAN	Homo sapiens hypoxanthine gene, exons 1-50
8722	21414	34657	3.74	2.0E-21	AU136778.1	EST_HUMAN	AU136778 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
10991	23695		1.55	2.0E-21	BE350127.1	EST_HUMAN	h099d01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER28 b3
11289	23950	37246	1.3	2.0E-21	BE973823.1	EST_HUMAN	MER29 repetitive element;
11289	23960	37247	1.3	2.0E-21	BE973823.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12272	24712		9.87	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1233	13982	26652	1.6	1.0E-21	AA557657.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1381	14128		2.62	1.0E-21	AI601264.1	EST_HUMAN	h462d04.x1 NCL CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28 b2
6396	19165		2.74	1.0E-21	AL076752.1	EST_HUMAN	MER29 repetitive element;
7092	19781	32847	6.6	1.0E-21	AI223104.1	EST_HUMAN	ae88d12.x1 Barstead colon HP1LRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
10484	23130		1.07	1.0E-21	5730335	NT	DKF-ZP4340830.r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKF-ZP4340830 5'
4377	17114	29747	6.65	9.0E-22	AI702438.1	EST_HUMAN	gg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gbM54241 QIM PROTEIN (HUMAN);
8502	21194	34339	1.27	9.0E-22	AI63201.2	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETNAR) mRNA
8502	21194	34337	1.27	9.0E-22	AI63201.2	NT	ts94d03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001

Page 245 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10661	23382	36622	2.63	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSOC505 5'
11707	24302	37627	1.34	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE200304 5'
620	13609		5.65	8.0E-22	BE144748.1	EST_HUMAN	CM04-HT0178-281058-078-105 HT0179 Homo sapiens cDNA
7797	20492		3.72	8.0E-22	AA048502.1	EST_HUMAN	X677a08.t1 Soares_pregnanl.uterus_NHPU Homo sapiens cDNA clone IMAGE:487868 5'
650	13428	28067	5.92	7.0E-22	AL165246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4250	16691	28616	2.21	7.0E-22	Q61898	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4877	17700	30307	0.99	7.0E-22	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8990	21282		1.38	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8731	21423	34568	3.65	7.0E-22	M78590.1	EST_HUMAN	EST007268 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBC07
8502	22155	35335	2.04	7.0E-22	AF009600.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TORBV12S2 region
4038	18783	28413	0.98	6.0E-22	AA045040.1	EST_HUMAN	zu55c10.t1 Soares_tesile_NHT Homo sapiens cDNA clone IMAGE:742867 5'
8140	20834		1.33	6.0E-22	AW029123.1	EST_HUMAN	w0507.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6424	19182	32188	3.76	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10217	22865	36077	7.63	5.0E-22	U60822.1	NT	Human cystoplatin (DMO) gene, exons 7, 8 and 9, and partial cds
12499	24854		2.22	5.0E-22	BF478511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3256888 3' similar to contains Alu repetitive element
3927	16380		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2
8004	20969	33827	0.45	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8312	25428		3.11	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10623	23316	36556	2.47	4.0E-22	BF218030.1	EST_HUMAN	BD1882813.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12657	24957		2.06	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
939	13708		1.89	3.0E-22	AI459879.1	EST_HUMAN	hm14h10.x1 NCI_CGAP_C014 Homo sapiens cDNA clone IMAGE:2156811 3' similar to gbl:19593 HIGH AFFINITY INTERLEUKIN-3 RECEPTOR 8 (HUMAN); contains L1.1 L1 repetitive element;
2576	15289	28028	0.92	3.0E-22	AI859038.1	EST_HUMAN	w66b54.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW:RL21_HUMAN
3502	18415		1.48	3.0E-22	D14718.1	NT	P48778 60S RIBOSOMAL PROTEIN L21;
4748	17480	30111	2.6	3.0E-22	AI090126.1	EST_HUMAN	q528d07.x1 Soares_pregnanl.uterus_NHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.2 MER12 repetitive element;
8129	20823		0.8	3.0E-22	BE158613.1	EST_HUMAN	QVC-HT0388-090200-059-112 HT0388 Homo sapiens cDNA
8134	20828	33983	2.46	3.0E-22	BE088941.1	EST_HUMAN	RCB-HT0707-150300-027-H10 B10707 Horle sapiens cDNA
8258	20952	34088	0.97	3.0E-22	X60680.1	NT	R.rattus RY205 mRNA for a potential ligand-binding protein
8258	20952	34089	0.97	3.0E-22	X60690.1	NT	R.rattus RY205 mRNA for a potential ligand-binding protein
1946	14881		2.29	2.0E-22	N24942.1	EST_HUMAN	w734d05.s1 Soares_melanocyte_NHMH Homo sapiens cDNA clone IMAGE:287369 3'
2526	15242	27981	2.15	2.0E-22	P24616	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3414	16172	28821	4.41	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4200	16941	26567	1.17	2.0E-22	AW611784.1	EST_HUMAN	PXN-ST0282-261193-001-d12 ST0282 Homo sapiens cDNA
5761	25075	31476	1.18	2.0E-22	W39458.1	EST_HUMAN	zz20071.r1 Soares_senescent_fibroblasts_NHSPF Homo sapiens cDNA clone IMAGE:322873 5' similar to
6094	18862	31628	3.58	2.0E-22	BF092116.1	EST_HUMAN	gg-XT7208 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
8002	22295	35440	1.53	2.0E-22	A1276522.1	EST_HUMAN	RCO-TU0076-15000-025-H12 TN0078 Homo sapiens cDNA
8098	22347	35540	0.69	2.0E-22	AA715315.1	EST_HUMAN	q17608.x1 Soares_NHHPIL_S1 Homo sapiens cDNA clone IMAGE:1876299 3' similar to contains
9698	22347	35541	0.69	2.0E-22	AA715315.1	EST_HUMAN	MER29.13 MER29 repetitive element ;
11761	24352	37684	1.88	2.0E-22	AA715315.1	EST_HUMAN	in04911.1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1210269 3'
11872	24946	30683	3.77	2.0E-22	AA715315.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1871	14609	27320	1.79	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2688	15302	28038	1.1	1.0E-22	U50871.1	NT	PM4-SN0020-010400-309-H02 SN0020 Homo sapiens cDNA
3405	16103	28814	1.37	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STIM2) gene, complete cds
7641	20306	33415	0.89	1.0E-22	BE084687.1	EST_HUMAN	Human DNA, SINE repetitive element
10451	23097	36328	0.79	1.0E-22	A366436.1	EST_HUMAN	MRO-BT0669-220200-002-H07 BT0669 Homo sapiens cDNA
10451	23097	36329	0.79	1.0E-22	A366436.1	EST_HUMAN	q209h07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020681 3' similar to contains MER29 b2
12704	24684	36329	5.86	1.0E-22	A366436.1	EST_HUMAN	MER29 repetitive element ;
3357	16312	28639	0.79	8.0E-23	AW802801.1	EST_HUMAN	IL2-UM0078-070400-061-F11 UM0078 Homo sapiens cDNA
3305	16065	28639	2.55	8.0E-23	AF188346.1	NT	Gallus gallus Desh12 protein (Desh12) mRNA, complete cds
10698	23642	36895	4.16	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GIG Homo sapiens cDNA clone GLCAW007 3'
3427	16184	3427	1.72	6.0E-23	AF198333.1	NT	Homo sapiens Nuclei (D. melanogaster)-like protein (NOT66L) mRNA
4235	16976	28601	1.39	8.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12005	24540	31105	1.5	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
12005	24540	31106	1.5	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12182	24963	31087	3.28	6.0E-23	AF224669.1	NT	(UBE2D3) genes, complete cds
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							q956c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
							SW3M10_MOUSE P23246 PROTEIN MOV-10 ;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
							(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin
							(CAL7), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
5358	18160	30844	4.09	5.0E-23	U82671.2	NT	

Page 247 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6145	25086	31893	3.93	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7337	25088	31893	3.37	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
8347	18117	32108	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6847	16117	32107	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7738	20434	33558	4.1	3.0E-23	AA130165.1	EST_HUMAN	335509.1 Scores: pregnant_virus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element;
9148	18179	35045	2.98	3.0E-23	Z70864.1	NT	Human endogenous retroviral element HC2
9148	18179	35046	2.98	3.0E-23	Z70864.1	NT	Human endogenous retroviral element HC2
10215	22953		1.18	3.0E-23	AW807927.1	EST_HUMAN	RC3-NN00068-270400-071-1071 NN00068 Homo sapiens cDNA
651	13429	26068	4.25	2.0E-23	AL288880.1	NT	Homo sapiens KIA0851 gene (partial), X13 gene and LZTFL1 gene
1120	15520		3.87	2.0E-23	M59270.1	NT	Human matrix Glia protein (MGF) gene, complete cds
2798	15503	28243	1.88	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2798	15503	28244	1.88	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3394	16123		1.46	2.0E-23	AL201458.1	EST_HUMAN	qs73f1.1 NC CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3705	16458		3.35	2.0E-23	SE165980.1	EST_HUMAN	MR3-H10487-150200-113-501 H10487 Homo sapiens cDNA
3958	16707	28346	3.65	2.0E-23	H58931.1	EST_HUMAN	Y16a02.1 Scores: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
3958	16707	28347	3.65	2.0E-23	H58931.1	EST_HUMAN	Y16a02.1 Scores: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
7772	20468		4.3	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8742	21434	34579	1.21	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11691	24530	246	2.46	2.0E-23	M32688.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12508	24960		2.87	2.0E-23	AF008650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TORBV12S2 region
4482	17228	29857	1.1	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4714	17448		5.56	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6820	19382		3.28	1.0E-23	BE378471.1	EST_HUMAN	601230459F1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3606653 5'
8254	20948	34085	4.6	1.0E-23	AA448097.1	EST_HUMAN	PTR5 repetitive element;
10570	23265	36503	2.05	1.0E-23	BE408643.1	EST_HUMAN	601301762F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
10570	23265	36504	2.05	1.0E-23	BE408643.1	EST_HUMAN	601301762F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
539	13322		1.84	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stradiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852768 3' similar to TRE19822 E19822 CA PROTEIN;
6337	18127	32121	1.53	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3853	16803			1.49	7.0E-24	AW807954.1	EST_HUMAN
5037	17805			0.85	7.0E-24	AL039498.1	EST_HUMAN
10536	20223			1.33	7.0E-24	AW303317.1	EST_HUMAN
890	13495			2.72	6.0E-24	AB007421.1	NT
818	13599			11.74	6.0E-24	AL183249.2	NT
3593	16703			7.9	5.0E-24	AJ228043.1	NT
7657	20321			0.58	5.0E-24	AF223391.1	NT
11595	24194			1.45	5.0E-24	AW614229.1	EST_HUMAN
8940	18928			3.85	4.0E-24	AA594178.1	EST_HUMAN
8981	21273			1.35	4.0E-24	AW813711.1	EST_HUMAN
11333	29801			1.95	4.0E-24	BE544822.1	EST_HUMAN
12361	24765			4.89	4.0E-24	AB026016.1	NT
12595	24651			1.77	4.0E-24	114183181	NT
8322	21015			2.85	3.0E-24	AW614871.1	EST_HUMAN
8377	21070			1.57	3.0E-24	AW602076.1	EST_HUMAN
8385	21940			4.33	3.0E-24	AL183252.2	NT
12438	24608			1.41	3.0E-24	BF12762.1	EST_HUMAN
2346	15059			2.72	2.0E-24	AA167559.1	EST_HUMAN
3719	20054			0.81	2.0E-24	AF088524.1	NT
7374	20056			0.65	2.0E-24	AJ003535.1	EST_HUMAN
7379	20058			3.28	2.0E-24	AL118758.1	EST_HUMAN
8539	21331			0.98	2.0E-24	AF6214.1	EST_HUMAN
8576	21369			0.84	2.0E-24	AF621759.1	EST_HUMAN
8754	22405			0.94	2.0E-24	AF621759.1	EST_HUMAN
11825	24409			1.31	2.0E-24	AW69552.1	EST_HUMAN
11825	24409			1.31	2.0E-24	AW69552.1	EST_HUMAN
12281	25377			7.44	2.0E-24	M28977.1	NT

Page 249 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1681	14435	27131	2.89	1.0E-24	7708340	NT	Homo sapiens CGI-127 protein (LOC51846), mRNA
2679	15388		1.83	1.0E-24	AW820184.1	EST_HUMAN	QV0-ST0284-100400-785-c10 ST0284 Homo sapiens cDNA
3020	15766	28433	1.49	1.0E-24	D96423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4237	16978		1.71	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7447	20223	33214	4.32	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7630	20268	33404	0.81	1.0E-24	BE144526.1	EST_HUMAN	MRO-H10168-271169-409-408 HT0168 Homo sapiens cDNA
7845	20540	33687	2.09	1.0E-24	AW801184.1	EST_HUMAN	OMO-NT1010-130300-281-407 NT1010 Homo sapiens cDNA
11689	24294	37618	1.31	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG1), mRNA
4839	17687	30275	2.33	7.0E-25	AA489944.1	EST_HUMAN	nc22a10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.52
							MER1 repetitive element;
8117	20811	33946	6.59	7.0E-25	AA489946.1	EST_HUMAN	nc06a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:890408 3' similar to contains THR.b2 THR repetitive element;
11701	24296	37622	3.28	7.0E-25	AA583540.1	EST_HUMAN	nt25h08.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
6893	17969		4.9	8.0E-25	W87623.1	EST_HUMAN	P39105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
7822	20288	33397	8.34	8.0E-25	7306360	NT	Z658107.1 Soares_fetal_liver_aplees_INFLS_S1 Homo sapiens cDNA clone IMAGE:416869 5'
1847	14393	27083	1.18	6.0E-25	AW860271.1	EST_HUMAN	IL3-CT0219-181169-031-D04 CT0219 Homo sapiens cDNA
11286	23947	37242	2.44	5.0E-25	AW879107.1	EST_HUMAN	EST3391217 IMAGE ressequences, MAGP Homo sapiens cDNA
1429	14176	26881	2.25	4.0E-25	T08107.1	EST_HUMAN	ys68h04.r1 Soares_fetal_liver_aplees_INFLS Homo sapiens cDNA clone IMAGE:121783 5'
3397	16155		3.04	4.0E-25	AW887671.1	EST_HUMAN	PM3-CT0093-280200-401-407 OT0093 Homo sapiens cDNA
4282	17021		2.83	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0593-140400-149-s11 HT0593 Homo sapiens cDNA
3314	16074	28725	3.98	3.0E-25	8823321	NT	Homo sapiens hypodermal protein FLJ20344 (FLJ20344), mRNA
3314	16074	28725	3.98	3.0E-25	8823321	NT	Homo sapiens hypodermal protein FLJ20344 (FLJ20344), mRNA
4837	17593	30180	0.75	3.0E-25	P26822	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6518	19284	32288	0.6	3.0E-25	AA603590.1	EST_HUMAN	nt27602.s1 NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61868 ZINC FINGER PROTEIN 65 (HUMAN);
8235	20229	34055	4.86	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							repetitive element;
10559	23635	38886	1.99	3.0E-25	AA676013.1	EST_HUMAN	nt30h10.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:916331 similar to contains L1.11 L1
1325	14075	28748	2.84	2.0E-25	5032158	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2306	15031	27798	6.42	2.0E-25	BE88016.1	EST_HUMAN	60181150QF1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2835	15259	27697	3.67	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4167	16907	29535	1.78	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4167	16907	29536	1.75	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16

Page 250 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8665	22317	35514	1.94	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stardust GS) Homo sapiens cDNA
355	13153	25764	1.03	1.0E-23	AL040229.1	EST_HUMAN	DKFZ494H0313.1 434 (synonym: h253) Homo sapiens cDNA clone DKFZ494H0313.5
1226	13978		2.02	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2435	16166	27890	1.03	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4808	17637	30160	2.84	1.0E-25	BE42737.1	EST_HUMAN	PM1-H1T0454-080100-002108 HT0454 Homo sapiens cDNA
6472	18239		0.78	1.0E-25	AA18080.1	EST_HUMAN	z445606.s1 Stratiagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:652627.3 similar to contains Alu repetitive element
6999	20100	32657	3.71	1.0E-25	AA382690.1	EST_HUMAN	nm54h11.31 NC1 CGAP K168 Homo sapiens cDNA clone IMAGE:1087749.3
7814	20509	33633	4.03	1.0E-25	AA1708078.1	EST_HUMAN	Z19604.s1 Soares, fetal, heart, N14-H16W Homo sapiens cDNA clone IMAGE:384822.3 similar to contains PTF6.13 PTR5 repetitive element
9446	22123	35302	0.75	1.0E-25	X60660.1	NT	R. retus RY205 mRNA for a potential ligand-binding protein
9446	22123	35303	0.75	1.0E-25	X60660.1	NT	R. retus RY205 mRNA for a potential ligand-binding protein
10980	23570	36821	3.05	1.0E-25	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12768	25024		2.18	1.0E-25	X51755.1	NT	Human lambdaide-immunoglobulin constant region complex (germline)
2487	15204	27945	1.41	9.0E-25	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C078
5607	18403		1.99	8.0E-28	D14547.1	NT	Human DNA, SINE repetitive element
1571	14318	27003	1.72	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3982	16711	29351	1.23	7.0E-26	X98211.1	NT	H sapiens DNA for endogenous retroviral like element
4138	16880	29508	2.27	7.0E-26	AW340153.1	EST_HUMAN	h02612.x1 Soares, NFL_T_OBC, S1 Homo sapiens cDNA clone IMAGE:2808366.3
5551	18348	31257	0.92	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11689	24284		8.45	7.0E-26	AA115695.1	EST_HUMAN	z330d08.r1 Stratiagene neuroepithelium NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:548943.5 similar to gb:AF14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12547	24985		1.64	7.0E-26	AW654559.1	EST_HUMAN	EST369528 MAGE reassessments, MAGEC Homo sapiens cDNA
2222	14950	27698	2.04	6.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3341	16100	28752	0.95	6.0E-26	AA206131.1	EST_HUMAN	z352h04.r1 Stratiagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271.5
10432	23078	36301	0.98	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10432	23078	36302	0.98	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11683	24278	37500	2.03	8.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1184	13809	26572	3.61	6.0E-26	AI708235.1	EST_HUMAN	as33h08.x1 Barstead aorta APLR88 Homo sapiens cDNA clone IMAGE:2319519.3 similar to WIP-F49C12.11 CE03371

Page 251 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (10p) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1154	13909	26573	3.61	5.0E-26	AF08235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371.
1535	14282		1.4	4.0E-26	AA329548.1	EST_HUMAN	EST:33446 Embryo, 12 week II Homo sapiens cDNA 5' and
9312	21976		3.72	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10558	23254	35491	2.75	4.0E-26	BE268187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635210 5'
1753	14495	27184	1.21	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1696	14732	27454	1.31	3.0E-26	AL045955.2	EST_HUMAN	z330408.1 Stralagene neuropeptide-like peptide (NLP) 133 (synonym: hias3) Homo sapiens cDNA clone DKFZp434068.5
2025	14760		3.15	3.0E-26	AA115895.1	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	16512	29148	1.04	3.0E-26	AA152494.1	EST_HUMAN	z33010.1 Stralagene codon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3760	16512	29149	1.04	3.0E-26	AA152494.1	EST_HUMAN	z33010.1 Stralagene codon (8637204) Homo sapiens cDNA clone IMAGE:4083278 5'
6811	19472	32455	1.78	3.0E-26	BF245458.1	EST_HUMAN	60168463F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
10826	23319		1.42	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11559	24158	37488	1.83	3.0E-26	AW876661.1	EST_HUMAN	QV2-P10012-040400-124-e08 PT0012 Homo sapiens cDNA
11659	24168	37489	1.83	3.0E-26	AW876661.1	EST_HUMAN	QV2-P10012-040400-124-e08 PT0012 Homo sapiens cDNA
11602	24201	37523	6.56	3.0E-26	AA583173.1	EST_HUMAN	nr37d05.s1 NCI CGAP_GCS Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
11858	24442	37783	1.35	3.0E-26	AF228925.1	NT	mus musculus harmonin isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
12724	24695		2.52	3.0E-26	AW073434.1	EST_HUMAN	ME330 repetitive element;
686	13442	26083	8.76	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1801	14599		3.07	2.0E-26	AL030099.2	EST_HUMAN	DKFZp566L171.s1 566 (synonym: hkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3225	15983	28642	5.89	2.0E-26	X86894.1	NT	Mus musculus mRNA for atrophic phosphoprotein, PEA-15
5147	17668		1.09	2.0E-26	AF073482.1	NT	Homo sapiens myotubularin related protein 7 mRNA, partial cds
10653	23344		2.7	2.0E-26	D87075.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11180	23848	37132	3	2.0E-26	AB01412.1	EST_HUMAN	1058a01.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185418 3' similar to contains Alu
11355	24001		2.45	2.0E-26	AF055088.1	NT	repetitive element/contains element MER20 repetitive element;
12108	24003		1.87	2.0E-26	AF055088.1	NT	Homo sapiens MHC class I region
133	12948	25591	5.18	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2040	14774	27503	1.37	1.0E-26	AL036363.2	EST_HUMAN	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
2693	15402		9.04	1.0E-26	AF281085.1	NT	DKFZp434H1910.1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434H1910 5'
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6740	19574		3.05	1.0E-26	BE165980.1	EST_HUMAN	MRG-110487-150200-113-g01 HIT0487 Homo sapiens cDNA
10809	23482		2.21	1.0E-26	AI038487.1	EST_HUMAN	DKFZ566C2148.1 556 (synonym: hfk22) Homo sapiens cDNA clone DKFZ566C2148.5
12348	25395		3.53	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45.6
7494	20156		1.11	9.0E-27	BF371227.1	EST_HUMAN	RC68-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9203	22082		4.14	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
11875	24454		5.72	9.0E-27	BF445553.1	EST_HUMAN	naa03-07.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:3250644.3 similar to contains OFR.11
10	12837	25450	3.93	9.0E-27	AI031402.1	EST_HUMAN	W49504.x1 NCI_CGAP_P19 Homo sapiens cDNA clone IMAGE:2406150.3 similar to contains THRLb2
544	13327		4.33	8.0E-27	AL163227.2	NT	THR repetitive element ; Homo sapiens chromosome 21 segment HS21C027
1395	14142	26819	59.39	8.0E-27	AW162737.1	EST_HUMAN	ea07108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295.3 similar to gb:K00555
1395	14142	26820	59.39	8.0E-27	AW162737.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN); TUBULIN ALPHA-1 CHAIN (HUMAN);
2184	14593	27826	1.37	8.0E-27	AW654776.1	EST_HUMAN	PM2-SN0018-220300-002-407 SN0018 Homo sapiens cDNA
3160	15943	28594	1.81	8.0E-27	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)(ADENINE
3348	16107	28782	0.81	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5808	18404	31317	1.02	8.0E-27	AW33214.1	EST_HUMAN	AV73214 HIT Homo sapiens cDNA clone HTFBCB06.6
6881	17857		2.83	8.0E-27	BE026560.1	EST_HUMAN	MR4-BT0388-260800-204-008 BT0388 Homo sapiens cDNA
6947	19429	32444	2.29	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751.5 similar to
9109	21797	34981	1.51	8.0E-27	AW657579.1	EST_HUMAN	REPETITIVE ELEMENT L1
9109	21797	34982	1.51	8.0E-27	AW657579.1	EST_HUMAN	CMF-CT0315-051289-058-007 CT0315 Homo sapiens cDNA
688	13444		1.23	7.0E-27	Z70984.1	NT	CMF-CT0315-051289-058-007 CT0315 Homo sapiens cDNA
5030	17750		2.25	7.0E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element HC2
8755	21448		1.19	7.0E-27	D66384.1	NT	h51112.x1 Scores, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2878879.3 similar to TR-076040
10550	23341		4.26	7.0E-27	AD271735.1	NT	Human mRNA for KIA0231 gene, partial cds
12484	24843		2.12	7.0E-27	AW723565.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
10627	23320	36588	2.75	6.0E-27	M26987.1	NT	AV723565 HTB Homo sapiens cDNA clone HTBAHE02.5
11804	24394	37728	1.57	6.0E-27	U93163.1	NT	Human nucleolar protein (B23) mRNA, complete cds Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds

Page 253 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10137	22785	35866	2.82	5.0E-27	BF66614.1	EST_HUMAN	602121491P1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278527 5'
10137	22785	35897	2.82	5.0E-27	BF66614.1	EST_HUMAN	602121491P1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278527 5'
6845	19407	32421	1.95	4.0E-27	6010659	NT	Mus musculus sperm tail associated protein (Slap), mRNA
7840	20535		1.07	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7883	20578		1.34	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9844	22268		0.7	4.0E-27	AW89059.1	EST_HUMAN	QV05-OT0033-070300-152-510 OT0033 Homo sapiens cDNA
11604	24203	37525	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2034	14769	27499	4.81	3.0E-27	X80958.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4238	16979	29604	1.06	3.0E-27	BE071824.1	EST_HUMAN	PMA-810527-060100-001-011 BT0527 Homo sapiens cDNA
5282	18058	30697	6.24	3.0E-27	AA077705.1	EST_HUMAN	7B4C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B4C08
7968	20361	33476	0.63	3.0E-27	BE070351.1	EST_HUMAN	7633D2.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9205	22084	35258	2.93	3.0E-27	BF03527.1	EST_HUMAN	601468531P1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3852086 5'
40	12663	25487	14.84	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1888	14825		5.12	2.0E-27	AA355345.1	EST_HUMAN	nc01b10.61 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000693 similar to gb:M17886 60S
3107	15872		10.39	2.0E-27	AW629172.1	EST_HUMAN	h01b12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976879 3' similar to TR:076040
3218	15981	28632	1.98	2.0E-27	AF111167.2	NT	O759-04 ORF2: FUNCTION UNKNOWN. ; Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3218	15981	28633	1.98	2.0E-27	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4009	16755	29385	1.36	2.0E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
5571	19340	32353	0.61	2.0E-27	H02655.1	EST_HUMAN	Y8560.1.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to SP-HMGQ_MOUSE C02591 HOMEBOX PROTEIN ;
7889	20884	33810	1.95	2.0E-27	AI886347.1	EST_HUMAN	w28907.x1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:2426268 3'
9169	21839		2.3	2.0E-27	AA851527.1	EST_HUMAN	h01b05.61 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1943737 similar to contains L1, L1, L1 repetitive element ;
9891	22342	35538	0.76	2.0E-27	X80658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
9835	22583	35782	1.28	2.0E-27	M76580.1	EST_HUMAN	EST007338 Fetal brain, Striatum (cat#636206) Homo sapiens cDNA clone HFBCF07
5835	22653	35793	1.28	2.0E-27	M76580.1	EST_HUMAN	EST007338 Fetal brain, Striatum (cat#636206) Homo sapiens cDNA clone HFBCF07
10875	23555	36802	4.11	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1.000746 5'
11469	14625		3.31	2.0E-27	AA355345.1	EST_HUMAN	nc01b10.61 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000693 similar to gb:M17886 60S
426	13212		1.51	1.0E-27	AL163249.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21C049

Page 254 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
978	13741	28404	1.34	1.0E-27	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4081	18006		0.98	1.0E-27	BE360127.1	EST_HUMAN	h05g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.53
6449	19217	32215	0.26	1.0E-27	6005955	NT	MER29 repetitive element;
6771	19515	32542	1.06	1.0E-27	F30158.1	EST_HUMAN	Homo sapiens Raf1a-derived POU-domain factor-1 (RPF-1), mRNA
6771	19515	32542	1.06	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
8508	21200	34346	0.98	1.0E-27	AB007823.1	NT	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
8854	21575		2.26	1.0E-27	BE079780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9822	22275	35463	2.55	1.0E-27	D87448.1	EST_HUMAN	ROC-BT0027-140200-071-E08 BT0027 Homo sapiens cDNA
11704	24299	37025	3.51	1.0E-27	AF111083.1	NT	Human mRNA for KIAA0280 gene, partial cds
137	12951		2.84	9.0E-28	BE348389.1	EST_HUMAN	Bos taurus latrophilin 3 splice variant b3h mRNA, complete cds
303	13107	25747	3.31	9.0E-28	AU126280.1	EST_HUMAN	hwt7c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3163188 3' similar to TR:Q07314 Q07314
10299	22837	36150	0.83	9.0E-28	AA174078.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C-RECURSOR, [3] TR:Q07280 TR:Q07313;
11951	24504		4.85	9.0E-28	BF377859.1	EST_HUMAN	ZP18g12.s1 Stragene fetal retina B37202 Homo sapiens cDNA clone NT2RP1000443 5'
12298	25245		2.48	8.0E-28	AW167671.1	EST_HUMAN	CM2-TN0140-070500-372-g01 TN0140 Homo sapiens cDNA
1153	13813	26576	7.89	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00094 Homo sapiens cDNA clone IMAGE:2782611 3' similar to
11142	23809	37089	3.38	7.0E-28	11417868	NT	TR:Q06902 Q66002 KIAA0555 PROTEIN, contains element MER22 repetitive element;
11910	24474		2.78	7.0E-28	AV735348.1	EST_HUMAN	AU142750 Y79AAT1 Homo sapiens cDNA clone Y79AAT1000824 5'
8817	21609		0.97	6.0E-28	AF016052.1	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12526	24073		2.35	6.0E-28	AA504582.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
310	13114		4.19	5.0E-28	AB21003.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
3960	16738	29372	1.44	6.0E-28	B79782.1	EST_HUMAN	aa00403.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains ALU
2631	15343	26087	1.68	4.0E-28	AW165065.1	EST_HUMAN	repetitive element/contains element PTR6 repetitive element;
2076	15742	28380	0.78	4.0E-28	4503316	NT	w018c07.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2455992 3' similar to contains THR.b1
3106	15871	28511	2.62	4.0E-28	BE409100.1	EST_HUMAN	THR repetitive element;
7230	18815	32988	1.69	4.0E-28	AI198941.1	EST_HUMAN	Y89F10.1 Source placenta NB2HP Homo sapiens cDNA clone IMAGE:148443 5'
							XN3G09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2865504 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-98;
							Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300733F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635306 5'
							q668f10.x1 Source testis NIH_T01 Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19603 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

Page 255 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10774	23457		3.08	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10928	23008		17.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10950	19916	32588	4.76	4.0E-28	AI198941.1	EST_HUMAN	q66f10.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12312	24734		1.84	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
1260	14009		2.88	3.0E-28	AF15582.1	NT	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5051	17770		1.05	3.0E-28	AF089860.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S9A2 to TORBV12S2 region
8728	21419	34592	1.89	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-073-109 HT0713 Homo sapiens cDNA
10653	23533	36778	2.09	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12344	24751		3.62	3.0E-28	AI811991.1	EST_HUMAN	w9807.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
87	12913	25551	10.6	2.0E-28	BE062197.1	EST_HUMAN	RC4-BT0254-220300-019-505 BT0254 Homo sapiens cDNA
1023	13783	28444	0.85	2.0E-28	4801912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1142	13897	26558	18.03	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2481	15189	27839	2.1	2.0E-28	AI348534.1	EST_HUMAN	q35806.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
6215	18889	31966	1.33	2.0E-28	BF22402.1	EST_HUMAN	ht76c03.x1 NCL CGAP_KW11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
6238	19012		5.07	2.0E-28	BF212905.1	EST_HUMAN	601814166F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
7843	20338	33766	0.71	2.0E-28	AF003273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9484	22137		5.54	2.0E-28	AW972305.1	EST_HUMAN	EST1364394 MAGE resequences, MAGL Homo sapiens cDNA
11614	24212	37536	1.84	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12322	24741		2.22	2.0E-28	H06378.1	EST_HUMAN	Y79c09.1 Homo sapiens infant brain INIB Homo sapiens cDNA clone IMAGE:44300 5'
1461	14208	28895	2.84	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2217	14945	27685	2.37	1.0E-28	BF333239.1	EST_HUMAN	QVH-BT0821-120900-360-503 BT0821 Homo sapiens cDNA
7759	20455		3.2	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC630391) mRNA
7917	20812		3.3	1.0E-28	8622793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9176	21848	35014	4.84	1.0E-28	AA308744.1	EST_HUMAN	EST179616 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to similar to retinoid LTR
9778	22427		8.73	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9778	22427	35834	8.73	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA

Page 256 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10422	23068		0.63	1.0E-28	AU149356.1	EST_HUMAN	AU149356 NT2RM4 Homo sapiens cDNA clone NT2RM4002146 3'
11915	24478		7.79	1.0E-28	AA054182.1	EST_HUMAN	Z51601.11 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:380448 5'
12651	28143		1.88	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12749	28346	30803	3.18	9.0E-29	AW663987.1	EST_HUMAN	h17g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878266 3'
12436	24806		3.32	8.0E-29	Q00130	SWISSPROT	HYPOPHYSICAL GENE 58 PROTEIN
1588	14344	27034	1.37	7.0E-29	AW668447.1	EST_HUMAN	EST1378221 MAGE sequences, MAGE Homo sapiens cDNA
12794	28045		7.13	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 46 kDa secretory protein, partial
581	13361	25889	16.66	6.0E-29	AB93748.1	EST_HUMAN	wb58001.x1 NCL CGAP_Brc25 Homo sapiens cDNA clone IMAGE:2465895 3' similar to TR:O15475
12201	24669		8.09	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN contains LTR7 b1 LTR7 repetitive element ;
12286	24717		1.72	6.0E-29	BF556037.1	EST_HUMAN	RC3-UT0082-210800-021-05 UT0082 Homo sapiens cDNA
8630	21322		5.36	6.0E-29	AW887541.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
3226	15959		1.84	4.0E-29	AT52367.1	EST_HUMAN	RC3-OT0091-170300-011-512 OT0091 Homo sapiens cDNA
5919	18704		7.81	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBc_cm15c02 random
7878	20874	33787	0.55	4.0E-29	AB78101.1	EST_HUMAN	GV14T0471-280300-121-ab5 HT0471 Homo sapiens cDNA
7979	20874	33798	0.55	4.0E-29	AB78101.1	EST_HUMAN	MER29.12 MER29 repetitive element ;
6644	21326	34480	6.21	4.0E-29	AB04988.1	NT	MER29.12 MER29 repetitive element ;
4381	17118	29751	1.4	3.0E-29	AB042287.1	NT	Human 80 kD heat shock protein gene, complete cds
4684	17418	30054	1.07	3.0E-29	BF333286.1	EST_HUMAN	Homo sapiens PIS gene for 6-pyruvylated hydrolytic synthesis, complete cds
6841	18629	31554	1.18	3.0E-29	BE314018.1	EST_HUMAN	GV1-8T0821-120900-360-b03 BT0821 Homo sapiens cDNA
6832	21324	34465	2.87	3.0E-29	D38044.1	NT	601162657F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350527 5'
9200	21869	35034	1.69	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
9431	22109		1.87	3.0E-29	AL169246.2	NT	x17703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
9859	22509		0.81	3.0E-29	BE350127.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
11255	23698	37185	1.47	3.0E-29	AA040083.1	EST_HUMAN	MER29 repetitive element ;
12102	24600		1.53	3.0E-29	D63882.1	NT	369201.f1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
12789	25376		7.53	3.0E-29	AA016177.1	EST_HUMAN	G1335769 GAG-POL POLYPOLYPROTEIN ;
480	13265	25900	1.72	2.0E-29	AF084898.1	NT	Human HELIM18 mRNA for HELIM18, complete cds
							z632e09.s1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:360712 3'
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

Page 257 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
480	13265	26901	1.72	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIG-6 (env) gene, complete cds
1523	14270	26955	6.62	2.0E-29	A063804.1	EST_HUMAN	w65d10.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR-O15548 O15546 HERV-E ENVELOPE GLYCOPROTEIN;
1623	14270	26956	6.62	2.0E-29	A063804.1	EST_HUMAN	w65d10.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR-O15548 O15546 HERV-E ENVELOPE GLYCOPROTEIN;
4248	16967	29610	1.63	2.0E-29	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068 ca71e04.x1 NCI CGAP_G02 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element;
5735	18527	31449	0.99	2.0E-29	A092459.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356960 3' similar to contains element MER6 repetitive element;
6037	18865	31830	1.48	2.0E-29	A1806418.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356960 3' similar to contains element MER6 repetitive element;
7459	18865	31830	1.36	2.0E-29	A1806418.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356960 3' similar to contains element MER6 repetitive element;
7876	20571	33693	1.16	2.0E-29	BE967157.1	EST_HUMAN	6014422D6F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
8471	21169	34313	0.63	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
8471	21169	34314	0.63	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
9408	22070	35241	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9408	22070	35242	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	35999	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	36000	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10877	23567	36804	1.31	2.0E-29	BF025947.1	EST_HUMAN	60166934F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952833 5'
11469	24063		2.04	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnal (SPF51), mRNA
11469	24100		1.73	2.0E-29	AW680701.1	EST_HUMAN	QV0-010032-090300-165-401 OT0032 Homo sapiens cDNA
8691	21383	34627	7.37	1.0E-29	AW198380.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10518	23164	36391	0.65	1.0E-29	X60658.1	NT	R. rattus RV43 mRNA for a potential ligand-binding protein
6437	19284	32255	2.97	9.0E-30	AA761216.1	EST_HUMAN	r220c07.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1268332 3' similar to contains MER4.b1 MER4 repetitive element;
11692	24631		1.76	9.0E-30	11422745	NT	Homo sapiens zincfin regulated transporter-like (ZRTL), mRNA
6227	19001		8.94	8.0E-30	F06688.1	EST_HUMAN	HSC22AF51 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
8193	20862	33994	3.72	8.0E-30	AA338373.1	EST_HUMAN	EST197317 Thyms1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
8593	21275	34412	3.1	8.0E-30	AI557072.1	EST_HUMAN	PT21.13 B11 tumor2 Homo sapiens cDNA 3'
1505	14281		1.03	7.0E-30	BE097133.1	EST_HUMAN	PM4-910724-150400-004-dt1 B10724 Homo sapiens cDNA
1766	14508	27209	1.79	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3165	15948	28598	2.3	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-112 BN0147 Homo sapiens cDNA
10437	23083	36310	0.48	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen sec2-10 mRNA, partial cds

Page 258 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12769	17897		3.38	6.0E-30	X51765.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3604	16742	29378	26.19	5.0E-30	AJ369992.1	EST_HUMAN	hg9203.x1 NCI_CGAP CLL7 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
6160	25178		6.44	5.0E-30	U97931.1	NT	Human acornitase hydrolase (ACOT2) gene, exon 7
10802	23485		1.95	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11103	23773	37047	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11103	23773	37048	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2139	14869	27559	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-060200-060-c06 DT0043 Homo sapiens cDNA
2139	14869	27600	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-060200-060-c06 DT0043 Homo sapiens cDNA
6758	17925	30560	0.63	4.0E-30	P11389	SWISSPROT	RETROVIRUS RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8803	21495	34541	2.82	4.0E-30	AW812488.1	EST_HUMAN	ENDONUCLEASE1
1129	13885		2.11	3.0E-30	AJ338551.1	EST_HUMAN	CM1-ST0181-081199-035-08 ST0181 Homo sapiens cDNA
3740	16493	28128	0.93	3.0E-30	AF128933.1	EST_HUMAN	qg9305.x1 Scores: total: 162528.9w Homo sapiens cDNA clone IMAGE:193820 3' similar to contains MER29.b2 MER29 repetitive element;
7852	20547		0.58	3.0E-30	AF078779.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-9
8385	21078		0.48	3.0E-30	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10333	22980	35200	1.7	3.0E-30	BE350127.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10465	23111	36342	0.63	3.0E-30	AB032689.1	NT	h0901.x1 NCI_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER29 b3 MER29 repetitive element;
10465	23111	36343	0.63	3.0E-30	AB032689.1	NT	h0901.x1 NCI_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER29 b3 MER29 repetitive element;
11168	23835	37116	2.48	3.0E-30	P34056	SWISSPROT	TRANSSCRIPTION FACTOR AP-2
660	13436	26077	0.92	2.0E-30	AW857315.1	EST_HUMAN	CMO-CT0307-370100-188-H03 CT0307 Homo sapiens cDNA
1062	13920		3.11	2.0E-30	F08688.1	EST_HUMAN	HSC23.F051 normalized infant brain cDNA Homo sapiens cDNA
1482	14209	26596	5.31	2.0E-30	BE175977.1	EST_HUMAN	RC8-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2720	14427	28165	8	2.0E-30	BE76232.1	EST_HUMAN	IL2-NT0101-280703-116-E04 NT0101 Homo sapiens cDNA
2920	10586	28531	6.39	2.0E-30	AF114195.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3769	19521	28160	2.26	2.0E-30	AW205391.1	EST_HUMAN	U1H-B1-ato-c-72-U1.x1 NCI_GAP Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4727	17459	30095	1.51	2.0E-30	BE268945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4727	17459	30095	1.51	2.0E-30	BE268945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6660	19420	32435	0.56	2.0E-30	BF500337.1	EST_HUMAN	601593208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138983 5'
8375	21068	34208	0.48	2.0E-30	AA011103.1	EST_HUMAN	2a9b10.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:3681188 5'
8435	21128	34265	4.66	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TF-ujwera) Homo sapiens cDNA clone GEN-570C01 5'

Page 259 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8533	21225	34366	3.61	2.0E-30	BE970617.1	EST_HUMAN	7637c12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284892 3' similar to SW:DHSA_HUMAN P31040 SUCONATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8533	21225	34367	3.61	2.0E-30	BE970617.1	EST_HUMAN	7637c12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284892 3' similar to SW:DHSA_HUMAN P31040 SUCONATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
9897	22547	35741	3.62	2.0E-30	AW971693.1	EST_HUMAN	h333d06.x1 NCI CGAP Kld12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR b3 THR repetitive element ;
8982	22630	35839	7.37	2.0E-30	AW470781.1	EST_HUMAN	C18639 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN:570C01 5'
280	13087	25729	18.33	1.0E-30	C18639.1	EST_HUMAN	C18639 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1 b3 MER1 MERT repetitive element ;
525	13309	25842	2.34	1.0E-30	AW488897.1	EST_HUMAN	h33b04.x1 Scores NF1_T_OBC_S1 Homo sapiens cDNA clone IMAGE:570C01 5'
699	13474	26122	2.62	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2209	14637	27675	7.16	1.0E-30	AA864377.1	EST_HUMAN	sc77b08.s1 Stratiogene lung (#637210) Homo sapiens cDNA clone IMAGE:888599 3'
2464	15182	27821	2.01	1.0E-30	BF447728.1	EST_HUMAN	602022560.F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4157981 5'
3030	15816	28461	0.94	1.0E-30	A4315045.1	EST_HUMAN	EST196989 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7824	20290	33369	2.48	1.0E-30	BF163230.1	EST_HUMAN	60160692.F1 NIH JMG2_18 Homo sapiens cDNA clone IMAGE:404684 5'
12581	25268	29135	0.85	1.0E-30	H56593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3748	16501	29135	0.81	9.0E-31	173025.1	EST_HUMAN	yc65d06.r1 Stratiogene liver (#637224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	16501	29135	0.81	9.0E-31	173025.1	EST_HUMAN	yc65d06.r1 Stratiogene liver (#637224) Homo sapiens cDNA clone IMAGE:85570 5'
8223	20917	34053	0.81	9.0E-31	R18214.1	EST_HUMAN	Y69308.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:U12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8223	20917	34054	0.81	9.0E-31	R18214.1	EST_HUMAN	Y69308.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:U12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8522	21214	34054	1.63	9.0E-31	Z38293.1	EST_HUMAN	RELATD PROTEIN RAB-2 (HUMAN);
8524	21216	34369	0.48	9.0E-31	AF078779.1	NT	HSC06F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
1054	13813	26473	2.41	8.0E-31	88223389	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
2414	15135	30214	4.6	8.0E-31	AL163208.2	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
4881	17560	30214	1.43	8.0E-31	P23275	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
4881	17560	30214	1.43	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
2874	15383	28123	3.29	7.0E-31	BES28517.1	EST_HUMAN	hw05t11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2874	15383	28123	3.29	7.0E-31	BES28517.1	EST_HUMAN	hw05t11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8300	20984	34130	0.86	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8300	20984	34131	0.86	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds

Page 260 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9166	21836		0.84	7.0E-31	BE40861.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12434	24805	31044	2.28	7.0E-31	X61785.1	NT	Human lambda-bi-immunoglobulin constant region complex (germline)
3657	16420		2.68	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8053	20747		4.37	6.0E-31	A505068.1	NT	Homo sapiens MHC class I region
8229	20923	34082	0.86	6.0E-31	BE350127.1	EST_HUMAN	hdb901.X1 NCI_CGAP_K013 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.03
12169	25195		1.99	6.0E-31	BE994488.1	EST_HUMAN	MER29 repetitive element;
187	13000	26540	3.59	5.0E-31	M60594.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
187	13000	26541	3.58	5.0E-31	M60594.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8344	21037		0.73	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
582	13362		5.18	4.0E-31	AJ271735.1	NT	706004.X1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR-Q18537 Q15337 SIMILAR TO POGO ELEMENT; contains L1/L1 repetitive element;
							Homo sapiens Xq pseudautosomal region; segment 1/2
1608	14352	27040	0.91	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN LUDP
1810	14550		1.57	4.0E-31	AL05280.2	NT	ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
2792	15487		1.23	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T)
12205	24672		1.88	4.0E-31	AJ230125.1	NT	Homo sapiens chromosome 21 segment HS21C080
12457	24826		1.88	4.0E-31	11430273	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens GGT1 gene, exon 1
							Homo sapiens KIA0369 gene product (KIA0369), mRNA
7238	18924	32999	12.23	3.0E-31	4825853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH) (NDUFB8) mRNA
7393	20072	33161	1.28	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8091	20765		2	3.0E-31	AL05200.2	NT	Homo sapiens chromosome 21 segment HS21C086
8479	22132	35312	3.7	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10468	23144	36371	0.84	3.0E-31	AA421242.1	EST_HUMAN	z06604.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731047 5'
10527	23224	36459	2.04	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11101	23771		3.95	3.0E-31	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3862085 5'
12819	25059		1.68	3.0E-31	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
1910	14647	27358	1.37	2.0E-31	AW83917.1	EST_HUMAN	QV24.T0051-263300-114-03.L1 T0051 Homo sapiens cDNA
2211	14939	27077	1.09	2.0E-31	AJ39388.1	EST_HUMAN	10449031 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:211672 3'
2339	15062	27800	1.88	2.0E-31	AL119245.1	EST_HUMAN	DKF26761G1613.J1 T61 (synonym: hamy2) Homo sapiens cDNA clone DKF26761G1513 5'
							aa891.1.31 Streptococcus felis relina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
2442	15161	27898	4.01	2.0E-31	AA458824.1	EST_HUMAN	THR12 THR repetitive element;

Page 261 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5193	18001	36624	0.81	2.0E-31	AW444468.1	EST_HUMAN	UHH-B3-ab5-f48-0-0-1-5' NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738833 3'
5624	18421	31334	3.57	2.0E-31	BE350127.1	EST_HUMAN	H090701.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_b3 MER28 repetitive element;
8875	21685		2.05	2.0E-31	AA87764.1	EST_HUMAN	nc0004.s1 NCL CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR-Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9107	21785	34859	3.84	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
8908	22457	36661	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUALB07 5'
8900	22457	36661	0.84	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUALB07 5'
8975	22623	35829	2.35	2.0E-31	BE40881.1	EST_HUMAN	601304.125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3538310 5'
8975	22623	35830	2.35	2.0E-31	BE40881.1	EST_HUMAN	601304.125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3538310 5'
12144	24632		1.58	2.0E-31	AF148812.1	NT	Homo sapiens hexokinase II gene, promoter region
12279	25413		1.75	2.0E-31	AI114627.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA (MAGE-B1) genes, complete cds
15	12842	25459	11.09	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1653	14404	27092	1.35	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27093	1.35	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27094	1.35	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4592	17327	29952	1.16	1.0E-31	AL134376.1	EST_HUMAN	DKFZ647B235_11 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ647B235 5'
4592	17327	29953	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZ647B235_11 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ647B235 5'
5210	18018	30640	3.79	1.0E-31	AW397679.1	EST_HUMAN	MR3-S10220-151299-028-c08_1 ST0220 Homo sapiens cDNA
6042	18622	31762	2.2	1.0E-31	AF048727.1	NT	Homo sapiens mitochondrial ccb1 repeat region
7189	19876	32948	1	1.0E-31	AF128145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10136	22784	35895	0.51	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10833	23515	36757	2.7	1.0E-31	AD86434.1	EST_HUMAN	qf2103.x1 NCL CGAP_Bir26 Homo sapiens cDNA clone IMAGE:1750769 3' similar to TR-Q10595 Q10595 FRAXIN.;
11830	24414	37752	1.48	1.0E-31	U08081.1	NT	Human germ-line T-cell receptor beta chain, TCRCV17S1A1T, TCRCV2S1, TCRCV10S1P, TCRCV28S1P, TCRCV16S1P, TCRCV15S1, TCRCV14S1A1T, HVB relic, TCRCV28S1P, TCRCV34S1, TCRCV14S1, TCRCV35S1, TCRCV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRCV1T, TCRCV1S2>
6942	18007	32312	2.38	9.0E-32	AV723976.1	EST_HUMAN	AV723976 H1B Homo sapiens cDNA clone HTBAAG01 5'
7492	20164		0.66	9.0E-32	11430322	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2070	14802	27530	2.48	8.0E-32	AD058770.1	EST_HUMAN	cc15609.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675394 3'

Page 262 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5394	18164	30887	0.97	8.0E-32	AW97214.1	EST_HUMAN	RC2-BN048-20300-015-04 BN048 Homo sapiens cDNA
4807	17538	30161	0.98	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KO) (P145)
12122	24814		8.18	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin (Ig) gene, part, with 5' breakpoint between cytosin and neighbouring non-amplified region
2735	15442	28180	1.01	6.0E-32	AI478104.1	EST_HUMAN	Imd34r10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159894 3' similar to contains MER29.13 MER29 repetitive element;
7263	16950		1.47	6.0E-32	BE686018.1	EST_HUMAN	601811530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3813087 5'
1011	13771	29431	18.78	5.0E-32	AF116027.1	NT	Homo sapiens PRO1181 mRNA, complete cds
910	13677		1.76	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
5148	17687		0.91	4.0E-32	AI685593.1	EST_HUMAN	w08h12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496847 3' similar to contains MER18.53
7503	20174	33266	2.94	4.0E-32	11432574	NT	MER18 repetitive element;
7503	20174	33267	2.94	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8257	20951		1.2	4.0E-32	BE094410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
443	13228	25872	3.7	3.0E-32	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1437	14184	26870	8.08	3.0E-32	AV731600.1	EST_HUMAN	AV731600 HTF Homo sapiens cDNA clone HTFAK07 5'
9294	21991	35135	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BM/FBHH12 5'
9294	21967	35136	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BM/FBHH12 5'
10843	23525	36768	3.57	3.0E-32	AA777621.1	EST_HUMAN	z05a07.s1 Scores_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR3 THR repetitive element;
12148	24534		3.51	3.0E-32	BE276068.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138701 5'
12507	17699	30586	2.97	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (Drosophila) homolog, translocated to, 4 (MLLT4) mRNA
12507	17699	30587	2.97	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (Drosophila) homolog, translocated to, 4 (MLLT4) mRNA
12658	24956		2.27	3.0E-32	BE276068.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138701 5'
6158	16935	31902	0.81	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6387	19156	32155	5.32	2.0E-32	Z38133.1	NT	H-sapiens mRNA for myosin
6387	19156	32156	5.32	2.0E-32	Z38133.1	NT	H-sapiens mRNA for myosin
8176	20370	34003	2.26	2.0E-32	AA114294.1	EST_HUMAN	z06a08.r1 Stragene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8176	20370	34004	2.26	2.0E-32	AA114294.1	EST_HUMAN	z06a08.r1 Stragene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
11859	24443	37784	2.06	2.0E-32	T18862.1	EST_HUMAN	bt20561 testis 1 Homo sapiens cDNA clone b12056
12763	25022	30961	2.42	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'

Page 263 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12763	25022	30862	2.42	2.0E-33	AY738446.1	EST_HUMAN	AY738446 CB Homo sapiens cDNA clone CBFA08 5'
3060	16955		1.07	1.0E-32	BE743269.1	EST_HUMAN	501879207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6855	16437	32463	7.02	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8494	21188	34326	8.08	1.0E-32	AA720574.1	EST_HUMAN	nv2192.81 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THRL3 THP repetitive element;
3474	16230		4.58	9.0E-33	BE327112.1	EST_HUMAN	hm07605.x1 NCI_CGAP_Luz4 Homo sapiens cDNA clone IMAGE:3182218 3' similar to TRC088539 O88539 WW DOMAIN BINDING PROTEIN 11;
6326	19069		4.05	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8887	21379	34623	1.96	9.0E-33	BF347280.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
10701	23392		5.22	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
58	12887	25517	3.14	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
68	12887	25518	3.14	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2168	14888	27622	2.29	7.0E-33	AI590115.1	EST_HUMAN	tor2809.x1 NCI_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2856	16385		6.46	7.0E-33	AY730058.1	EST_HUMAN	AY730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
3236	16998		9.3	7.0E-33	AW671307.1	EST_HUMAN	EST383396 MAGE resequences, MAGE Homo sapiens cDNA
8845	21637		1.56	7.0E-33	X64850.1	NT	Human NLRP mRNA for leukocyte common antigen-related papillate (protein-tyrosine phosphatase) (EC 3.1.3.48)
10732	23419	36660	2.41	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
11213	23876	37162	1.93	7.0E-33	AW671588.1	EST_HUMAN	EST383396 MAGE resequences, MAGE Homo sapiens cDNA
12127	24619	31090	4.34	7.0E-33	AA601416.1	EST_HUMAN	not6h01.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element;
3720	16473		0.94	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5976	18758	31720	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
5976	18758	31720	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8478	21170	34315	9.33	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8903	21295	34438	3.09	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9910	22559	35754	1.12	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
9910	22559	35755	1.12	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1770	14512		1.46	6.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-402 FT0169 Homo sapiens cDNA
1874	14612		1.19	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1891	14628	27337	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1891	14628	27338	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

Page 264 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2270	14393		1.29	5.0E-33	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
10148	22768	36010	0.8	5.0E-33	AW264678.1	EST_HUMAN	qx33111.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10148	22768	36011	0.8	5.0E-33	AW264678.1	EST_HUMAN	qx33111.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1106	13953		2.16	4.0E-33	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2121	14852	27581	1.84	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2419	15140		2.02	4.0E-33	AA628921.1	EST_HUMAN	af51511.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains AU repetitive element; contains MER28.b2 MER28 repetitive element ;
2547	15292	27898	4.15	4.0E-33	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4450	17186	26811	2.15	4.0E-33	AW263349.1	EST_HUMAN	U1-H-B12-ah1-c03-0-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	16122	30779	24.73	4.0E-33	AA035053.1	EST_HUMAN	z71408.1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:510038 5' similar to
6289	18072	32057	0.87	4.0E-33	8383994	NT	glx12871.m1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6289	18072	32058	0.87	4.0E-33	8383994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1067	13825		5.5	3.0E-33	BE350127.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1068	13825		3.89	3.0E-33	BE350127.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
2451	15695		0.82	3.0E-33	AV647851.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10338	22895	36203	1.04	3.0E-33	AA881610.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
102	12843		3.21	2.0E-33	AI160189.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
4385	17122		6.39	2.0E-33	BE159039.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
4925	17653	30285	28.91	2.0E-33	AA626683.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5033	17753	30386	2.75	2.0E-33	11421332	NT	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5033	17753	30386	2.75	2.0E-33	11421332	NT	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6329	18059	32087	1.81	2.0E-33	AI27482.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
8988	21693		2.18	2.0E-33	AI052256.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10513	23159	36384	1.48	2.0E-33	11421332	NT	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10513	23159	36385	1.48	2.0E-33	11421332	NT	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11046	23716	36985	1.26	2.0E-33	AA453847.1	EST_HUMAN	h059p1.x1 NCL CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3

Page 265 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8	12835		1.16	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5166	17873	30485	2.48	1.0E-33	4502556	NT	Homo sapiens calcitriol/calcimodulin-dependent protein kinase IV (CAMK4) mRNA
5601	18269	31108	0.58	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7307	19390	33087	1.04	1.0E-33	M13975.1	NT	Homo sapiens protein kinase G beta-II type (PRKG2) mRNA, complete cds
9820	28432		0.84	1.0E-33	U06822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11282	23953	37281	1.83	1.0E-33	AW098818.1	EST_HUMAN	QV3-BN0047-200200-102-303 BN0047 Homo sapiens cDNA
11603	24259	37581	3.32	1.0E-33	U08022.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12407	24780		2.21	1.0E-33	A027191.1	EST_HUMAN	w889c05.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2452410.3
12570	12835		4.07	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12802	24914	31005	1.41	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCNC12.5
12780	25034		1.61	6.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2168	14897	27631	0.68	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
7659	20343	33466	0.66	8.0E-34	BE089882.1	EST_HUMAN	MR4BT0399-200100-001-H03 BT0399 Homo sapiens cDNA
1426	14173	28858	2.27	7.0E-34	T70943.1	EST_HUMAN	y015e05.r1 Soares fetal liver spleen cDNA clone IMAGE:108320.5
8900	14173	28858	0.66	7.0E-34	T70943.1	EST_HUMAN	y015e05.r1 Soares fetal liver spleen cDNA clone IMAGE:108320.5
12191	24902		3.05	7.0E-34	H12806.1	EST_HUMAN	y14c10.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:148722.5
458	13243	25884	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
458	13243	25885	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
12011	24644	31107	2.13	6.0E-34	U03885.1	NT	Mus musculus DAB2/2 hair-specific (hcd-1) gene
1873	14811		2.9	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5002	17725	30328	3.91	6.0E-34	U30893.1	NT	Human epigenetic factor SRP55-1 (SRP55-1) mRNA, complete cds
8765	21457	34507	1.37	5.0E-34	AF078178.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10550	23348	36482	2.24	5.0E-34	AB037858.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11219	23882		1.78	5.0E-34	AI163203.2	NT	Homo sapiens chromosome 21 segment HS21C009
1991	14727	27449	1.84	4.0E-34	AB04897.1	EST_HUMAN	1994c06.x1 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:2249184.3
5770	18591	31488	0.94	4.0E-34	AA081773.1	EST_HUMAN	ak35c01.r1 Soares testis cDNA clone IMAGE:1407936.3
8936	21627	34769	1.26	4.0E-34	BF209778.1	EST_HUMAN	60187480P1 NIH MGC 54 Homo sapiens cDNA clone IMAGE:4102213.5
6133	16516	31886	0.78	3.0E-34	M37277.1	NT	Human Ig gamma H-chain D-region genes, partial cds
11100	23710		3.14	3.0E-34	BF05327.1	EST_HUMAN	60145553F1 NIH MGC 58 Homo sapiens cDNA clone IMAGE:3862088.5
8950	21541	34697	1.16	2.0E-34	AI678101.1	EST_HUMAN	wd35g06.x1 Soares NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2330170.3 similar to contains MER28.12 MER29 repetitive element;

Page 266 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8850	21541	34688	1.16	2.0E-34	A1678101.1	EST_HUMAN	wc35g06.x1 Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
11113	23783	37057	1.34	2.0E-34	P51805	SWISSPROT	MER2912 MER29 repetitive element ;
11113	23783	37058	1.34	2.0E-34	P51805	SWISSPROT	PLEXN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1494	14241	28928	6.53	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLATOR 3) (ANT 3)
3993	16416	29055	1.32	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arthralgia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4051	16706	29425	0.97	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4051	16706	29426	0.97	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4449	17182	31788	3.44	1.0E-34	BE5071414.1	EST_HUMAN	RC2-B10508-240403-916-h08 B10508 Homo sapiens cDNA
6047	18827	31789	2.05	1.0E-34	BE874952.1	EST_HUMAN	601484430F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3886999 5'
9225	21904	35076	0.45	1.0E-34	P23266	SWISSPROT	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9595	22249	35434	7.71	1.0E-34	AL036635.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN F6
11138	23805	37083	1.39	1.0E-34	BE781780.1	EST_HUMAN	DKFZ564A1563.1 564 (synonym: MR2) Homo sapiens cDNA clone DKFZ564A1563 5'
11138	23805	37084	1.39	1.0E-34	BE781780.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11153	23820	37100	1.82	1.0E-34	11439598	NT	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
12372	25350		1.65	1.0E-34	AA807097.1	EST_HUMAN	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12553	24949		4.22	1.0E-34	AL163210.2	NT	cc31c11.1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb-X68203
3539	16389	28028	1.2	9.0E-35	AW663302.1	EST_HUMAN	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
219	13028		7.71	6.0E-35	6031160	NT	Homo sapiens chromosome 21 segment HS21C010
1730	14472	27171	3.43	8.0E-35	BF599937.1	EST_HUMAN	hm77006.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2668787 5'
1730	14472	27172	3.43	8.0E-35	BF599937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
4814	17545	30170	2.69	8.0E-35	BF183195.1	EST_HUMAN	hm33a08.x1 NCI CGAP K1d11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
10599	23283	36522	2.42	8.0E-35	BE378480.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
121189	24611		3.95	8.0E-35	BF596282.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
6953	19162	32163	2.05	7.0E-35	11425417	NT	60123648F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
1391	14136	28815	1.83	6.0E-35	AA757115.1	EST_HUMAN	60218492T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
1860	14696	27409	2.09	6.0E-35	6005975	NT	Homo sapiens phosphatidylinositol glycan class L (PIGL), mRNA
4030	16775	29405	0.84	6.0E-35	AW297191.1	EST_HUMAN	hm53R03.x1 Source_fetus_NHT Homo sapiens cDNA clone 1306387 3'
							Homo sapiens zinc finger protein 208 (ZNF208), mRNA
							U1-H-BWO-ajd-4-09-0-U1.s1 NCI CGAP_Su66 Homo sapiens cDNA clone IMAGE:2731433 3'

Page 287 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7798	20493	33615	3.84	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8610	21302	34445	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8610	21302	34449	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9555	22218	35403	0.88	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0358 gene, partial cds
9803	22464	35555	3.17	6.0E-35	AB037788.1	NT	Homo sapiens mRNA for KIAA1355 protein, partial cds
1704	14447	27146	1.36	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2187	15482	28232	1.07	5.0E-35	AB007886.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3008	16776	28424	1.7	5.0E-35	6912639	NT	Homo sapiens RING1 and YY1 binding protein (RYBP), mRNA
4376	17113	29746	1.7	5.0E-35	AF023288.1	NT	Homo sapiens cdk2 kinase (CLK2), protein; cdk2, glucocorticoidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoidase pseudogene; and thymopendin3 (THBS3) gene, partial cds
8084	20778		3.99	5.0E-35	BE800992.1	EST_HUMAN	601431084FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917729 5'
8109	20803	33936	2.35	5.0E-35	AI208765.1	EST_HUMAN	6038405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
8109	20803	33937	2.35	5.0E-35	AI208765.1	EST_HUMAN	6038405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
11130	23798		2.46	5.0E-35	AA001786.1	EST_HUMAN	2184102.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428016 5'
1413	14161	26846	16.86	4.0E-35	BE257607.1	EST_HUMAN	601109719FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3390405 5'
1811	14561	27265	4.87	4.0E-35	H91193.1	EST_HUMAN	Y498407.r1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTRS repetitive element ;
4753	17485		0.72	4.0E-35	AF03528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7108	19706		1.81	4.0E-35	BE350127.1	EST_HUMAN	h09501.x1 NCJ_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER28.b3 MER29 repetitive element ;
8416	21109	34248	8.88	4.0E-35	AL045598.1	EST_HUMAN	DKFZp434L148.r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434L148 5'
11729	24322	37846	1.78	4.0E-35	AW303317.1	EST_HUMAN	X71703.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER18.12 MER19 repetitive element ;
1573	14320	27006	7.78	3.0E-36	BE288182.1	EST_HUMAN	801125260FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345093 5'
2330	15055		1.5	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5256	18062	30690	31.47	3.0E-35	BF433100.1	EST_HUMAN	7c25509.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;
5256	18062	30691	31.47	3.0E-35	BF433100.1	EST_HUMAN	7c25509.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;

Page 268 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6889	22050		1.42	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10074	22722	36593	1.12	3.0E-35	AW003063.1	EST_HUMAN	hnc03a05.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW_P01_1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE];
106	15535	25597	1.88	2.0E-35	N88995.1	EST_HUMAN	K69322 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1165	13610	26582	1.55	2.0E-35	T11009.1	EST_HUMAN	REPETITIVE ELEMENT
2215	14943	27683	5.73	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
3305	16066	28714	1.12	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3305	16066	28715	1.12	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3545	16300		0.84	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3890	16640	28279	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16640	28280	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4821	17356		2.57	2.0E-35	H49239.1	EST_HUMAN	Xt18at12.1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:274079 5'
5065	18294	31192	2.7	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-198-b04 BT0701 Homo sapiens cDNA
7004	19680	32749	0.95	2.0E-35	BE532538.1	EST_HUMAN	GM2-MT0125-280700-287-G02 MT0125 Homo sapiens cDNA
7004	19686	32750	0.95	2.0E-35	BE532538.1	EST_HUMAN	GM2-MT0125-280700-287-G02 MT0125 Homo sapiens cDNA
7775	20471	33593	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAY10 5'
7775	20471	33594	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAY10 5'
10597	23398	36626	2.24	2.0E-35	X99417.1	NT	H. sapiens PROS-27 mRNA
11817	18294	31192	1.28	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-198-b04 BT0701 Homo sapiens cDNA
11889	16066	28714	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11889	16066	28715	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12062	24577	31120	1.39	2.0E-35	BE904978.1	EST_HUMAN	601468774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3698699 5'
12062	24577	31121	1.39	2.0E-35	BE904978.1	EST_HUMAN	601468774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3698699 5'
12572	24800		5.95	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C910
12597							K69322 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
12689	15535	25597	1.98	2.0E-35	N88995.1	EST_HUMAN	REPETITIVE ELEMENT
45	12874	25490	6.81	1.0E-35	AA631949.1	EST_HUMAN	hnc1616 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	12874	25497	6.81	1.0E-35	AA631949.1	EST_HUMAN	hnc1616 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	13500	26165	19.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0182-131056-008-d12 ST0182 Homo sapiens cDNA

Page 269 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
735	13509	28168	19.5	1.0E-35	AW398473.1	EST_HUMAN	L2-ST0162-131089-008-012 ST0162 Homo sapiens cDNA
889	13658		1.3	1.0E-35	T87947.1	EST_HUMAN	ycf3a01.r1 Scores fetal spleen INFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2844	15268	27686	1.88	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233) mRNA
2770	15475	28217	1.09	1.0E-35	BE350127.1	EST_HUMAN	h03g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28 b3
2770	18476	28218	1.09	1.0E-35	BE350127.1	EST_HUMAN	MER28 repetitive element ;
3140	15904	28549	1.81	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCB1L) mRNA
3161	15924	28570	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GIC Homo sapiens cDNA clone GLOC6F08 3'
3161	15924	28571	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GIC Homo sapiens cDNA clone GLOC6F08 3'
4388	17125	29756	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4388	17125	29757	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4728	18222	30934	1.41	1.0E-35	11526238	NT	Homo sapiens chromatin assembly factor 1, subunit B (p50) (CHAF1B), mRNA
7393	20083	33141	0.88	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7541	20211	33311	1.18	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9442	25125	35297	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLAGE3000382 3'
9442	25125	35298	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLAGE3000382 3'
10477	23123	36352	0.7	1.0E-35	BF589584.1	EST_HUMAN	head608.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR.O31341
10477	23123	36353	0.7	1.0E-35	BF589584.1	EST_HUMAN	OS1341 BETA-GALACTOSIDASE ;
11758	24349	37680	1.46	1.0E-35	AB028950.1	NT	OS1341 BETA-GALACTOSIDASE ;
11758	24349	37681	1.46	1.0E-35	AB028950.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11768	24359		1.81	1.0E-35	AB25118.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
11917	25313		1.37	1.0E-35	1418274	NT	prom7a.7.D01.7 bivariate Homo sapiens cDNA 5'
12121	24613		1.63	1.0E-35	11418110	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12471	24637		2.13	1.0E-35	BE702832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
9729	21817	34983	0.66	8.0E-38	AA348480.1	EST_HUMAN	90158483F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
2931	15697	28344	1.1	7.0E-36	AW857570.1	EST_HUMAN	EST54939 Hippocampus II Homo sapiens cDNA 5' end similar to endogenous retrovirus 9, 5' LTR
3116	15881		3.94	7.0E-36	4557488	NT	CM7-CT0315-091289-058-407 CT0315 Homo sapiens cDNA
7554	20224	33327	5.92	7.0E-36	U06672.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7554	20224	33328	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and UN
7554	20224	33328	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and UN

Page 270 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14734	27456	2	6.0E-36	7706822	NT	Homo sapiens nitfurin 2 (NINJ2), mRNA
2418	15139		6.58	6.0E-36	AB03548.1	NT	Homo sapiens TSG1 gene, exon 12
3630	16383	28023	0.71	6.0E-36	BF515101.1	EST_HUMAN	U1HJBJT-antiv-c-12.0.U1.s1.NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5248	18084	30682	3.54	6.0E-36	AI435169.1	EST_HUMAN	1983008.x1 Soares NSF FR_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128106 3' similar to gbAI11948 PANCREATIC SECRETORY TRYPsin INHIBITOR PRECURSOR (HUMAN);
7009	19701	32756	3.57	6.0E-36	AF780143.1	EST_HUMAN	h008102.x1 NCI CGAP Cot4 Homo sapiens cDNA clone IMAGE:3096927 3' similar to SW1MA2_HUMAN
8650	21242	34385	2.33	6.0E-36	AF208161.1	EST_HUMAN	P52292; IMPORTIN ALPHA-2 SUBUNIT;
10125	22773		0.51	6.0E-36	C16927.1	EST_HUMAN	Homo sapiens synclin precursor, mRNA, complete cds
11536	24136	37443	3.11	6.0E-36	AI380499.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN:635C11 5'
134	12849	26592	10.74	6.0E-36	AJ271735.1	NT	h05609.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
2755	15460	28821	8.79	5.0E-36	BE386498.1	EST_HUMAN	MEF8 repetitive element;
3569	16562	29891	1.45	5.0E-36	AL163203.2	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4739	17468	30104	2.15	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C039
4736	17468	30105	2.15	5.0E-36	5729729	NT	Homo sapiens AP15-liko 1 (AP15L.1), mRNA
7686	20350	33464	0.61	5.0E-36	11076227	NT	Homo sapiens AP15-liko 1 (AP15L.1), mRNA
11887	12849	25592	3.83	6.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12168	24950	31103	3.45	5.0E-36	11417862	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1203	13955	28618	1.69	4.0E-36	BE010038.1	EST_HUMAN	Homo sapiens calcitriol binding protein 1 (KIA03036), mRNA
1423	14770	28856	1.03	4.0E-36	P10268	SWISSPROT	PMS-BN0176-10040-001-g04 BN0176 Homo sapiens cDNA
1840	14386	27074	1.61	4.0E-36	BE382574.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ;
2219	14947		2.13	4.0E-36	AW247772.1	EST_HUMAN	ENDONUCLEASE)
3349	15106	28763	0.82	4.0E-36	BE389289.1	EST_HUMAN	601285674.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
3348	18108	28764	0.82	4.0E-36	BE389289.1	EST_HUMAN	2820020.Sprfme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2620020 5'
6629	18428		0.84	4.0E-36	R64023.1	EST_HUMAN	601282286.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3904188 5'
5964	18748		2.36	4.0E-36	M33320.1	NT	601282286.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3904188 5'
7553	20223	33326	1.63	4.0E-36	M33320.1	NT	Y19031.1 Soares placenta Nb2HJp Homo sapiens cDNA clone IMAGE:136713 5'
8453	21146	34285	1.62	4.0E-36	DB7675.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8453	21145	34286	1.62	4.0E-36	DB7675.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
10608	23589	36833	2.84	4.0E-36	AA000370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12183	24655		2.09	4.0E-36		EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12227	24169		7.3	4.0E-36	AV158929.1	NT	z.69e10.r1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:143250 5'
						EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
						EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 1 (NFATC1), mRNA
						EST_HUMAN	AV1755629.Tp Homo sapiens cDNA clone TPGAB01 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12798	25047		1.44	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
690	13455	20100	2.59	3.0E-36	AF09810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
1484	14231	20917	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1484	14231	26918	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2207	15022	27157	1.21	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4407	17203	20926	5.88	3.0E-36	10181130	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
11050	23720	30691	1.59	3.0E-36	BF035327.1	EST_HUMAN	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3167	15630	28579	2.38	2.0E-36	BE299267.1	EST_HUMAN	601168631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862066 5'
4804	17631	30246	6.45	2.0E-36	AW680378.1	EST_HUMAN	601108348F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5396	18108	30892	3.1	2.0E-36	AF287747.1	NT	QV0-070530-240300-174-H04 OT0030 Homo sapiens cDNA
5758	18540	31471	3.95	2.0E-36	T08756.1	EST_HUMAN	Mus musculus p47-phox gene, complete cds
6481	19248	32248	12.22	2.0E-36	T69229.1	EST_HUMAN	EST05948 Infant Brain, Banto Scores Homo sapiens cDNA clone HIBJ28 5' end
6288	21955	35126	1.07	2.0E-36	BF512784.1	EST_HUMAN	Y044407.1 Strataene liver (8937224) Homo sapiens cDNA clone IMAGE:35508 5'
9449	21969	35172	0.79	2.0E-36	4507848	EST_HUMAN	U1H-BW7-enu-e-1-0.U1e1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9449	21969	35173	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
6685	19334	28304	1.81	1.0E-36	BE408310.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
2141	14871	27603	1	1.0E-36	BE146523.1	EST_HUMAN	601300638F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2141	14871	27604	1	1.0E-36	BE146523.1	EST_HUMAN	RC1-H1T0217-131189-021-h07 HT0217 Homo sapiens cDNA
2159	14928	27664	1.36	1.0E-36	BF673761.1	EST_HUMAN	RG1-H1T0217-131189-021-h07 HT0217 Homo sapiens cDNA
3330	16090		1.18	1.0E-36	AF156862.1	NT	602138493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
5910	18899	31527	1.29	1.0E-36	4827064	NT	Homo sapiens human endogenous retrovirus W provC-19 probease (pro) gene, partial cds
							Homo sapiens zinc finger protein 147 (zinc finger protein) (ZNF147) mRNA
							Homo sapiens zinc finger protein 147 (zinc finger protein) (ZNF147) mRNA
							wk37c12.1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307892 3' similar to contains Alu repetitive element
6090	18866		4.19	1.0E-36	AI897714.1	EST_HUMAN	Y03910.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN
6256	18069	32052	1.21	1.0E-36	R26012.1	EST_HUMAN	Y03910.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN
6299	19069	32053	1.21	1.0E-36	R26012.1	EST_HUMAN	Y03910.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN
6952	19345	32359	0.73	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229.1 1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
7323	20009	33087	0.85	1.0E-36	11428108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7326	20000	33088	0.85	1.0E-36	11428108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7860	20355	33679	5.13	1.0E-36	AA148034.1	EST_HUMAN	z551a12.1 Strataene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7860	20355	33680	5.13	1.0E-36	AA148034.1	EST_HUMAN	z551a12.1 Strataene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7652	20647	33770	1.34	1.0E-36	AA420467.1	EST_HUMAN	nc60608.t1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
7652	20647	33771	1.34	1.0E-36	AA420467.1	EST_HUMAN	nc60608.t1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
8079	20773	33902	0.61	1.0E-36	AI141888.1	EST_HUMAN	AI141888 THYRO1 Homo sapiens cDNA clone THYRO1001033 6'
8079	20773	33903	0.61	1.0E-36	AI141888.1	EST_HUMAN	AI141888 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8927	21618	34782	2.71	1.0E-36	AW103658.1	EST_HUMAN	wa2307.x1 NCI CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2814357 3'
10014	22662	35978	3.88	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1028-010600-156-H01 N1023 Homo sapiens cDNA
10226	22874	36088	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-C70278-040500-017-at10 G70278 Homo sapiens cDNA
10226	22874	36087	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-C70278-040500-017-at10 G70278 Homo sapiens cDNA
10887	23547	37347	4.17	1.0E-36	AW504143.1	EST_HUMAN	U1HF-ENO-de-c-33-O-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
11354	24044	37302	1.45	1.0E-36	AI005636.1	EST_HUMAN	RC-BT091-210169-110 BT091 Homo sapiens cDNA
11393	23969	37303	1.45	1.0E-36	AI005636.1	EST_HUMAN	RC-BT091-210169-110 BT091 Homo sapiens cDNA
11393	23969	37303	1.45	1.0E-36	AI005636.1	EST_HUMAN	RC-BT091-210169-110 BT091 Homo sapiens cDNA
12060	24575		3.81	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12501	24858		3.03	1.0E-36	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C013
12747	25011		3.23	1.0E-36	AF202723.1	NT	Homo sapiens Srd1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7281	18665	33042	2.12	9.0E-37	AW009277.1	EST_HUMAN	wa80507.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7281	18665	33043	2.12	9.0E-37	AW009277.1	EST_HUMAN	wa80507.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12309	24733		1.35	8.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
3350	18106	28765	0.99	8.0E-37	4757978	NT	Homo sapiens chimoth (chimothrin) 2 (CHN2) mRNA
5168	17677		1.58	8.0E-37	BE698077.1	EST_HUMAN	CMX-U7003-050600-505-309 UT0003 Homo sapiens cDNA
5738	18530	31451	3.75	8.0E-37	BE330127.1	EST_HUMAN	HO9801.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29 b3
5738	18530	31452	3.75	8.0E-37	BE330127.1	EST_HUMAN	HO9801.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29 b3
5787	18578	31507	8.24	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
7764	20479		6.22	8.0E-37	X87344.1	NT	H. sapiens DMA, DMB, HUA-Z1, PP2, LMP2, TAP1, LMP7, DOB, DQ82 and RING8, 9, 13 and 14 genes
1262	14011		3.03	7.0E-37	AL042800.1	EST_HUMAN	DKFZ434E0422_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZ434E0422 5'
1738	14480	27179	0.97	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1738	14480	27180	0.97	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10657	23348	36955	8.09	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12 PTR5 repetitive element;

Page 273 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10811	23494	38729	2.26	7.0E-37	AF169870.1	EST_HUMAN	tm87g03.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168140 3' similar to contains L1.b3 L1 repetitive element;
8338	21031	34168	1.34	6.0E-37	AF169880.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12624	24928		2.94	6.0E-37	AF202723.1	NT	Homo sapiens Sad1, unc-84 domain protein 2 (SUN2) mRNA, partial cds
6002	18783	31744	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178038 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6002	18783	31746	3.9	6.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8654	21346	34490	0.9	5.0E-37	AV760211.1	EST_HUMAN	AV760211 NPC Homo sapiens cDNA clone NPCBIGH08 5'
10837	23519		4	6.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12065	24672		6.86	5.0E-37	AF140773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2423	16144		2.12	4.0E-37	AF140774.1	EST_HUMAN	280604.x1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6184	18970	31845	0.61	4.0E-37	AW794502.1	EST_HUMAN	ROB-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
6286	21935	35109	0.74	4.0E-37	AA843806.1	EST_HUMAN	ad0902.x1 Soares, parathyroid, tumor, NBHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2010	14745	27472	3.2	3.0E-37	AL048556.1	EST_HUMAN	DKFZp434L2418.1_1 434 (synonym: h153) Homo sapiens cDNA clone DKFZp434L2418
2010	14746	27473	3.2	3.0E-37	AL048556.1	EST_HUMAN	DKFZp434L2418.1_1 434 (synonym: h153) Homo sapiens cDNA clone DKFZp434L2418
2065	15731		3.15	3.0E-37	AV051150.1	EST_HUMAN	EST173222 MAGE resources, MAGEF Homo sapiens cDNA
5774	18555	31494	0.92	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G087.1 547 (synonym: h187) Homo sapiens cDNA clone DKFZp547G087 5'
7455	20129	33221	0.71	3.0E-37	AI748952.1	EST_HUMAN	sl34c05.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:237986 3' similar to TR-Q13537
372	13197	25842	0.66	2.0E-37	D89700.1	NT	Q13537 SIMILAR TO POGO ELEMENT ;
372	13197	25843	0.68	2.0E-37	D89700.1	NT	Homo sapiens mRNA for AML1, complete cds
1058	13816	26477	2.64	2.0E-37	D58780.1	NT	Homo sapiens mRNA for AML1, complete cds
1058	13816	26478	2.64	2.0E-37	AF131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1899	14892	27405	1.97	2.0E-37	AL169247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3873	18623	29281	4.78	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 17-hydroxylase, cerebrolendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4998	17693		0.93	2.0E-37	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5304	18109		0.66	2.0E-37	BF035327.1	EST_HUMAN	601456031FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
6561	19326	32533	3.46	2.0E-37	AA346720.1	EST_HUMAN	EST152831 Fetal heart II Homo sapiens cDNA 5' end
7695	20590	33720	0.46	2.0E-37	BE537764.1	EST_HUMAN	601067834FT NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453657 5'
7695	20590	33721	0.46	2.0E-37	BE537764.1	EST_HUMAN	601067834FT NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453657 5'
7637	20652	33769	2.88	2.0E-37	BF204032.1	EST_HUMAN	601891917FT NIH_MGC 17 Homo sapiens cDNA clone IMAGE:411408 5'
11549	24148	37459	11.22	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDPT1) mRNA, complete cds
12784	23037		3.54	2.0E-37	114176721	NT	Homo sapiens pascadolin (pascadolin) homolog 1, containing BRCT domain (PES1), mRNA
2081	14813	27546	4.93	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3192	18955		1.06	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3943	19593	28332	0.72	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4888	17615	30234	2.35	1.0E-37	BF37117.1	EST_HUMAN	QY0-FN0180-280700-318-ct0 FN0180 Homo sapiens cDNA
5914	18689		0.84	1.0E-37	7303360	NT	Mus musculus ologelin (Olog), mRNA
8113	20807	35940	1.25	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8634	21328	34488	2.67	1.0E-37	AA171406.1	EST_HUMAN	zp21162.11 Stradiogene neuroepithelium (#837251) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.92 L1 repetitive element:
10597	23291	36528	2.68	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12583	24786		2.81	1.0E-37	BE771814.1	EST_HUMAN	CV3-FT0096-140700-243-407 FT0096 Homo sapiens cDNA
5600	18483	31402	2	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC66768), mRNA
1200	13952	26916	2.02	8.0E-38	11436865	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2502	19219	27992	1.8	8.0E-38	BF346221.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12420	13952	26916	1.8	8.0E-38	11436865	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4197	16938	29593	0.73	7.0E-38	H19082.1	EST_HUMAN	yn5107.11 Soares adult brain N263-B557 Homo sapiens cDNA clone IMAGE:171973 5'
5039	17758		1.31	7.0E-38	AF297263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
3037	15903	28450	1.2	6.0E-38	BF030033.1	EST_HUMAN	60146572F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3869348 5'
5502	18300	31159	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5502	18300	31200	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7228	16913	32866	0.57	6.0E-38	8923130	NT	Homo sapiens hypophelical protein FLJ20128 (FLJ20128), mRNA
11818	24480		2.57	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12995	24783	31038	12.79	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P23M, complete cds
12767	25161	30900	1.7	6.0E-38	11418164	EST_HUMAN	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
710	13484	26133	1.38	5.0E-38	AV071819.1	EST_HUMAN	EST383908 IMAGE resequences, MAGL Homo sapiens cDNA
2485	15173	27612	0.99	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
3949	16446	29066	0.85	5.0E-38	7548804	NT	Homo sapiens deiodinase, iodothyronine, type 1 (DIO2), transcript variant 2, mRNA
3917	16687	29307	0.92	5.0E-38	T83107.1	EST_HUMAN	yt404067.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
3917	16687	29308	0.92	5.0E-38	T83107.1	EST_HUMAN	SP-OLF3_MOUSE P23275 OLFACTORY RECEPTOR :
6930	18686	32712	1.48	5.0E-38	BE871610.1	EST_HUMAN	SP-OLF3_MOUSE P23275 OLFACTORY RECEPTOR :
116	12636	29575	4.59	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
116	12636	29576	4.59	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2093	14824		5.25	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3684	16437		2.18	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-1/ixp) (HIRIP4), mRNA

Page 275 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
3836	16587	29224	1.76	3.0E-38 P93338	SSU72 PROTEIN	
3836	16587	29225	1.76	3.0E-38 P63538	SSU72 PROTEIN	
4574	17309		1.47	3.0E-38 BE278301.1	EST_HUMAN	001157633FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504272 5'
6695	25097	32430	8.11	3.0E-38 AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7144	19931	32500	0.66	3.0E-38 AW302461.1	EST_HUMAN	xc0401.x1 NCI_CGAP_Brm63 Homo sapiens cDNA clone IMAGE:2827009 3'
7468	20160	33252	8.26	3.0E-38 BF373694.1	EST_HUMAN	CM3-FT0181-140700-241-07 FT0181 Homo sapiens cDNA
8548	21240	34383	2.1	3.0E-38 H85494.1	EST_HUMAN	y68804.r1 Soares melanocyte 2N0HM Homo sapiens cDNA clone IMAGE:249775 5'
8548	21240	34384	2.1	3.0E-38 H85494.1	EST_HUMAN	y68804.r1 Soares melanocyte 2N0HM Homo sapiens cDNA clone IMAGE:249775 5'
8872	22522		2.24	3.0E-38 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12630	17696	30488	1.65	3.0E-38 11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
48	12878	25504	1.4	2.0E-38 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	14106	26781	2.96	2.0E-38 5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1641	14387	27076	2.21	2.0E-38 AA437353.1	EST_HUMAN	zw303d01.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
1641	14387	27076	2.21	2.0E-38 AA437353.1	EST_HUMAN	zw303d01.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
2008	15120	27865	1.45	2.0E-38 W76571.1	EST_HUMAN	SW:MA12, RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
5632	18427	31339	0.69	2.0E-38 Z28534.2	NT	z86g08.r1 Soares_fetal_N8HT19W Homo sapiens cDNA clone IMAGE:345684 5'
5632	18427	31340	0.69	2.0E-38 Z28534.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7619	20285	33395	1.46	2.0E-38 AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8592	21076		4.38	2.0E-38 BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8763	21485	34631	0.56	2.0E-38 F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-1803
8864	21555	34700	2.04	2.0E-38 AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor H320 (H320) mRNA, complete cds
9121	21809		1.08	2.0E-38 BE222256.1	EST_HUMAN	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710
10245	22893	39212	1.71	2.0E-38 D63479.2	NT	GMO POLYPROTEIN. ;
10346	22893	39212	1.71	2.0E-38 D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11200	23865	37151	1.37	2.0E-38 AA595480.1	EST_HUMAN	nc34g03.x1 NCI_CGAP_P123 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11200	23865	37152	1.37	2.0E-38 AA595480.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11472	24073	37392	5.79	2.0E-38 BE712760.1	EST_HUMAN	nc34g03.x1 NCI_CGAP_P123 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11472	24073	37392	5.79	2.0E-38 BE712760.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11638	24238	37557	3.52	2.0E-38 AF190501.1	NT	QV2HT10696-080600-293-405 HT0598 Homo sapiens cDNA
						Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds

Page 276 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	24236	37558	3.52	2.0E-38	AF180501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11971	24517		3.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCA3407.5'
11973	24518		2.06	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12260	24706	31081	8.45	2.0E-38	H55541.1	EST_HUMAN	CHR2201560 Chromosome 22 exon Homo sapiens cDNA clone C22_788.5'
12323	24742		1.43	2.0E-38	S74906.1	NT	ET bataypyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
12777	25031		3.76	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULT23), mRNA
							z026027.1 Soares, Iestis, NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1071	13829		2.55	1.0E-38	AA401570.1	EST_HUMAN	MER19 repetitive element
1992	14728	27450	2.53	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2012	14747	27476	1.11	1.0E-38	7861860	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2468	16216	27960	2.34	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4390	17029	29655	1.23	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4390	17029	29658	1.23	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4558	17283	29921	1	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10500 (FLJ10600), mRNA
5937	18719	31678	4.71	1.0E-38	7305360	NT	Mus musculus dogelin (Obg), mRNA
7304	19987	33063	3.15	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
8051	21740	34898	0.71	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10500 (FLJ10600), mRNA
6910	21977	35160	5.13	1.0E-38	BE350127.1	EST_HUMAN	h89d01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146259 3' similar to contains MER29.b3
10301	22948	36163	0.58	1.0E-38	R18512.1	EST_HUMAN	MER29 repetitive element
11588	24187	37503	1.28	1.0E-38	7602108	NT	Y66038.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30488.5'
12118	25140		2.2	1.0E-38	AL163284.2	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
53	12882	25510	15.3	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C008
1373	14121	28798	1.48	8.0E-39	4758220	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16KD (ATP6C) mRNA
							Homo sapiens estrogen receptor-binding fragment-associated gene 6 (EBAG6) mRNA
1821	14560		1.27	8.0E-39	AB23404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 6 (EBAG6) mRNA
2087	14819	27550	5.79	7.0E-39	AL163227.2	NT	W33310.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2394491 3' similar to TR:P87690 P87690
10711	23400	36859	2.24	6.0E-39	BF531828.1	EST_HUMAN	POL PROTEIN
							Homo sapiens chromosome 21 segment HS21C027
12898	24979		1.66	8.0E-39	BE670394.1	EST_HUMAN	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
987	13760	28412	1.57	5.0E-39	AF003528.1	NT	7634d03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284359 3' similar to WP-R151.6
							CE00828
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Page 277 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORT SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2884	15750	26387	8.62	5.0E-39	AI750154.1	EST_HUMAN	aa2654.4.x1 Bartled codon HPLR37 Homo sapiens cDNA clone IMAGE:2374083 3' similar to TRQ15408
12410	24783		2.04	5.0E-39	11420289	NT	Q15408 UNIDENTIFIED PROTEIN FLJ10843 (FLJ10803), mRNA
537	13320	25854	6.78	4.0E-39	AB016810.1	NT	Homo sapiens hypothetical protein FLJ10843 (FLJ10803), mRNA
3559	13314	25951	0.87	4.0E-39	AL163210.2	NT	Chlorobacter ethiops mRNA for ribosomal protein S4, complete cds
7674	20660	33761	1.27	4.0E-39	AA682949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	aa2904.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9228	21907	35079	0.56	4.0E-39	D84116.1	NT	ORF.b1 ORF repetitive element
12427	24802		4.47	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12534	24878		2.71	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens DNA for prostacyclin synthase, exon 2
46	12875	25498	14.86	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
46	12875	25499	14.86	3.0E-39	AA631949.1	EST_HUMAN	Q70-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
46	12875	25500	14.86	3.0E-39	AA631949.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25500	14.86	3.0E-39	AA631949.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11983	24511	37257	4.35	3.0E-39	AI084557.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11983	24511	37268	4.35	3.0E-39	AI084557.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12006	24541		5.82	3.0E-39	H37603.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
677	13346		6.8	2.0E-39	BE406203.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
892	13461		14.03	2.0E-39	AI525118.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
1009	13769		4.2	2.0E-39	AF000573.1	NT	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
1520	14287		11.91	2.0E-39	AI372218.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
1596	14702	27416	3.28	2.0E-39	AA720574.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
2634	15346	28039	1.84	2.0E-39	AL163248.2	NT	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
4370	17108	29743	1.46	2.0E-39	BF370207.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
5403	18203	30807	4.21	2.0E-39	AA505860.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
7269	19893	33026	2.36	2.0E-39	AA080867.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
7431	20108	33195	0.72	2.0E-39	AL163202.2	NT	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
7431	20108	33196	0.72	2.0E-39	AL163202.2	NT	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
8209	22003	34036	0.67	2.0E-39	AF078719.1	NT	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
8394	22003		0.55	2.0E-39	AA984551.1	EST_HUMAN	IMF16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6626	22179		0.73	2.0E-39	AI060660.1	EST_HUMAN	363563.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:2263052 3'
11409	24058	37365	2.97	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
1503	14249	26939	3.71	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQT1 gene
1503	14249	26937	3.71	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQT1 gene
1521	14268	26952	4.24	1.0E-39	7657020	NT	Homo sapiens KVLQT1 gene
4098	16841	29487	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4098	16841	29468	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4612	17347	29680	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364085 IMAGE resequences, MAG8 Homo sapiens cDNA
4612	17347	29681	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364085 IMAGE resequences, MAG8 Homo sapiens cDNA
4654	17368	30021	8.96	1.0E-39	7657020	NT	Homo sapiens DKFZ343P211 protein (DKFZ343P211), mRNA
5274	18079	30735	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA), mRNA
5274	18079	30736	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA), mRNA
5542	16339	31248	1.97	1.0E-39	T60976.1	EST_HUMAN	3228068.r1 Sources fetal liver spleen 1NF.L3 Homo sapiens cDNA clone IMAGE:1094022 5' similar to contains Alu repetitive element/contains LTR1 repetitive element ;
5578	18375	31267	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5578	18375	31269	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6727	19591		1.57	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7264	18948	33025	1.8	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8462	21154	34297	1.03	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12357	24761		1.34	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
542	13325	25957	1.68	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1213	13963	26929	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1213	13963	26930	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1432	14179	26965	6.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3766	16517	29155	0.97	9.0E-40	4603784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3856	17878	29343	3.89	9.0E-40	AB030370.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3903	18602	28449	0.84	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HLA cDNA library Homo sapiens cDNA clone 7H15A04
3903	18603		3.35	8.0E-40	BE306541.1	EST_HUMAN	601288058FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 6'
7616	20282	33390	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7616	20282	33391	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10813	23466	36732	2.27	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2730	15437	28174	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST10527 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
2730	15437	28175	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST10527 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
5549	18636		2.24	6.0E-40	BE604769.1	EST_HUMAN	h24091.x1 NCL_CGAP_G03 Homo sapiens cDNA clone IMAGE:3210480 3'
6055	18635		1.11	6.0E-40	7661889	NT	Homo sapiens KIAA0211 gene product [KIAA0211], mRNA
6836	19498	32622	3.66	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6836	19498	32523	3.66	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
8877	22527	35722	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
8877	22527	35723	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
1869	14607	27316	1.78	4.0E-40	AI686005.1	EST_HUMAN	H91801.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TRQ73505 O73505
2101	14832		2.27	4.0E-40	AF003528.1	NT	POL PROTEIN-1; Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4356	17064	20720	9.03	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7788	20481	33606	0.5	4.0E-40	AI127831.1	EST_HUMAN	AI127831.NT2R22 Homo sapiens cDNA clone N12R22002172 5'
7690	20585	33714	6.22	4.0E-40	AI127831.1	EST_HUMAN	m346r0.1 NCL_CGAP_B14 Homo sapiens cDNA clone IMAGE:1222122
8653	21644	34793	6.17	4.0E-40	BE009416.1	EST_HUMAN	PMD-BN0167-070500-002-H12 BN0167 Homo sapiens cDNA
8653	21644	34794	5.17	4.0E-40	BE009416.1	EST_HUMAN	PMD-BN0167-070500-002-H12 BN0167 Homo sapiens cDNA
10616	23309	36548	3.03	4.0E-40	AV1841585.1	EST_HUMAN	RC1-CH0017-120200-312-e04 CN0017 Homo sapiens cDNA
11111	16854	29481	1.02	3.0E-40	AI625949.1	EST_HUMAN	wh1207.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2380549 3'
6543	18308	32313	7.02	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8260	20974	34115	3.62	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8363	21559	34704	1.25	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9111	21799	34683	1.42	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11232	23895	37182	8.38	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
11553	24162	37473	2.23	3.0E-40	AW118769.1	EST_HUMAN	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TRQ16804
317	13120		8.53	2.0E-40	AI220306.1	EST_HUMAN	Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERV5 ; qp520b.x1 Soares_bas1s_NHT Homo sapiens cDNA clone IMAGE:1838847 3'

Page 280 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
777	13549		1.61	2.0E-40	AW303868.1	EST_HUMAN	x72410.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE
1818	14557		0.92	2.0E-40	AV731601.1	EST_HUMAN	P97461.40S RIBOSOMAL PROTEIN S5 ;
1927	14663	27375	1.58	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1927	14663	27376	1.56	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2084	14796	27522	1.21	2.0E-40	AI068562.1	EST_HUMAN	w80411.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2814716 3' similar to TR:Q61829 Q91929
2106	14895	27650	2.48	2.0E-40	6463592	NT	ZINC FINGER PROTEIN ;
2695	15404		1.44	2.0E-40	BE275932.1	EST_HUMAN	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
3123	16598	28529	4.28	2.0E-40	6463592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
4843	17573	30187	1.66	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C090
4843	17573	30188	1.68	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C090
863	19632		1.78	1.0E-40	AA256985.1	EST_HUMAN	nc09a09.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1007608
2627	15339	28083	0.93	1.0E-40	BF036981.1	EST_HUMAN	801460376T1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3863803 5'
2692	15401		1.34	1.0E-40	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z156 Q9Z156
2741	15447	28185	1.18	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17 ;
2741	15447	28186	1.18	1.0E-40	BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4087736 5'
3282	18053		1.27	1.0E-40	4507142	NT	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4087736 5'
4571	17309	29934	4.52	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6161	18938	31907	0.75	1.0E-40	W92708.1	EST_HUMAN	z79711.1.t1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6161	18938	31908	0.75	1.0E-40	W92708.1	EST_HUMAN	z79711.1.t1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6987	19680	32721	1.77	1.0E-40	AA573201.1	EST_HUMAN	h4204.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:895167 3'
6987	19680	32728	1.77	1.0E-40	AA573201.1	EST_HUMAN	h4204.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:895167 3'
7133	19820	32868	0.69	1.0E-40	P26808	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
10334	23516	36768	8.34	1.0E-40	AI146246.1	EST_HUMAN	AI146246.N12R44 Homo sapiens cDNA clone NT2RMA002122 3'
11694	24289	37612	1.89	1.0E-40	AA614255.1	EST_HUMAN	nc09a03.s1 NCL CGAP_P03 Homo sapiens cDNA clone IMAGE:1116681 similar to TR:G1136406
11694	24289	37613	1.89	1.0E-40	AA614255.1	EST_HUMAN	G1136408 KIA0173 PROTEIN ;
12376	25274		10.09	1.0E-40	BF334112.1	EST_HUMAN	h139408 KIA0173 PROTEIN ;
7822	20517	33643	1.62	8.0E-41	AL163203.2	NT	MR2-CT07222-211089-002-e10 CT07222 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C003

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
809	15593	26246	1.24	7.0E-41	A1834394.1	EST_HUMAN	WP0404.x1 NCL CGAP_K0411 Homo sapiens cDNA clone IMAGE:2463955 3'
809	15593	26247	1.24	7.0E-41	A1834394.1	EST_HUMAN	WP0404.x1 NCL CGAP_K0411 Homo sapiens cDNA clone IMAGE:2463955 3'
4809	17344	29976	0.92	7.0E-41	BE389592.1	EST_HUMAN	60128207.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
4809	17344	29977	0.92	7.0E-41	BE389592.1	EST_HUMAN	60128207.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5183	17691	30507	1.2	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ131188 (FLJ131188), mRNA
5918	18703	31656	3.49	7.0E-41	11416208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6260	19034	32009	0.61	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
6895	17671	30528	0.68	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIST1) gene, exons 3 and 4
11411	24050	37366	2.23	7.0E-41	4758446	NT	Homo sapiens guanine nucleotide binding protein 10 (GNNG10) mRNA
11631	24228	37552	1.73	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12782	25271		4.35	7.0E-41	11417872	NT	Homo sapiens p53 (p53) homolog 1, containing BRCT domain (P53), mRNA
274	13081	25724	1.19	6.0E-41	A3037183.1	NT	Homo sapiens DSCR5p mRNA, complete cds
2104	14835	27559	2.04	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (OSGRL1), mRNA
4433	17169	29787	0.91	6.0E-41	BE597816.1	EST_HUMAN	601340485.F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3682677 5'
7871	20566	33692	1.44	6.0E-41	BF513783.1	EST_HUMAN	U1H-BW1-Lamp-B-05-D-U1.1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1795	14535	27244	1.11	6.0E-41	T82628.1	EST_HUMAN	yc33810.x1 Stratiocyt lung (#637270) Homo sapiens cDNA clone IMAGE:76628 3'
4087	16830		1.07	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6452	19220		2.29	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251169-002-F11 BT0341 Homo sapiens cDNA
382	13169		2.42	4.0E-41	BE156316.1	EST_HUMAN	Q10-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1076	13534	28492	1.28	4.0E-41	AU118344.1	EST_HUMAN	AU118344 HEMBAT Homo sapiens cDNA clone HEMBAT1005683 5'
1388	14135	28810	15.51	4.0E-41	A027117.1	EST_HUMAN	ow45606.s1 Soares_perathrydrol_tumor_NhpHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1398	14135	26811	16.51	4.0E-41	A027117.1	EST_HUMAN	ow45606.s1 Soares_perathrydrol_tumor_NhpHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1403	14150	26830	1.88	4.0E-41	AB006881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1632	14378	27065	6.08	4.0E-41	A1500408.1	EST_HUMAN	Trn96c04.x1 NCL CGAP_Bn28 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OTR.b1 OFR repetitive element;
2891	15659	28302	3.55	4.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2891	15659	28303	3.55	4.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4124	16668	29493	2.24	4.0E-41	X02985.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element

Page 282 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	19184			4.0E-41	AV758295.1	EST_HUMAN	AY758295 BM Homo sapiens cDNA clone BMFH008 5'
6593	22246	35430	7.24	4.0E-41	BF304983.1	EST_HUMAN	60188099F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11871	24266		11.07	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'
12546	25164		1.83	4.0E-41	AV708431.1	EST_HUMAN	AV708431 AOC Homo sapiens cDNA clone ADCARE02 5'
12727	24998	30971	1.69	4.0E-41	BE887118.1	EST_HUMAN	601330831P1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
927	13594	26333	2.68	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4301	17040	29687	2.45	3.0E-41	AB026988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5404	18204	30508	7.78	3.0E-41	X87068.1	NT	H. sapiens mRNA for putative p84 GLOP protein
6288	19081	32043	1.59	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7159	19848	32916	0.71	3.0E-41	AA356168.1	EST_HUMAN	ESTB4893 Jurkat T-cells VI Homo sapiens cDNA 5' end
11730	24323	37647	1.26	3.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 of 1710.81 Soares, total 1605 N22HF8, 9w Homo sapiens cDNA clone IMAGE:1031947 3'
11624	24485		1.52	3.0E-41	AA309768.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
12458	24825	26987	1.48	3.0E-41	BF125622.1	NT	Human ribosomal protein L28a mRNA, complete cds
1817	14299	27399	5.17	2.0E-41	U43701.1	NT	EST336818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
1951	14698	27399	1.84	2.0E-41	AA331940.1	EST_HUMAN	Human mRNA for KIAA0207 gene, complete cds
2216	14944	27684	1.54	2.0E-41	X86962.1	NT	G. gorilla DNA for ZNF83 gene homolog
2284	14990	27730	3.34	2.0E-41	X86931.1	NT	Human ribosomal protein L23a mRNA, complete cds
2831	14299	26687	4.85	2.0E-41	U43701.1	NT	X208504.1 Soares, total 1605 N22HF8, 9w Homo sapiens cDNA clone IMAGE:785939 5'
3321	16081	28731	1.41	2.0E-41	AA448546.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C087
4579	17314	29542	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4579	17314	29843	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
5141	17859	30475	0.9	2.0E-41	AW236547.1	EST_HUMAN	xm4708.v1 NCL CGAP_G05 Homo sapiens cDNA clone IMAGE:2887363 3' similar to TR:070343 070343 PPAR GAMMA COACTIVATOR 1.
6530	19286	32300	0.76	2.0E-41	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
7572	20241	33346	8.08	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (Itihed5) mRNA, complete cds
7987	20662	33786	1.45	2.0E-41	M65944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
7987	20662	33787	1.45	2.0E-41	M65944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
7985	20690	33818	1.12	2.0E-41	AA328285.1	EST_HUMAN	EST37723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
8874	21695	34710	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 165
6317	21684	35155	0.82	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9317	21884	35166	0.52	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11408	24071	37379	2.76	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3201	15994	28616	1.05	1.0E-41	BE898735.1	EST_HUMAN	601446647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3949803 5'

Page 283 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3201	15684	28817	1.05	1.0E-41	BE869733.1	EST_HUMAN	6014846741 NH_MGC_08 Homo sapiens cDNA clone IMAGE:3849803 5'
4529	17284	29887	14.08	1.0E-41	6878468	NT	Mus musculus tubulin alpha 8 (Tubaf8), mRNA
6749	17918	30582	0.66	1.0E-41	H99075.1	EST_HUMAN	X17802.x1 Soares melanocyte 2N61M Homo sapiens cDNA clone IMAGE:262061 3'
6918	21985	35157	1.69	1.0E-41	A1217688.1	EST_HUMAN	d75c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755958 3'
11111	23781	37056	1.66	1.0E-41	AW847812.1	EST_HUMAN	U3-C10213-190200-Q40-F08 C10213 Homo sapiens cDNA
12054	24571		2.81	1.0E-41	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8418	21111		1.14	9.0E-42	BE179191.1	EST_HUMAN	RCO-HT0613-210300-032-201 HT0613 Homo sapiens cDNA
9072	21761	34922	3.49	9.0E-42	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9072	21761	34923	3.49	9.0E-42	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
450	13236	25875	7.71	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2102	14833	27587	0.92	8.0E-42	AB026958.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12093	25277		4.4	8.0E-42	AA493886.1	EST_HUMAN	hm7cd2.s1 NCL CGAP_Tm1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
12111	25154		1.56	8.0E-42	AW086092.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG mRNA
911	13578		2.58	7.0E-42	AL183285.2	NT	OF1 repetitive element
9143	21874	35038	1.67	7.0E-42	AL204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C086
11128	23795	37071	1.3	7.0E-42	AA589592.1	EST_HUMAN	d58012.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11128	23795	37072	1.3	7.0E-42	AA589592.1	EST_HUMAN	m23907.x1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1848	14598	27299	3.21	6.0E-42	AF012872.1	NT	m23907.x1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1848	14598	27300	3.21	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2287	15012		3.55	6.0E-42	AW236556.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
5381	18181	30871	1.63	6.0E-42	AB028950.1	NT	Xp25003.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.11 L1
5381	18181	30871	1.63	6.0E-42	AB028950.1	NT	repetitive element
132	12247		7.53	5.0E-42	AJ21735.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
428	13214	25859	1.41	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
474	13260		2.57	5.0E-42	5730038	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
476	13261		2.74	5.0E-42	5730038	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6597	18550	32363	1.04	5.0E-42	11433003	NT	h3191.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
6597	18550	32364	1.04	5.0E-42	11433003	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
							Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6704	19919	32662	3.12	5.0E-42	11417957	NT	Homo sapiens myobulbin related protein 3 (MTMR3), mRNA
7101	19789	32854	1.59	5.0E-42	AF071599.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7111	20375	33499	0.67	5.0E-42	4826977	NT	Homo sapiens reelin (RELN) mRNA
8677	21369	34575	3.65	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10920	23600	38849	2.44	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
739	13510	25167	6.09	4.0E-42	AF050668.1	NT	Homo sapiens MHC class 1 region
736	13510	26168	5.09	4.0E-42	AF050668.1	NT	Homo sapiens MHC class 1 region
1044	13803	26462	3.46	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4171	16911	29541	1.22	4.0E-42	X59417.1	NT	H. sapiens PIROS-27 mRNA
4202	16943	29670	1.07	4.0E-42	AF243219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4223	16964	29589	4.15	4.0E-42	AF243219.1	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4543	17278	29909	15.12	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
10645	23241	36475	1.56	4.0E-42	AW618630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10545	23241	36476	1.98	4.0E-42	AW618630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11389	23995	37297	1.8	4.0E-42	BF033327.1	EST_HUMAN	60146531 F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662088 5'
1468	14213	26602	2.61	2.0E-42	BF376834.1	EST_HUMAN	RC3-TN0079-11080-024-g07 TN0079 Homo sapiens cDNA
2413	15134	26602	2.61	2.0E-42	AW808344.1	EST_HUMAN	RC3-TN0079-270400-011-h10 NN0079 Homo sapiens cDNA
2425	15146	27879	2.22	2.0E-42	AW250059.1	EST_HUMAN	2819293.3p1m6 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5670	18466	31379	7.8	2.0E-42	AW653088.1	EST_HUMAN	EST367438 IMAGE sequences, MAGC Homo sapiens cDNA
5870	18466	31380	7.8	2.0E-42	AW653088.1	EST_HUMAN	EST367438 IMAGE sequences, MAGC Homo sapiens cDNA
6654	19416	32429	1.43	2.0E-42	AJ052586.1	EST_HUMAN	ow83d05x1 Soares, fetal_liver, spleen, TNF.LS_51 Homo sapiens cDNA clone IMAGE:1653417 3'
6741	22392	35096	1.92	2.0E-42	BE639919.1	EST_HUMAN	601661284 F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447820 6'
9935	22603	35807	0.86	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
9935	22603	35808	0.87	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
11742	24334	37660	1.97	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C346
717	13490	29143	1.21	1.0E-42	X57147.1	NT	Human endogenous retrovirus pH1.1 (ERV9)
1019	13779	28441	1.1	1.0E-42	AW265009.1	EST_HUMAN	U1-H131-5aff-04-04-U1.s1 NC1_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1079	13937	28495	1.18	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1079	13937	28496	1.18	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1220	15563	28541	16.49	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1220	15563	28542	16.49	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1696	14439	27137	1.13	1.0E-42	11423219	NT	Homo sapiens rce [LOC51201], mRNA
2546	15291	27998	1.63	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2954	15730	28380	10.26	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog-like) (ORCSL) mRNA, and translated products
3695	16449	29088	2.6	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3905	16655	29296	1.17	1.0E-42	AL163282	NT	Homo sapiens chromosome 21 segment HS21C067
4221	16952	29587	1.92	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4554	17269	29918	0.75	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST10197-161059-012-403 ST10197 Homo sapiens cDNA
4697	17431	30062	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4697	17431	30063	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4728	17460	30097	6.02	1.0E-42	5905798	NT	Homo sapiens retinoid receptor 3 (RTR3) mRNA
6044	17763	30378	1.08	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5044	17763	30379	1.08	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5956	22634	35844	4.03	9.0E-43	4757668	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
637	13416	26052	19.69	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08.5'
637	13416	26053	19.69	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08.5'
684	13459	26104	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26105	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26106	6.03	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
9512	18408	31321	0.76	8.0E-43	H13852.1	EST_HUMAN	J08411.1 Soares placenta Nc2HP Homo sapiens cDNA clone IMAGE:2822251.5'
3632	16385	26025	6.42	7.0E-43	AW248442.1	EST_HUMAN	2822251.5 Soares NIH JMG-7 Homo sapiens cDNA clone IMAGE:2822251.5'
8687	21359		4.09	7.0E-43	AB38748.1	EST_HUMAN	wp68b01.x1 NGL CGAP Brn25 Homo sapiens cDNA clone IMAGE:2466985.3' similar to TR:O15475
1321	14070		10.45	6.0E-43	AA461800.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN, contains LTR7 b1 LTR7 repetitive element;
2600	15314		2.25	6.0E-43	AV708201.1	EST_HUMAN	ne72003.s1 NGL CGAP Ew1 Homo sapiens cDNA clone IMAGE:509803 similar to gb:L05095.60S
6219	18993	31899	2.24	6.0E-43		NT	RIBOSOMAL PROTEIN L30 (HUMAN);
6808	19469	32492	2.09	6.0E-43	AW468897.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10.6'
9751	22402	35607	2.16	6.0E-43	AA1195154.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
11044	23714		2.55	6.0E-43	AL119159.1	EST_HUMAN	h430304.x1 Soares NFL T, GBC, S1 Homo sapiens cDNA clone IMAGE:2910991.3' similar to contains
138	12853		2.64	5.0E-43	AL163213.2	NT	z35068.r1 Soares NIH-MMPu_S1 Homo sapiens cDNA clone IMAGE:665410.5' similar to TR:G529641
							z35068.r1 Soares NIH-MMPu_S1 COMPLETE CDS, contains element PRT7 repetitive element;
							DKFZ6761L1712.1 T1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ6761L1712.5'
							Homo sapiens chromosome 21 segment HS21C013

Page 286 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
490	13276	26909	4.55	5.0E-43	AA382780.1	EST_HUMAN	EST166033 Testis 1 Homo sapiens cDNA 5' end
2850	16618	28264	1.52	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
8213	19463	32484	1.17	5.0E-43	AG13509.1	EST_HUMAN	W22407.X1 NCL CGAP Brn82 Homo sapiens cDNA clone IMAGE:2280452 3'
8602	19463	32484	0.72	5.0E-43	AG13509.1	EST_HUMAN	W22407.X1 NCL CGAP Brn82 Homo sapiens cDNA clone IMAGE:2280452 3'
8778	21470		0.46	5.0E-43	H74277.1	EST_HUMAN	3449412.1 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:228510 5'
8248	21927	35098	0.47	5.0E-43	AA044450.1	EST_HUMAN	245502.1 Soares pregnant uterus NHPU Homo sapiens cDNA clone IMAGE:486698 5' similar to
8248	21927	35098	0.47	5.0E-43	AA044450.1	EST_HUMAN	245502.1 Soares pregnant uterus NHPU Homo sapiens cDNA clone IMAGE:486698 5' similar to
9264	22018	35188	4.44	5.0E-43	AA465283.1	EST_HUMAN	gb-D2808 N-ACETYLGLUTAMINE SYNTHASE (HUMAN);
10297	22944	36158	2.31	5.0E-43	AF733244.1	EST_HUMAN	gb-D2808 N-ACETYLGLUTAMINE SYNTHASE (HUMAN);
10355	22982	36201	1.21	5.0E-43	ALJ49110.1	EST_HUMAN	gb-D2808 N-ACETYLGLUTAMINE SYNTHASE (HUMAN);
10683	23354	36593	5.29	5.0E-43	AV186307.1	EST_HUMAN	gb-D2808 N-ACETYLGLUTAMINE SYNTHASE (HUMAN);
10891	23571	36822	1.84	5.0E-43	W29011.1	EST_HUMAN	gb-D2808 N-ACETYLGLUTAMINE SYNTHASE (HUMAN);
952	15519	26383	5.9	4.0E-43	AF003528.1	NT	005210.3 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591
6178	17687	30502	1.02	4.0E-43	AI058338.1	EST_HUMAN	PV14 GENE. ;
6276	18048	30206	0.7	4.0E-43	6986006	NT	DKFZp434D0119.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D0119
7030	19722		2.32	4.0E-43	11416783	NT	MR2-SN0007-290400-004-002 SN0007 Homo sapiens cDNA
8077	20771	33900	5.21	4.0E-43	AI244341.1	EST_HUMAN	6564 Homo sapiens retina cDNA randomly primed sublibrary Homo sapiens cDNA
8077	20771	33901	5.21	4.0E-43	AI244341.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
10213	22861	36074	1.23	4.0E-43	8005687	EST_HUMAN	q747h03.x1 NCL CGAP Brn23 Homo sapiens cDNA clone IMAGE:1669013 3'
11275	23936	37226	1.68	4.0E-43	T77390.1	EST_HUMAN	Homo sapiens glycyl-IRNA synthetase (GARS), mRNA
12030	24556		3.05	4.0E-43	R20950.1	EST_HUMAN	Homo sapiens prolidase beta 6 (PCDH6), mRNA
1181	13943		4.59	3.0E-43	AF223391.1	NT	q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
1600	14434	27130	2.07	3.0E-43	X07860.1	NT	MER10 repetitive element;
3558	16313	29860	1.31	3.0E-43	S69002.1	EST_HUMAN	q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
4258	16998	29829	1.04	3.0E-43	AA548154.1	EST_HUMAN	q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
							q76a02.x1 NCL CGAP_Ku83 Homo sapiens cDNA clone IMAGE:1665354 3' similar to contains MER10.13
							MER10 repetitive element;
	</						

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6803	18583	31518	0.72	3.0E-43	D34813.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6294	19038	32013	2.24	3.0E-43	7305360	NT	Mus musculus otodectin (Otog), mRNA
6284	19038	32014	2.24	3.0E-43	7305360	NT	Mus musculus otodectin (Otog), mRNA
6528	19390	32404	4.29	3.0E-43	U85487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8063	20757		8.38	3.0E-43	AA459824.1	EST_HUMAN	aa88111.s1 Stratiens retina 937202 Homo sapiens cDNA clone IMAGE:538413 3' similar to contains
8719	21411	34554	1.87	3.0E-43	7661721	NT	THRL2 THR repetitive element
8764	22415	35622	0.56	3.0E-43	11420217	NT	Homo sapiens typhoid protein (HSA011916), mRNA
179	12991		7.57	2.0E-43	A1190784.1	EST_HUMAN	cd81c09.x1 Sox6, testis_NHT Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains PTR.7.3
6983	19152	32151	1.13	2.0E-43	BE222778.1	EST_HUMAN	huc3a08.x1 NCJ_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
6983	19152	32152	1.13	2.0E-43	BE222778.1	EST_HUMAN	huc3a08.x1 NCJ_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
7178	19602	32553	1.32	2.0E-43	AW207390.1	EST_HUMAN	UHL-B1-af1-a-09-0-J1.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721713 3'
8207	20801		6.59	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11156	23623		4.94	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stratiens Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1645	14391	27080	2.04	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1645	14391	27081	2.94	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1700	14443	27142	1.57	1.0E-43	AL163284.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21Q84
2727	15434	28170	3.85	1.0E-43	BF346283.1	EST_HUMAN	BD022313P1 NCJ_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:4157665 5'
5325	18128	30788	0.74	1.0E-43	4865544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6514	19279	32280	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6514	19279	32281	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6870	17947	30542	1.36	1.0E-43	R18751.1	EST_HUMAN	Y94060.1 Sox6 Infant brain 1N18 Homo sapiens cDNA clone IMAGE:34732 5' similar to
7833	20528	33655	1.13	1.0E-43	AF175265.1	NT	SP-BD38_MOUSE P26668 BRAIN PROTEIN DN38
7865	20660		4.03	1.0E-43	AF108400.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8736	21428	34574	25.49	1.0E-43	AW958076.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
10189	22937	36052	0.68	1.0E-43	AW953229.1	EST_HUMAN	EST1375749 IMAGE sequences, MAGB Homo sapiens cDNA
10884	23594	36812	8.11	1.0E-43	A1684861.1	EST_HUMAN	EST1365269 IMAGE sequences, MAGB Homo sapiens cDNA
11338	24028	37332	4.78	1.0E-43	11424378	NT	w878101.x1 NCJ_CGAP_KR11 Homo sapiens cDNA clone IMAGE:2464705 3'
11975	24520		3.04	1.0E-43	AL137084.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12253	24698	31079	1.89	1.0E-43	A1675416.1	EST_HUMAN	DKFZ576D1015.r1 T81 (synonym: hamy2) Homo sapiens cDNA clone DKFZ576D1015 5'
							w889004.x1 NCJ_CGAP_P228 Homo sapiens cDNA clone IMAGE:2313775 3'

Page 288 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12669	24835	31032	3.41	8.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
870	13639	26309	6.23	8.0E-44	A1222895.1	EST_HUMAN	q123g01.x1 Soares NFL_T1 GGC_S1 Homo sapiens cDNA clone IMAGE:184552 3'
870	13639	26310	6.23	8.0E-44	A1222895.1	EST_HUMAN	q123g01.x1 Soares NFL_T1 GGC_S1 Homo sapiens cDNA clone IMAGE:184552 3'
8437	21129	34298	2.67	8.0E-44	X84354.1	NT	H.sapiens DNA for Cere GMP-PDE gene
10238	22884	36058	0.47	8.0E-44	11423497	NT	H.sapiens small proline-rich protein 2C (SPRR2C), mRNA
10238	22884	36059	0.47	8.0E-44	11423497	NT	H.sapiens small proline-rich protein 2C (SPRR2C), mRNA
11117	23787	37054	3.78	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11698	24283	37608	1.38	8.0E-44	L28135.1	NT	Homo sapiens myosin mRNA, partial cds
12207	24673	31073	4.09	8.0E-44	11627380	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12248	25009	30978	1.38	8.0E-44	11418089	NT	Homo sapiens putative nuclear protein (HRHFB2122), mRNA
12589	25186	30808	2.55	8.0E-44	11418089	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
644	13423		0.69	7.0E-44	R06035.1	EST_HUMAN	y88901.r1 Soares fetal liver spleen NFILS Homo sapiens cDNA clone IMAGE:124620 5'
2228	14956	27698	1.08	7.0E-44	5031880	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2688	15732	28381	2.58	7.0E-44	AF048726.1	NT	Homo sapiens mitisatellite ms32 repeat region
2988	15732	28382	2.58	7.0E-44	AF048726.1	NT	Homo sapiens chromosome 21 segment HS21C084
3843	16594	29231	2.54	7.0E-44	AL183284.2	NT	Homo sapiens chromosome 21 unknown mRNA
4217	16958	29581	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4217	16958	29582	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5142	17880	30476	1.01	7.0E-44	4505949	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
8085	20779	33908	2.28	7.0E-44	AU159839.1	EST_HUMAN	AU159839 789A.1 Homo sapiens cDNA clone Y8AA100466 3'
6012	18763	31766	0.94	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU.P Human fetal Brain Whole tissue Homo sapiens cDNA
11781	24372	37702	1.76	6.0E-44	AW954050.1	EST_HUMAN	EST388120 MAGE resequencing, MAGE Homo sapiens cDNA
266	13102		3.3	5.0E-44	AJ289380.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
323	13124		2.72	5.0E-44	AJ289380.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7768	20483	33607	4.96	6.0E-44	AI588523.1	EST_HUMAN	1540402.x1 NC1 CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9284	22038		2.34	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element;
3408	16167	28916	3.75	4.0E-44	AL163303.2	NT	AU124571 NT20M Homo sapiens cDNA clone NT2RM400218 5'
7370	20050	33131	0.98	4.0E-44	BE683178.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8169	20863	33995	0.76	4.0E-44	L21948.1	NT	601503601F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8777	21469		0.61	4.0E-44	BE176818.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11202	23868	37153	5.38	4.0E-44	U90878.1	NT	RC3-H10585.01A00-023-008 H10585 Homo sapiens cDNA
3034	15859	28900	5.77	3.0E-44	AA166851.1	EST_HUMAN	Homo sapiens carboxy terminal LIM domain protein (CLIM1) mRNA, complete cds
							Zp18505.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3870	16620	29280	1.37	3.0E-44	AA337234.1	EST_HUMAN	EST42288 Endometrial tumor Homo sapiens cDNA 5' end similar to alpha-1-antitrypsinase F
6419	22097	33259	0.65	3.0E-44	AF005273.1	NT	Sus scrofa domestica submandibular apomucin mRNA, complete cds
1027	13787	26446	2.64	2.0E-44	4826585	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1027	13787	26447	2.64	2.0E-44	4826585	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1185	13937	28602	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1185	13937	28603	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1289	14038	28711	4.09	2.0E-44	AF133395.1	NT	Homo sapiens RAB39 (RAB39) mRNA, complete cds
1347	14095	28770	1.3	2.0E-44	BE48525.1	EST_HUMAN	hw14q06.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2147	14877	27612	2.22	2.0E-44	AF070051.1	NT	P22069 OXYSTEROL-BINDING PROTEIN.
2618	15327	28873	1.31	2.0E-44	5901833	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3463	16219	28873	1.13	2.0E-44	D97675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4531	17268	29898	1.54	2.0E-44	AW694379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6004	18785	31747	1.87	2.0E-44	11449301	NT	PM4-SN0016-120500-003-a04 SN0018 Homo sapiens cDNA
6759	19527	30602	3.31	2.0E-44	AF038968.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9) mRNA
7313	19596	33074	4.57	2.0E-44	11419226	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7313	19596	33075	4.57	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34156	0.87	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34156	0.87	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIA00917), mRNA
8517	21209	34352	1.59	2.0E-44	BE339056.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIA00917), mRNA
11883	24456		1.82	2.0E-44	BE244902.1	EST_HUMAN	601268914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3673366 5'
12760	25020		1.4	2.0E-44	11528263	NT	TCBAP1E2765 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2765
51	12880	25507	2.43	1.0E-44	7657334	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
51	12880	25508	2.43	1.0E-44	7657334	NT	Homo sapiens Mismatch repair-related kinase (MINK), mRNA
569	13347	25975	2.44	1.0E-44	AW653132.1	EST_HUMAN	Homo sapiens Mismatch repair-related kinase (MINK), mRNA
1175	13928		1.9	1.0E-44	AW694603.1	EST_HUMAN	RC1-CT0249-030300-026-H12 CT0249 Homo sapiens cDNA
1567	14314		3.78	1.0E-44	AL163303.2	NT	RC1-BNG039-110300-012-301 BNG039 Homo sapiens cDNA
2221	14849	27687	3.74	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2221	14940	27688	3.74	1.0E-44	AA434554.1	EST_HUMAN	zr53d02r1 Scores: total: 7689, 9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element;
2221	14940	27688	3.74	1.0E-44	AA434554.1	EST_HUMAN	zr53d02r1 Scores: total: 7689, 9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element;

Page 290 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2280	15590	27746	0.96	1.0E-44	AA398099.1	EST_HUMAN	288g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2763	15468	28211	1.44	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor IG-HI enhancer 3, JM11 protein, JM4 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel, a2
3712	18465		3.73	1.0E-44	AA455893.1	EST_HUMAN	ad01cd02.x1 Soares_NHNP4_S1 Homo sapiens cDNA clone IMAGE:311934 3'
5648	17767	30395	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5048	17767	30398	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8163	20857	33988	0.98	1.0E-44	AW967073.1	EST_HUMAN	EST1379147 IMAGE: ressequences, MAGJ Homo sapiens cDNA
8163	20857	33989	0.98	1.0E-44	AW967073.1	EST_HUMAN	EST1379147 IMAGE: ressequences, MAGJ Homo sapiens cDNA
8544	21248	34390	0.69	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
8824	21515	34759	0.69	1.0E-44	AI337183.1	EST_HUMAN	q489g07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone DQ8BYE03 5'
10938	23016		4.04	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DQ8 Homo sapiens cDNA clone IMAGE:2009028 3'
11516	24116	37427	3.92	1.0E-44	1002864	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK63A9.2), mRNA
11583	24182	37499	3.17	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150959-011-C08 CT0198 Homo sapiens cDNA
11583	24182	37497	3.17	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150959-011-C08 CT0198 Homo sapiens cDNA
4539	17274	29905	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4539	17274	29907	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6552	18317	32328	1.31	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
2527	15243	27682	3.12	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5023	17744	30355	6.41	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6414	19182	32181	0.68	8.0E-45	AW692763.1	EST_HUMAN	OMA-NN0005-130300-283-508 NN0005 Homo sapiens cDNA
8006	20701	33830	0.91	8.0E-45	AA377565.1	EST_HUMAN	EST106893 Synovial sarcoma Homo sapiens cDNA 5' and
1545	14291		1.01	9.0E-45	AI875425.1	EST_HUMAN	W69606.x1 NCI_CGAP_F728 Homo sapiens cDNA clone IMAGE:2313902 3' similar to contains L1.11 L1 repetitive element;
3990	16709		4.09	6.0E-45	AW157570.1	EST_HUMAN	au8307.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW-R13A, A Human P40429 68S RIBOSOMAL PROTEIN L19A ;
12555	25378		1.95	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
872	13641		1.03	6.0E-45	AL169203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1985	14731	27453	3.65	5.0E-45	BF333927.1	EST_HUMAN	OM4-CN0044-180200-315-401 CN0044 Homo sapiens cDNA
3204	15967	28921	1.79	5.0E-45	AI523768.1	EST_HUMAN	tg9407.x1 NCI_CGAP_CLI1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW.PAX1_MOUSE
5425	18224	30935	8.76	5.0E-45	AA397781.1	EST_HUMAN	P08084 PAIRED BOX PROTEIN PAX1 ;
5928	18713	31669	1.31	5.0E-45	Y18933.1	NT	x72d03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
							Homo sapiens MCP-1 gene and enhancer region

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5929	18713	31670	1.31	5.0E-46	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5974	18768	31717	0.79	5.0E-46	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
5974	18768	31718	0.79	5.0E-46	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6056	18874	31842	1.02	5.0E-46	11466268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6056	18874	31843	1.02	5.0E-46	11466268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8174	20868	34000	0.73	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8639	21630	34773	1.95	6.0E-46	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11697	24292	37617	2.60	5.0E-46	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1121	13877	26558	0.58	4.0E-45	X95928.1	NT	H. sapiens ART4 gene
2289	15014	27750	2.42	4.0E-45	BE295922.1	EST_HUMAN	601184440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3539425 5'
8855	21546		0.82	4.0E-45	AA226220.1	EST_HUMAN	nc28607.61 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1
4065	16083		1.35	3.0E-45	T71480.1	EST_HUMAN	repetitive element
6142	18920	31890	1.36	3.0E-46	6753651	NT	xd3507.71 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:110245 5'
8350	21043	31891	1.36	3.0E-46	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8660	21382	34520	3.74	3.0E-45	4758451	EST_HUMAN	AY723976 HTB Homo sapiens cDNA clone HTBAACG01 5'
10206	22554	36068	13.43	3.0E-46	AL183227.2	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10206	22554	36068	13.43	3.0E-46	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12870	25314		2.35	3.0E-45	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
2508	15223		2.21	2.0E-46	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3029	15765	28441	1.22	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8429	19197	32184	5.15	2.0E-46	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7510	20181	33274	1.22	2.0E-46	BE782184.1	EST_HUMAN	601467703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8314	21007	34145	0.78	2.0E-45	AW834834.1	EST_HUMAN	RQ3-L10001-150200-032-411 L10001 Homo sapiens cDNA
6485	22138	35318	0.48	2.0E-45	A1636786.1	EST_HUMAN	tu56a07.x1 NC1_CGAP_K108 Homo sapiens cDNA clone IMAGE:2232562 3'
10705	25130	36633	18.26	2.0E-46	BE934350.1	EST_HUMAN	MRO-HT10923-180600-201-602 HT10923 Homo sapiens cDNA
11129	23797	37073	4.16	2.0E-46	A4458770.1	EST_HUMAN	aa87112.1 Sra1e gene fetal retina 937/202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11488	24089	37400	1.76	2.0E-46	AW270280.1	EST_HUMAN	TR.G114599 G114599 R-SLY1.
12711	24087		3.63	2.0E-45	11418157	NT	x672a03.x1 NC1_CGAP_O440 Homo sapiens cDNA clone IMAGE:2745668 3'
120	13785		-1.6	1.0E-45	BE386655.1	EST_HUMAN	xp72a03.x1 NC1_CGAP_O440 Homo sapiens cDNA clone IMAGE:2745668 3'
							Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
							601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
400	13185		2.17	1.0E-48	BE398858.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360183 5'
460	13245	25837	1.38	1.0E-46	4508412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1161	13306	26559	1.70	1.0E-45	7657280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3101	15866	28507	7.42	1.0E-45	U32169.1	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3483	16240	28897	1.38	1.0E-46	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3590	16316	28992	1.19	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
4442	17178	29804	5.01	1.0E-45	BE396633.1	EST_HUMAN	6011239116F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3619803 5'
4877	17411		1.04	1.0E-46	H57443.1	EST_HUMAN	y05502.F1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:204395 5'
7930	20025	33782	0.77	1.0E-45	11422268	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
7930	20625	33753	0.77	1.0E-45	11422268	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8905	21197	34341	0.98	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9019	21709	34691	5.08	1.0E-45	BE887843.1	EST_HUMAN	601811228F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3612535 5'
9422	22100	35272	1.22	1.0E-45	AB002287.1	NT	Human mRNA for KIAA0299 gene, partial cds
11734	24327	37651	1.33	1.0E-45	7016570	NT	Homo sapiens alpha-catenin-like protein (VR22), mRNA
12097	24592	31125	0.93	1.0E-46	11416059	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12263	24708		11.18	1.0E-46	11526297	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12360	24711		5.28	1.0E-46	11418157	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAPT), mRNA
12680	24969	30991	2.6	1.0E-46	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8127	20821	33958	1.7	9.0E-48	8910293	NT	Mus musculus keratin complex 2, gene 5q (Krt2-5q), mRNA
8532	21224		5.86	9.0E-48	AL163209.2	EST	Homo sapiens chromosome 21 segment HS21C09
10378	23024	36239	11.23	9.0E-48	AW24584.1	EST_HUMAN	2822448 SpRime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822448 5'
2443	15162	27899	13.53	8.0E-48	A1433261.1	EST_HUMAN	182208.x1 NCI CGAP_Gsc4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:00314_rna2
2443	15162	27900	13.53	8.0E-48	A1433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7953	20848		5.89	8.0E-48	BE167244.1	EST_HUMAN	182208.x1 NCI CGAP_Gsc4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:00314_rna2
2232	14960	27700	1.03	7.0E-46	U46307.1	NT	TUBULIN BETA-1 CHAIN (HUMAN);
4541	17278		3.38	7.0E-46	BE395165.1	EST_HUMAN	RC3-H10508-260200-012-C12 H10508 Homo sapiens cDNA
4795	17487		1.33	7.0E-46	BE064386.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
5951	18733	31692	4.01	7.0E-48	8922708	NT	60127292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618118 5'
8402	19171	32170	1.14	7.0E-48	BF105845.1	EST_HUMAN	RC4-B10310-110300-015-H10 B10310 Homo sapiens cDNA
2759	15464	28207	3.00	6.0E-48	A1884381.1	EST_HUMAN	RC4-B10310-110300-015-H10 B10310 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
							601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
							wm3108.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
							MER19 repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2759	15464	28208	3.99	6.0E-46	AI884381.1	EST_HUMAN	wtm3109.x1 NCI_CGAP_Lu4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element ;
6038	18818	31779	10.94	6.0E-46	AI635448.1	EST_HUMAN	tt6810.x1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE ;
7116	19804	32988	0.72	6.0E-46	AW513244.1	EST_HUMAN	nc4264.x1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:2706854 3' similar to gb:U08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
11384	23175		2.04	6.0E-46	BE74971.1	EST_HUMAN	601478409F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3880995 5'
198	13012		8.9	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3519	16275	28929	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsli_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3519	16275	28930	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsli_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6636	18398	32413	1.86	5.0E-46	BF590442.1	EST_HUMAN	naa3807.x1 NCI_CGAP_Lu11 Homo sapiens cDNA clone IMAGE:3298757 3' similar to TR:O76202 O76202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
6942	19542	32570	4.29	5.0E-46	BF347235.1	EST_HUMAN	602021764F1 NCI_CGAP_Brn67 Homo sapiens cDNA
6925	18687	32738	0.62	5.0E-46	AW68283.1	EST_HUMAN	QV4-S10212-120100-975-f09 S10212 Homo sapiens cDNA
6515	22168	36390	0.47	5.0E-46	AA398381.1	EST_HUMAN	262208.s1 Scarsa_testis_NHT Homo sapiens cDNA clone IMAGE:726926 3'
625	13405		1.4	4.0E-46	AA601143.1	EST_HUMAN	nc54609.x1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_maf1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1689	14442	27140	8.88	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008938 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1699	14442	27141	6.86	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008938 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2743	15469	28198	2.62	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4384	17121	28753	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4384	17121	28754	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
6350	18163	30834	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
6350	18163	30835	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12513	24683	31014	2.71	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2X ₆ , complete cds
2755	14888	27618	0.9	3.0E-46	5453620	NT	Homo sapiens solute carrier family 35 (CHP-salic acid transporter), member 1 (SLC35A1), mRNA
2429	15784	27894	0.95	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4392	17100	28735	0.79	3.0E-46	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4724	17456	30091	1.2	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c, 1.1, 2) germline; (p-Light-Lambda; VLambda

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4724	17458	30082	1.2	3.0E-46	Z73680.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
8847	21339	34483	7.59	3.0E-46	AI031462.1	EST_HUMAN	Y19004.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2
11564	24163	37474	2.19	3.0E-46	D31765.1	NT	THR repetitive element.
817	13598	26255	7.64	2.0E-46	AA468546.1	EST_HUMAN	Human mRNA for KIAA0081 gene, partial cds
1554	14301		1.55	2.0E-46	AA678246.1	EST_HUMAN	ne0609.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element.
1637	14383	27070	3.43	2.0E-46	U78027.1	NT	247611.s1 Soares_fetal_liver_spleen_1NF.LS_31 Homo sapiens cDNA clone IMAGE:431998 3'
4917	17645	30258	1.2	2.0E-46	AA399286.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
7384	20064	33142	7.67	2.0E-46	8910569	NT	z69602.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW_RSP1_MOUSE Q01730 RSP-1 PROTEIN.1
7668	20663		1.46	2.0E-46	BE589151.1	EST_HUMAN	Mus musculus sperm tail associated protein (Stap), mRNA
12257	25179		1.5	2.0E-46	H46391.1	EST_HUMAN	601445137f1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849287 5'
12575	25170	30902	3.38	2.0E-46	AW277214.1	EST_HUMAN	y32801.r1 Soares_fetal_liver_spleen_1NF.LS_Homo sapiens cDNA clone IMAGE:206977 5'
1211	13951	26628	7.67	1.0E-46	4502884	NT	xq78608.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1566	14313	26809	1.23	1.0E-46	7662177	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
1566	14313	27000	1.23	1.0E-46	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2279	15005	27745	3.44	1.0E-46	AW978516.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2399	15120	27857	3.06	1.0E-46	H67330.1	EST_HUMAN	EST390625 IMAGE:resquences, MAGP Homo sapiens cDNA
3243	18005	28654	4.65	1.0E-46	AA631912.1	EST_HUMAN	EST480685 WATM1 Homo sapiens cDNA clone 480685
4918	17649		3.17	1.0E-46	AB023197.1	NT	np78602.x1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:376717 H.sapiens MT-11 mRNA (HUMAN);
5613	18409	31322	0.88	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
5688	25080	31617	6.14	1.0E-46	8923762	NT	762307.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5688	25080	31618	6.14	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
10770	18409	31322	5.27	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11747	24338	37665	1.53	1.0E-46	AW023178.1	EST_HUMAN	df50433.y1 Morton_Fetal_Cochlea_Homo sapiens cDNA clone IMAGE:3843705 3'
11747	24338	37666	1.53	1.0E-46	AW023178.1	EST_HUMAN	df50433.y1 Morton_Fetal_Cochlea_Homo sapiens cDNA clone IMAGE:2486861 5'
12044	24564	31115	2.28	1.0E-46	BF631102.1	EST_HUMAN	df50603.y1 Morton_Fetal_Cochlea_Homo sapiens cDNA clone IMAGE:2486861 5'
12044	24564	31116	2.28	1.0E-46	BF631102.1	EST_HUMAN	60207228f1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215398 5'
12778	25032		2.37	1.0E-46	AW15377.1	EST_HUMAN	60207228f1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215398 5'
1750	13522		6.18	9.0E-47	AJ271735.1	NT	A7116377 DGB_Homo sapiens cDNA clone DOBAIE03 5'
							Homo sapiens Xq pseudobulbar region; segment 1/2

Page 295 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4879	17606	30229	3.02	9.0E-47	AW770928.1	EST_HUMAN	h183604.x1 NCL CGAP_L1024 Homo sapiens cDNA clone IMAGE:3005534 3' similar to TR.O75703 O75703
6294	19057	32037	0.9	8.0E-47	11425439	NT	HYPOPHYSICAL 12.4 KD PROTEIN.
12631	26270	30725	2	9.0E-47	11417968	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1801	14541	27252	6.88	8.0E-47	Y11836.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801	14541	27252	6.88	8.0E-47	Y11836.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2722	15426	28187	1.04	8.0E-47	5453556	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3024	15790	28438	1.99	8.0E-47	AJ228043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R6E) mRNA
3613	16366	29009	0.68	8.0E-47	AB041928.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366	29010	0.68	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
12604	25169	34210	1.38	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
2550	15265	28000	1.68	8.0E-47	AL163246.2	NT	AV683284 GSK Homo sapiens cDNA clone GRCASH11 5'
8592	21284	34423	0.49	8.0E-47	U77054.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9176	21846	35012	0.76	8.0E-47	AB05169.1	EST_HUMAN	HS177054 Human Homo sapiens cDNA clone N7
9812	22265	35450	0.68	8.0E-47	AB042824.1	NT	1258602.x1 NCL CGAP_X4811 Homo sapiens cDNA clone IMAGE:2266559 3'
9812	22265	35451	0.68	8.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6482	19248	32246	6.67	5.0E-47	11423972	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
10586	23387	32246	5.27	5.0E-47	M78690.1	EST_HUMAN	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
1379	14126	28801	3.29	4.0E-47	4557568	NT	EST100736 Rat brain, Striatum (caudate) Homo sapiens cDNA clone HFBGF07
6733	19567	32599	1.9	4.0E-47	BE938398.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
8378	21072	34210	2.42	4.0E-47	BE616483.1	EST_HUMAN	MR2-TN108-280800-201-404 TNF108 Homo sapiens cDNA
8378	21072	34211	2.42	4.0E-47	BE616483.1	EST_HUMAN	601280485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8516	21206	34351	0.81	4.0E-47	AW693777.1	EST_HUMAN	601280485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
11635	24232		2.83	4.0E-47	AW15509.1	EST_HUMAN	RC3-BN0034-220300-015-005 BN0034 Homo sapiens cDNA
531	13315	25980	2.05	3.0E-47	BE007634.1	EST_HUMAN	Q64907.x1 NCL CGAP_L1024 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
531	13315	25981	2.05	3.0E-47	BE007634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
789	13571	26327	6.45	3.0E-47	NG7483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3659721 5'
624	13691	26356	10.26	3.0E-47	AL163284.2	NT	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3659721 5'
3269	16058	28707	0.79	3.0E-47	U63181.1	NT	y54604.s1 Scarsa, multiple sclerosis, 2N5HNSP Homo sapiens cDNA clone IMAGE:277327 3'
3948	16598		5.77	3.0E-47	UG3181.1	NT	Homo sapiens chromosome 21 segment HS21C084
4328	17068	28698	1.32	3.0E-47	M12959.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5922	18707	31659	5.41	3.0E-47	AW408900.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
							Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
							UHLF-BMD-404-07-04.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5922	18707	31690	5.41	3.0E-47	AW040860.1	EST_HUMAN	U1HF-BMO-adv-d-07-0-UL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6469	19236		1.78	3.0E-47	A1222413.1	EST_HUMAN	qH0407.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1943713 3'
8732	21424	34599	0.71	3.0E-47	AW683769.1	EST_HUMAN	EST1375859 IMAGE resequencing, MAGH Homo sapiens cDNA
8732	21424	34570	0.71	3.0E-47	AW683769.1	EST_HUMAN	EST1375859 IMAGE resequencing, MAGH Homo sapiens cDNA
143	12898	25600	1.61	2.0E-47	45053181	NT	Homo sapiens myosin phosphatase, large subunit 2 (MYPT2), mRNA
947	13713	26377	2.69	2.0E-47	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C09
947	13713	26378	2.69	2.0E-47	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C09
1590	14307		0.98	2.0E-47	AB69279.1	EST_HUMAN	w956502.x1 NCL_CGAP_G03 Homo sapiens cDNA clone IMAGE:2478851 3'
1590	14307		0.98	2.0E-47	AB69279.1	EST_HUMAN	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1598	14334	27022	1.75	2.0E-47	7662109	NT	ng43h12.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
1673	14418	27111	3.41	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens ling finger protein (C3HC4 type) 8 (RNF8), mRNA
4313	17052	29677	2	2.0E-47	4504888	NT	nt23a907.x1 NCL_CGAP_F11 Homo sapiens cDNA clone IMAGE:914652
4351	17090	29722	1.5	2.0E-47	AA569592.1	EST_HUMAN	nt23a907.x1 NCL_CGAP_F11 Homo sapiens cDNA clone IMAGE:914652
4351	17090	29722	1.5	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4471	17208	29832	1.66	2.0E-47	5174648	NT	EST1377239 IMAGE resequencing, MAGH Homo sapiens cDNA
4761	17463	30121	1.3	2.0E-47	AW685168.1	EST_HUMAN	Homo sapiens regulator of G-protein signaling 5 variant form (RGS5), mRNA, complete cds
5099	18490	31411	1.12	2.0E-47	AF073921.1	NT	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
5987	18673	31615	1.23	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
5987	18673	31616	1.23	2.0E-47	BE778475.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7568	25116		1.43	2.0E-47	L09731.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7884	20559	33685	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7884	20559	33686	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8618	21310	34452	1.67	2.0E-47	AF071771.1	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
5889	22051	35222	0.77	2.0E-47	11526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11451	23218	30451	1.27	2.0E-47	M76125.1	NT	Human tyrosine kinase receptor (src) mRNA, complete cds
12077	25312	30709	1.75	2.0E-47	R42423.1	EST_HUMAN	y92608.x1 Scores Infant brain NIH Homo sapiens cDNA clone IMAGE:20965 3' similar to contains OFR repetitive element
1384	14131	26804	7.35	1.0E-47	A1333429.1	EST_HUMAN	q956h03.x1 Scores_Fetal_Jung_NHRL19W Homo sapiens cDNA clone IMAGE:1931189 3'
5017	17736	30347	1.96	1.0E-47	AW613906.1	EST_HUMAN	RC3-ST0197-130400-017-H02 ST0197 Homo sapiens cDNA
6944	19426	32441	6.79	1.0E-47	A1880886.1	EST_HUMAN	af19408.x1 Barstead acra HPLR56 Homo sapiens cDNA clone IMAGE:2355688 3' similar to gb:M22995
8767	21459		0.56	1.0E-47	AW964648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10254	22902	38112	2.28	1.0E-47	330115.1	NT	h18441.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region

Page 297 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1607	14353	27041	3.03	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAGNA1E) gene, exons 7-48, and partial cds, alternatively spliced
3544	16258	28950	0.82	9.0E-48	BF356847.1	EST_HUMAN	CM2-MT0100-310700-290-070 MT0100 Homo sapiens cDNA
5594	18388	31239	0.86	9.0E-48	BE888195.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 6'
5594	18388	31300	0.88	9.0E-48	BE888193.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6010	18791	31754	0.66	9.0E-48	AI833188.1	EST_HUMAN	at75003.x1 Baricled cdon HPL R87 Homo sapiens cDNA clone IMAGE:2377859 3' similar to TR:O60844
6131	18909	31877	0.64	9.0E-48	AU123240.1	EST_HUMAN	Q60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN ;
11080	23730	37002	3.09	9.0E-48	BE393913.1	EST_HUMAN	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM100978 5'
1228	13878		1.44	9.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1229	13878		1.7	9.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3132	16597	28541	4.38	9.0E-48	AW768477.1	EST_HUMAN	Hk81b03.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3132	16597	28542	4.38	9.0E-48	AW768477.1	EST_HUMAN	Hk81b03.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3911	16691	28302	0.79	9.0E-48	4504119	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
478	13264		1.27	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
479	13264		17.09	7.0E-48	AB033035.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
1483	14230	28916	0.98	7.0E-48	9132719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1634	14380	27067	3.89	7.0E-48	5730338	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
6460	19227	32227	27.21	7.0E-48	11418831	NT	Homo sapiens SET domain and malin transposase fusion gene (SETMAR) mRNA
5867	18749	31710	0.91	9.0E-48	AB006955.1	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
6889	19005	32645	1.08	9.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
7365	25111	33123	0.98	9.0E-48	AB046844.1	NT	Homo sapiens BNX non-receptor tyrosine kinase (BNX), mRNA
7365	25111	33124	0.98	9.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9022	21712	34866	2.07	9.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9441	22119	35236	1.74	9.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9588	22241	35425	3.2	9.0E-48	AA189080.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11008 (FLJ1008), mRNA
3304	17878	28713	1.94	9.0E-48	4828881	EST_HUMAN	z445006 c1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains A1u repetitive element
8474	21168	34310	1.25	9.0E-48	BE084410.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
11603	24202	37524	3.96	9.0E-48	AB060289.1	EST_HUMAN	RCABT0311-141188-011-105 BT0311 Homo sapiens cDNA
10978	23558	35803	3.06	9.0E-48	AI620420.1	EST_HUMAN	MRO-NT0039-010500-002-068 NT0039 Homo sapiens cDNA
1384	14112	28786	1.27	9.0E-48	AV680954.1	EST_HUMAN	tu47a02.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:2284154 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1869	14705	27422	15.26	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
1869	14705	27423	15.26	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3622	16375	28017	0.76	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
5834	18594	31519	2.47	3.0E-48	BE084571.1	EST_HUMAN	P65555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6919	18655	32701	0.84	3.0E-48	AF087913.1	NT	MR2-B10657-060400-201+10 BT10657 Homo sapiens cDNA
8290	20984		3.41	3.0E-48	AA659930.1	EST_HUMAN	Human endogenous retrovirus HENV-P-T47D
10784	23467	35708	9.32	3.0E-48	BF514170.1	EST_HUMAN	nv0303.571 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5b1
44	12873	25495	1.71	2.0E-48	AA631940.1	EST_HUMAN	PTP3 repetitive element ;
1197	13549		5.15	2.0E-48	H24278.1	EST_HUMAN	U-H-BW1-ep1-a-10-0-J1.x1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:308287 3'
4485	17231	28661	1.42	2.0E-48	BE246065.1	EST_HUMAN	Imc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone GR17-26
5724	18516	31436	0.61	2.0E-48	AA613171.1	EST_HUMAN	ym55a10.r1 Scores Infant brain 1N18 Homo sapiens cDNA clone IMAGE:52182 5' similar to
5724	18516	31437	0.61	2.0E-48	AA613171.1	EST_HUMAN	SP-M6B_MOUSE P35803 MEMBRANE GLYCOPROTEIN ;
7419	20096	33182	4.77	2.0E-48	AB040341	NT	TCBAP1D3842 Pedialtic pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo
7419	20096	33183	4.77	2.0E-48	AB040341	NT	sapiens cDNA clone TCBAP3842
7432	20109	33197	3.35	2.0E-48		EST_HUMAN	nc18g01.x1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
8253	20547	34084	1.33	2.0E-48	AV743451.1	EST_HUMAN	nc18g01.x1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
12041	17688	30486	4.27	2.0E-48	AA465007.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
12687	26232	30820	1.86	2.0E-48	BE137154.1	EST_HUMAN	Homo sapiens v-v1 avian reticuloendothelias viral oncogene homolog A (nuclear factor of kappa light
12716	13549		1.34	2.0E-48	H24278.1	EST_HUMAN	polyptide gene enhancer in B-cells 3 (p65) (REL A), mRNA
54	12883	26511	2.3	1.0E-48	7706534	NT	AV743451 CB Homo sapiens cDNA clone C80CGG10 5'
853	13623	26293	17.13	1.0E-48	4502168	NT	z80c03.r1 Scores ovary tumor NBH-OT Homo sapiens cDNA clone IMAGE:810062 5'
1273	14023	26691	3.77	1.0E-48	5032032	NT	601303004F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
1911	14648	27350	30.36	1.0E-48	AL163302.2	NT	ym55a10.r1 Scores Infant brain 1N18 Homo sapiens cDNA clone IMAGE:52182 5' similar to
3481	16236	26884	0.96	1.0E-48	AL163246.2	NT	SP-M6B_MOUSE P35803 MEMBRANE GLYCOPROTEIN ;
5061	17760	30398	1.8	1.0E-48	M10976.1	NT	Homo sapiens c16p11 resistance-associated overexpressed protein (LOC51747), mRNA
6195	18971	31946	1.17	1.0E-48	AI869077.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
							Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
							Homo sapiens chromosome 21 segment HS21C102
							Homo sapiens chromosome 21 segment HS21C046
							Human endogenous retroviral DNA (4-1), complete retroviral segment
							Id17cd1.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075804 3' similar to TR:O14598 O14598
							SIMILARITY TO U73941 ;

Page 299 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6195	18771	31947	1.17	1.0E-48	AB89077.1	EST_HUMAN	Id17301.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2079604 3' similar to TR:O14988 O14988 SIMILARITY TO U73941:
6407	18178		0.94	1.0E-48	Y18020.1	NT	Homo sapiens NF2 gene
6500	19265	32268	0.71	1.0E-48	AB028894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6500	19266	32267	0.71	1.0E-48	AB028894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7157	19844	32813	2.52	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
8730	21422	34566	0.76	1.0E-48	4759695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8730	21422	34567	0.76	1.0E-48	4759695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9133	21801	34960	0.84	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9198	21838	35004	6.4	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9481	22134	35314	5.33	1.0E-48	BF304683.1	EST_HUMAN	601880696F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10269	22917	35127	4.08	1.0E-48	11423938	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10269	22917	35128	4.08	1.0E-48	11423938	NT	Homo sapiens B cell linker protein (SLP65), mRNA
2002	14737	27461	1.13	8.0E-49	AB028497.1	NT	Mus musculus MyoP2 mRNA for myosin containing PDZ domain, complete cds
5992	18744	31704	3.43	8.0E-48	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
5992	18744	31705	3.43	8.0E-48	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8194	20888	34026	3.17	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
9889	22539	35733	1.15	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type 1 mRNA, complete cds
135	13171	28814	1	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
135	13171	28815	1	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
384	13171	28814	1.73	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
384	13171	28815	1.73	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
385	13171	28814	2.94	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
385	13171	28815	2.94	7.0E-49	8728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
1199	13551	28815	3.4	7.0E-49	AL163284.2	NT	Homo sapiens proteasome 21 segment HS21C084
5373	18173	30892	2.11	7.0E-49	AI807191.1	EST_HUMAN	W726H04.x1 Scores, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2356883 3' similar to TR:O54923 O54923 RSEC15:
5383	18183	30873	1.46	7.0E-49	AL120937.1	EST_HUMAN	DKFZp762C033.1 762 (synonym: hmal2) Homo sapiens cDNA clone DKFZp762C033.3
5716	18173	30862	0.87	7.0E-49	AI807191.1	EST_HUMAN	w25H04.x1 Scores, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2356883 3' similar to TR:O54923 O54923 RSEC15:
102	13005	25646	12.12	8.0E-49	AW731740.1	EST_HUMAN	bc55g06.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20692 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4085	16837	29464	1.27	8.0E-49	AL162081.1	EST_HUMAN	DKFZp761A138.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138.3

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6349	18118	32109	0.94	0.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone IMAGE:000148 5'
7314	19897	33076	0.69	0.0E-49	AW511235.1	EST_HUMAN	H044602.1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O965936
8633	22285	35478	0.45	0.0E-49	9910293	NT	O96596 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
9533	22285	35479	0.45	0.0E-49	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-5g), mRNA
11248	23910	37202	2.6	0.0E-49	AW452218.1	EST_HUMAN	U141813-10c-40c-01 U1 N1 C1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11661	24257	37579	2.8	0.0E-49	AA386556.1	EST_HUMAN	EST77626 Pancreas tumor III Homo sapiens cDNA 5' end
11661	24257	37580	2.8	0.0E-49	AA386556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
12362	25151	37580	2.03	0.0E-49	AA707667.1	EST_HUMAN	229c08.s1 Soares_feld_liver_salad1_INFLS S1 Homo sapiens cDNA clone IMAGE:451694 3'
695	13470	28117	7	0.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
695	13470	28118	7	0.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1786	14527	27235	3.49	0.0E-49	AA172421.1	EST_HUMAN	z029c07.r1 Striatogene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:610890 5' similar to
2764	15459	28201	4.26	0.0E-49	U17714.1	NT	TR:G333229 G333226 RTV/L-H PROTEIN, contains LTR7.13 L TR7 L TR7 repetitive element ;
3267	16029	28678	2.84	0.0E-49	11436355	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
512	13296	25927	47.84	0.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC633862), mRNA
7172	19858	32930	0.95	0.0E-49	11525737	NT	CE08703 ;
7172	19858	32931	0.95	0.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylglucosaminyltransferase 8
7710	20374	33468	0.9	0.0E-49	7682209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylglucosaminyltransferase 8
8763	21455	34604	0.47	0.0E-49	11425374	NT	Homo sapiens (GALNT8), mRNA
8763	21455	34605	0.47	0.0E-49	11425374	NT	Homo sapiens KIAA0523 gene product (KIAA0523), mRNA
12221	25368		4.21	0.0E-49	AA210798.1	EST_HUMAN	Homo sapiens copine III (CPNE3), mRNA
12306	24730		4.1	0.0E-49	AF240788.1	NT	z08005.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:982877 5'
547	15330	25961	1.73	0.0E-49	X65568.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2654	15934		1.8	0.0E-49	AA016131.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
4923	17651	30284	2.33	0.0E-49	U46989.1	NT	z051005.r1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:300594 5' similar to contains 1.13 L1
7319	20002	33081	11.87	0.0E-49	H33479.1	EST_HUMAN	repetitive element ; Human type IV collagen (COL4A6) gene, exon 40
							EST25a12 WATM1 Homo sapiens cDNA clone 25a12

Page 301 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11272	23933	37226	1.88	3.0E-49	A4337561.1	EST HUMAN	EST 42872 Endometrial tumor Homo sapiens cDNA 5' end
646	13425		2.64	2.0E-49	BE165980.1	EST HUMAN	MR3-H10487-160200-113-q01 HT10487 Homo sapiens cDNA
3216	15979	28930	1.64	2.0E-49	N26446.1	EST HUMAN	YK23d06.r1 Soares melanocyte 2N5NHM Homo sapiens cDNA clone IMAGE:282571 5'
							q28d02.1 Soares, senescent, fibroblasts, NHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to
							gb1M31470 RAS-LIKE PROTEIN TC10 (HUMAN) contains Alu repetitive element contains element MER22
							repetitive element 1
4746	17478	30110	0.66	2.0E-49	AI167357.1	EST HUMAN	UI-H814-qps-d-02-q1.1 NCJ CGAP Sub8 Homo sapiens cDNA clone IMAGE:3088534 3'
4758	17490	30116	0.74	2.0E-49	BF611846.1	EST HUMAN	UI-H814-qps-d-02-q1.1 NCJ CGAP Sub8 Homo sapiens cDNA clone DCSALB01 5'
6937	19390	32414	1.71	2.0E-49	AV717898.1	EST HUMAN	EST102558 Fetal brain, Striatum (cell433208) Homo sapiens cDNA clone HFB0CY60
7998	20893		1.74	2.0E-49	N88033.1	EST HUMAN	Homo sapiens SINGA isoform (SINGA) gene, complete cds, alternatively spliced
12316	26250		2.07	2.0E-49	AF163864.1	NT	601459531FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3962088 5'
879	13848		5	1.0E-49	BF035327.1	EST HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
1546	14292	26976	1.11	1.0E-49	4557887	NT	601115769F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3358273 5'
1794	14534	27243	4.82	1.0E-49	BE255216.1	EST HUMAN	60120033F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052032 5'
5276	18080	30737	6.82	1.0E-49	BF131007.1	EST HUMAN	YH4804.r1 Soares adult brain N26HBB57 Homo sapiens cDNA clone IMAGE:171703 5' similar to
							SP-C8041_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G17 GAMMA-1 SUBUNIT 1
5986	18767	31731	0.88	1.0E-49	K18291.1	EST HUMAN	EST1376713 IMAGE: ressequences, MAGH Homo sapiens cDNA
5992	18773	31736	6.55	1.0E-49	AW054640.1	EST HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCYD11 5'
7117	19806	32660	0.82	1.0E-49	AV703000.1	EST HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCYD11 5'
7117	19906	32870	0.82	1.0E-49	AV703000.1	EST HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620883 5'
7123	19811	32876	3.55	1.0E-49	BE988110.1	EST HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620883 5'
7123	19811	32879	3.65	1.0E-49	BE988110.1	EST HUMAN	YH7812.s1 Soares, placenta, 80gbweeks, 2N6HPP82dW Homo sapiens cDNA clone IMAGE:288406 3' similar to gb-X65873 KINESIN HEAVY CHAIN (HUMAN);
7200	19886	32960	2.21	1.0E-49	N25894.1	EST HUMAN	YH7812.s1 Soares, placenta, 80gbweeks, 2N6HPP82dW Homo sapiens cDNA clone IMAGE:288406 3' similar to gb-X65873 KINESIN HEAVY CHAIN (HUMAN);
7200	19886	32981	2.21	1.0E-49	N25894.1	EST HUMAN	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUGLO1), mRNA
7977	20872	33785	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUGLO1), mRNA
7977	20872	33786	0.69	1.0E-49	11321580	NT	Homo sapiens RNA binding motif protein 7 (LOC61120), mRNA
8575	21267		0.68	1.0E-49	9894184	NT	601300592F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
8581	21582	34721	1.29	1.0E-49	BE40840.1	EST HUMAN	DKFZP4402423 J1 434 (synonym: HES3) Homo sapiens cDNA clone DNFBZ434D2423 5'
10026	22974	35989	1.98	1.0E-49	AL043128.2	EST HUMAN	AV761477 NPD Homo sapiens cDNA clone NPDAWE04 5'
10979	23654	36007	1.43	1.0E-49	AV761477.1	EST HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11261	23942	37236	3.32	1.0E-49	11427368	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12215	24677		2.46	1.0E-49	11418322	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
4937	17695		1.4	9.0E-60	AF101473.1	NT	

Page 302 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6310	25421		0.95	9.0E-50	BE28758.1	EST_HUMAN	601170250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
168	12989	25619	2.56	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
702	13477	26125	4.04	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
702	13477	26125	2.54	8.0E-50	X65097.2	NT	Homo sapiens mRNA for VIP receptor 2
1768	14500	27201	2.82	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2703	15410	28147	1.48	8.0E-50	4826553	NT	Homo sapiens capping protein (actin filament) muscle Z line, beta (CAPZB), mRNA
2833	14691		15.7	8.0E-50	D90334.1	NT	Homo sapiens hepatocyte growth factor(HGF) gene, exon 18
11385	23692	37293	1.29	8.0E-50	AA633467.1	EST_HUMAN	nm62406.s1 NCI CGAP_B2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05439
605	13593	26015	0.76	7.0E-50	BE088591.1	EST_HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS(BRAN (HUMAN);
6587	19804	32843	1.08	7.0E-50	BF091922.1	EST_HUMAN	QV6-BT0793-260400-211-408 BT0703 Homo sapiens cDNA
6587	19804	32844	1.06	7.0E-50	BF091922.1	EST_HUMAN	RC6-BT0073-150600-011-A12 TN0073 Homo sapiens cDNA
7205	19590	32666	0.6	7.0E-50	AA627822.1	EST_HUMAN	RC6-BT0073-150600-011-A12 TN0073 Homo sapiens cDNA
10558	23047	36584	7.65	7.0E-50	AB72137.1	EST_HUMAN	ng38e12.s1 NCI CGAP_C68 Homo sapiens cDNA clone IMAGE:1148209 3' similar to gb:X65891 60S
4309	17048		0.98	6.0E-50	BE784381.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
8112	20805		5.97	6.0E-50	BE044076.1	EST_HUMAN	nm55611.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439008 3'
10717	23406	36248	12.6	6.0E-50	AA312079.1	EST_HUMAN	h036104.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:36943677 5'
10717	23406	36647	12.8	6.0E-50	AA312079.1	EST_HUMAN	h036104.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1785	14526	27233	1.1	5.0E-50	BF332938.1	EST_HUMAN	MER29 repetitive element;
1785	14526	27234	1.1	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
8990	21680		5.26	5.0E-50	AA557863.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
897	13665		1.71	4.0E-50	AA601143.1	EST_HUMAN	CMD-BT0792-300500-308-505 BT0792 Homo sapiens cDNA
3441	16197	28847	0.99	4.0E-50	AL163248.2	NT	CMD-BT0792-300500-308-505 BT0792 Homo sapiens cDNA
6268	16041	32016	0.98	4.0E-50	1140663	NT	h045HT0.s1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.b3 PTR5
7135	19822	32888	1.95	4.0E-50	BE087538.1	EST_HUMAN	repetitive element;
1631	14657		4.13	3.0E-50	IM6048.1	NT	nm54400.s1 NCI CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_mn1
3283	16054	28703	1.24	3.0E-50	AA748142.1	EST_HUMAN	PIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3734	16487	28124	1.14	3.0E-50	AA755254.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens cystinyl-RNA synthetase (CARS), mRNA
							QV4-BT0681-280300-127-412 BT0681 Homo sapiens cDNA
							Human endogenous retrovirus RTVL-H2
							nm53008.s1 NCI CGAP_K163 Homo sapiens cDNA clone IMAGE:1328267 3'
							CNAYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CNAYAS
							Cardiomyopathy associated gene 5

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6987	19584	32818	1.52	3.0E-50	11421514	NT	Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC53232), mRNA
7544	20214	33314	4.85	3.0E-50	AF233438.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7544	20214	33315	4.85	3.0E-50	AF233438.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8481	21173	34318	0.71	3.0E-50	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9718	22369	35597	1.21	3.0E-50	AB046918.1	NT	Homo sapiens mRNA for KIAA1868 protein, partial cds
9727	22378	35590	0.69	3.0E-50	11418514	NT	Homo sapiens T-complex 10 (a murine top homolog) (TCP10), mRNA
10077	22725	35942	0.47	3.0E-50	Y18276.1	NT	Mus musculus mRNA for neurobeachin
10415	23061	36280	1.03	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0359 gene, partial cds
11045	23715	36884	1.61	3.0E-50	11436955	NT	Homo sapiens G12-associated binder 2 (KIAA0571), mRNA
11441	23208	39439	5.35	3.0E-50	AJ245821.1	NT	Homo sapiens CTL2 gene
760	13532		5.38	2.0E-50	AF050065.1	NT	Homo sapiens MHC class I region
1057	13815	28476	5.57	2.0E-50	4557762	NT	Homo sapiens midline 1 (Optiz/BEB syndrome) (MID1) mRNA
1424	14171	28857	2.25	2.0E-50	AF198303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
6769	19513	32539	0.59	2.0E-50	AU124068.1	EST_HUMAN	AU124068 NT2R42 Homo sapiens cDNA clone NT2R42001609 5'
8215	20509	34044	1.02	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8215	20509	34045	1.02	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8355	21048	34186	10.04	2.0E-50	X06565.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8355	21048	34187	10.04	2.0E-50	X06565.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9784	22435	35641	1.61	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 5g (K12-5g), mRNA
9784	22435	35642	1.61	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 5g (K12-5g), mRNA
11960	24256		1.8	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
449	13255	25874	1.92	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C09
2385	15087		9.48	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10093	22741	35656	1.57	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
5933	18678	31624	1.21	9.0E-51	AW511225.1	EST_HUMAN	Id44602.x1 Soares, JNF, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6130	18608	31876	0.71	9.0E-51	AA744637.1	EST_HUMAN	O95936 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
8572	21284	34403	0.65	9.0E-51	AI761154.1	EST_HUMAN	in67103.61 NCI CCAP CGB1 Homo sapiens cDNA clone IMAGE:1293381 3'
9224	21903	35075	1.23	9.0E-51	AA043738.1	EST_HUMAN	ab23504.35 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841688 3' similar to
							SW-PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							2451c09.71 Soares, pregnant uterus, NHKPU Homo sapiens cDNA clone IMAGE:489932 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9400	22002	35231	0.66	9.0E-51	AI791154.1	EST_HUMAN	ab22604.x5 Stragelens lung (#637210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW-PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9400	22082	36232	0.66	9.0E-51	AI791154.1	EST_HUMAN	ab22604.x5 Stragelens lung (#637210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW-PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11455	22222	36459	1.89	9.0E-51	H89078.1	EST_HUMAN	hw2408.11 Marton Fetal Coclella Homo sapiens cDNA clone IMAGE:263210 5'
11455	22222	36457	1.89	9.0E-51	H89078.1	EST_HUMAN	hw2408.11 Marton Fetal Coclella Homo sapiens cDNA clone IMAGE:263210 5'
11823	18908	31878	1.43	9.0E-51	AA744837.1	EST_HUMAN	hw87103.1 NCL CGAP GC81 Homo sapiens cDNA clone IMAGE:1283381 3'
4405	17142	29770	1.45	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4405	17142	28771	1.45	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4530	17265	29868	8.43	8.0E-51	AA610842.1	EST_HUMAN	hw89409.1 NCL CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb-X12871_mnt1
7592	20222	33325	2.24	8.0E-51	11439587	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
8384	21639		1.13	8.0E-51	AI138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NT-CC-38), mRNA
11812	20222	33325	2.02	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NT-CC-38), mRNA
3015	15781	28430	0.9	7.0E-51	AW274720.1	EST_HUMAN	hw34403.1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR-Q82340
3276	16037	28687	1.45	7.0E-51	AW869218.1	EST_HUMAN	Q92340 A TYPICAL PKC SPECIFIC BINDING PROTEIN ;
4140	18988	28518	1.37	7.0E-51	AL079628.1	EST_HUMAN	QV410028-200400-180-406 NT0028 Homo sapiens cDNA
4146	18988	29520	1.37	7.0E-51	AL079628.1	EST_HUMAN	DKFZP434B2229.11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434B2229 5'
4318	17057	29681	2.71	7.0E-51	AW295903.1	EST_HUMAN	DKFZP434B2229.11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434B2229 5'
11688	24281	37603	1.34	7.0E-51	AF167449.1	NT	U1-HWYO-epb-05-05-JUL1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:2729817 3'
1072	14708	27426	4.06	6.0E-51	7657266	NT	Homo sapiens HSP-C331 mRNA, partial cds
3468	16222	29878	14.73	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
5901	19588	31634	1.56	6.0E-51	X01788.1	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
5912	19586	31648	9.95	6.0E-51	AF070083.1	NT	Human haptoglobin related (Hprl) gene exon 3
5912	19586	31649	9.95	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6693	19580	32615	1.02	6.0E-51	4506736	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6792	19589	32654	0.97	6.0E-51	11410751	NT	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RP-S8KB1) mRNA
6988	17943	30540	2.2	6.0E-51	11429693	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56999), mRNA
9035	21726	34878	0.69	6.0E-51	11429525	NT	Homo sapiens cerebral cell adhesion molecule (CCAM146), mRNA
9035	21726	34879	0.69	6.0E-51	11429525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9982	22235	35419	2.18	6.0E-51	7681635	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6602	22314	38511	0.67	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11221	23884	37169	1.51	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL-17R), mRNA
11515	24115	37425	1.52	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11515	24115	37428	1.52	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
774	13546	26207	11.81	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
785	13557	26219	1.98	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
970	15557	26400	0.85	6.0E-51	AL132204.1	NT	Novel human gene mapping to chromosome X
1603	14349	27038	0.89	6.0E-51	5031890	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2001	16318	28052	8.67	5.0E-51	AJ007558.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3025	16875	29318	1.52	6.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3025	16875	29317	1.52	6.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
11249	23911	37203	4.18	5.0E-51	5803198	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
1163	13908	26571	3.65	3.0E-51	AI897348.1	EST_HUMAN	t81c09.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
4292	17031	29859	1.97	3.0E-51	AL159142.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
7479	20152	33246	3	3.0E-51	R16914.1	EST_HUMAN	Human hnRNP C2 protein mRNA
8738	21430		4.86	3.0E-51	M29063.1	NT	Human hnRNP C2 protein mRNA
8686	25430		0.47	3.0E-51	AW563777.1	EST_HUMAN	Human hnRNP C2 protein mRNA
357	13155	25766	2.01	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1683	14427	27124	5.16	2.0E-51	AA233352.1	EST_HUMAN	z39a05.11 Striatum NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR-G332229 G333228 RTVL-H PROTEIN. contains LTR7.13 LTR7 repetitive element;
3716	10469	29107	1.97	2.0E-51	AI492415.1	EST_HUMAN	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'
4458	17184	28820	0.78	2.0E-51	AW137826.1	EST_HUMAN	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'
5352	18155	30837	0.7	2.0E-51	AI732951.1	EST_HUMAN	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'
5352	18155	30838	0.7	2.0E-51	AI732951.1	EST_HUMAN	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'
5925	18709	31663	3.66	2.0E-51	BE782015.1	EST_HUMAN	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'
7209	18894		0.81	2.0E-51	AF210927.1	NT	UJH-B11-eql-492-0-11.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2131732 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7357	20038	33116	1.08	2.0E-51	7682349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0868), mRNA
8599	21261	34432	1.72	2.0E-51	BE001994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858613 5'
8599	21261	34433	1.72	2.0E-51	BE001994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858613 5'
8932	21623	34768	0.96	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISG1), mRNA
9412	22060	35281	1.45	2.0E-51	A1917078.1	EST_HUMAN	ts74d07.x1 NCI_CGAP_CG8 Homo sapiens cDNA clone IMAGE:2236880 3' similar to SW:TRKG_HUMAN
9503	22156	35336	0.68	2.0E-51	BE165980.1	EST_HUMAN	P16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
9519	22172	35355	0.6	2.0E-51	AB007828.1	NT	MR3-HT1047-150200-119-401 HT10487 Homo sapiens cDNA
9519	22172	35355	0.6	2.0E-51	AB007828.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10332	22879	36199	1.77	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10370	23016	36232	2.67	2.0E-51	AA378659.1	EST_HUMAN	EST161298 Synovial sarcoma Homo sapiens cDNA 5' end
11298	18155	30837	8.32	2.0E-51	A1732851.1	EST_HUMAN	td33409.x6 NCI_CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
11298	18155	30838	8.32	2.0E-51	A1732851.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
12523	24870	31017	2.1	2.0E-51	11419159	NT	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
112	12934	25571	6.74	1.0E-51	4503528	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11b)(2)(p13)(q24)) (MLL14), mRNA
1479	14226	30294	20.32	1.0E-51	AV742248.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA
4559	17684	30294	1.32	1.0E-51	BE776038.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
5305	18110	30769	4.1	1.0E-51	T18862.1	EST_HUMAN	60146495F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3858246 5'
7549	20219	33322	0.84	1.0E-51	A1572532.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
7803	20498	33918	0.81	1.0E-51	BF434359.1	EST_HUMAN	td339502.x1 Soares NIH/NHLBI ST Homo sapiens cDNA clone IMAGE:2089108 3'
11793	25434	36520	2	1.0E-51	AV760590.1	EST_HUMAN	7c86602.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644051 3' similar to TR:P87892 P87892
10587	23282	36520	1.39	8.0E-52	R91638.1	EST_HUMAN	PROTEASE;
10587	23282	36521	1.39	9.0E-52	R91638.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSCB02 5'
12301	24726		5.36	9.0E-52	AA777621.1	EST_HUMAN	X11004.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196557 5' similar to
148	12963	25505	9.99	8.0E-52	AA720574.1	EST_HUMAN	SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION;
1482	14229	28915	1.65	8.0E-52	X84900.1	NT	X11004.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196557 5' similar to
							SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION;
							td368047.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
							contains THR13 THR repetitive element;
							tw27g02.s1 NCI_CGAP_CG80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
							THR repetitive element;
							H.sapiens mRNA for laminin-5, alpha3b chain

Page 307 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1650	14398	27085	3.13	8.0E-52	U1898028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1650	14395	27086	3.13	8.0E-52	U1898028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3976	14396	27085	6.6	8.0E-52	U1898028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3976	14398	27086	6.6	8.0E-52	U1898028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7417	20094	33178	0.67	8.0E-52	U1416685	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7417	20094	33179	0.67	8.0E-52	U1416685	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8911	21602	34745	2.04	7.0E-52	W56471.1	EST_HUMAN	z559a03.r1 Soares_papillary_thyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1164	13918		0.76	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271239-Q49-307 BT0537 Homo sapiens cDNA
1689	14433	27129	4.27	6.0E-52	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5841	18438	31349	0.86	6.0E-52	U1203704.1	EST_HUMAN	ig44104.x1 Soares_breast_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11170	23837	37119	1.94	8.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NC1_OGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281871 5' similar to SW:PG5M_MOUSE_Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR
9222	21959	35132	0.6	5.0E-52	U1437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1723	14466	27165	1.32	4.0E-52	U4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1), mRNA
1780	14521	27225	1.02	4.0E-52	U4758843	NT	Homo sapiens nucleoporin 155kD (NUP155), mRNA
3906	16959	29287	0.89	4.0E-52	U4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
5204	18012	30633	1.33	4.0E-52	U4506132	NT	Homo sapiens phosphatidylyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA
5204	18012	30634	1.33	4.0E-52	U4506132	NT	Homo sapiens phosphatidylyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA
7938	20633	33760	1.74	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818808 5'
8432	21125	34293	5.48	4.0E-52	U1417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12143	24631		5.11	4.0E-52	U1418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12627	24930		5.22	4.0E-52	AB02059.1	NT	Homo sapiens DNA for Human P2X ₂ complete cds
4071	16815		10.57	3.0E-52	U1437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
549	13332	25962	2.88	2.0E-52	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
549	13332	25963	2.88	2.0E-52	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

Page 308 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2503	15220	27663	2.04	2.0E-52	BE207575.1	EST_HUMAN	b66607.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb.X16403 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2740	15446		6.03	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4020	17648	30260	2.13	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
4952	17678	30287	1.29	2.0E-52	AI141802.1	EST_HUMAN	ga56a05.s1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
4952	17678	30288	1.29	2.0E-52	AI141802.1	EST_HUMAN	ga56a05.s1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5917	18413	31328	4.11	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-050-E12 CT0214 Homo sapiens cDNA clone IMAGE:1690784 3'
6274	19047	32024	1.86	2.0E-52	11141868	EST_HUMAN	Homo sapiens interferon 21 receptor (IL21R), mRNA
6813	19376	32390	0.99	2.0E-52	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6843	19543	32571	1.17	2.0E-52	AI792146.1	EST_HUMAN	ga5612.y5 NCI_CGAP_B72 Homo sapiens cDNA clone IMAGE:1608311 5'
8551	21243		9.03	2.0E-52	AF147860.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
8834	21528	34672	0.81	2.0E-52	AA78795.1	EST_HUMAN	245g05.s1 Soares_fetal_liver_spleen_1 INFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9379	21954		0.88	2.0E-52	4756789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10015	22653	35879	5.83	2.0E-52	6730038	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
10015	22653	35880	5.83	2.0E-52	6730038	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
11185	23832	37111	3.15	2.0E-52	AB31462.1	EST_HUMAN	W48c04.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element;
11165	23832	37112	3.15	2.0E-52	AB31462.1	EST_HUMAN	W48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element;
11178	23845	37131	3.09	2.0E-52	AV16377	EST_HUMAN	AV16377 DOB Homo sapiens cDNA clone DCBAIE03 5'
11325	24016		1.72	2.0E-52	AV16377.1	EST_HUMAN	AV16377 DOB Homo sapiens cDNA clone IMAGE:344038 5'
11618	24215		2.76	2.0E-52	W70280.1	EST_HUMAN	245g12.r1 Soares_fetal_heart_NDPH19W Homo sapiens cDNA clone IMAGE:344038 5'
11618	24215		2.76	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
11981	25408	30601	24.36	2.0E-52	AW236297.1	EST_HUMAN	xn72a07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700039 3' similar to contains ALU repetitive element; contains element LTR2 repetitive element;
12350	24796		4.49	2.0E-52	AB08985.1	EST_HUMAN	W67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TRQ16859
520	13304	25937	1.96	1.0E-52	AA834445.1	EST_HUMAN	Q16859 CARBOXYL ESTERASE
1350	14068	26773	37.84	1.0E-52	4504026	NT	2475h12.r1 Soares_gelatin_NHT Homo sapiens cDNA clone IMAGE:743879 3'
2537	15252		0.9	1.0E-52	4502238	NT	Homo sapiens glutamate-aminoligase (glutamine synthase) (GLUL) mRNA
3055	15821	28465	2.67	1.0E-52	S61070.1	NT	Homo sapiens erythroferrone D (ARSD), transcript variant 1, mRNA
5250	15056	30984	4.35	1.0E-52	M29426.1	NT	poly(ADP-ribose) polymerase 1 (PARP1), human, endogenous retroviral element RTVL-Hp1, Genomic, 600 nt
6300	18073	32059	2.51	1.0E-52	U38954.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6300	18073	32059	2.51	1.0E-52	U38954.1	NT	Human PMS2 related (hPMSR2) gene, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	20012	33080	5.31	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8364	21057		1.2	1.0E-52	AF163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8037	21176	34940	0.75	1.0E-52	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10478	23122		1.03	1.0E-52	AW020370.1	EST_HUMAN	d18g05.v7 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10486	23132		1.39	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10865	23356	35596	1.81	1.0E-52	U48266.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (PTPCCAAX1) mRNA, complete cds
10740	23427		2.09	1.0E-52	11425321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3771	16523	29191	1.05	9.0E-53	4506004	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4359	17097	29732	1.86	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CSF1A1) gene, exon 3
12188	24680		3.18	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4132793 5'
12800	25285		4.92	7.0E-53	AI421782.1	EST_HUMAN	164107.x1 NCI_CGAP_Bln23 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR.11
5089	17805	30422	1.02	6.0E-53	BE295719.1	EST_HUMAN	THR repetitive element
4078	16822	26448	2.28	5.0E-53	4758543	NT	601175776F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3630946 5'
12238	24688		1.58	5.0E-53	AW813553.1	EST_HUMAN	Homo sapiens heterogenous nuclear ribonucleoprotein C (C11C2) (HNRPO) mRNA
48	12877	25502	2.78	4.0E-53	AL163285.2	NT	RC3-ST0187-151059-011-010 ST0197 Homo sapiens cDNA
4771	17503	30125	1.03	4.0E-53	7705414	NT	Homo sapiens chromosome 21 segment HS21C085
9316	21883		0.68	4.0E-53	AI813037.1	EST_HUMAN	Homo sapiens hook1 protein (HOOK1), mRNA
9659	22308		0.57	4.0E-53	FI3080.1	EST_HUMAN	MSB04.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2278327 3'
11175	23842	37128	2.78	4.0E-53	BF128701.1	EST_HUMAN	HSC3J0041 normalized infant brain cDNA Homo sapiens cDNA clone e-3id04
	23842	37127	2.78	4.0E-53	BF128701.1	EST_HUMAN	601810689F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							601810689F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2655	15375	28114	1.77	3.0E-53	AB026598.1	NT	
4549	17284	28914	0.74	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UNC081 Homo sapiens cDNA
5339	18142	30803	0.7	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5338	18336	31243	0.82	3.0E-53	11526287	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6101	18879		0.85	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
6888	19690	32740	1.04	3.0E-53	Y10388.3	NT	H. sapiens gdf gene
6998	19690	32741	1.04	3.0E-53	Y10388.3	NT	H. sapiens gdf gene
8203	20097	34034	12.52	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
8758	21450	34587	0.65	3.0E-53	10895090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8895	21848		8.41	3.0E-53	5901953	NT	Homo sapiens GGFRI oncogene partner (GFP), mRNA
11828	24410	37746	2.78	3.0E-53	8823598	NT	Homo sapiens hypothetical protein FLJ20944 (FLJ20944), mRNA

Page 310 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	13231		5.82	2.0E-53	AA369556.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' and
2327	15062	27788	2.79	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2538	15263		8.73	2.0E-53	4502316	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) 31KD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
2729	15438	28172	1.48	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2729	15439		1.49	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3239	18001	28651	3.72	2.0E-53	AF1983822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4038	18781	29411	2.53	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5340	18143	30804	2.57	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT03056-17060D-001-g03 CT03056 Homo sapiens cDNA
5340	18143	30805	2.67	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT03056-17060D-001-g03 CT03056 Homo sapiens cDNA
7770	20466	33590	1	2.0E-53	AW976598.1	EST_HUMAN	EST139707 MAGE resequences, MAGE Homo sapiens cDNA
8306	21975		3.82	2.0E-53	AW245878.1	EST_HUMAN	2822955.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822665 5'
1428	14175	26860	1.51	1.0E-53	AJ271736.1	NT	Homo sapiens Xa pseudautosomal region, segment 2/2
3404	16162	28813	1.08	1.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6593	18390	32370	1.52	1.0E-53	BF364201.1	EST_HUMAN	GM4-NN1028-150800-543-e02 NN1028 Homo sapiens cDNA
7147	18834	32803	0.68	1.0E-53	BE012071.1	EST_HUMAN	RC6-BN1058-270400-031-C01 BN1058 Homo sapiens cDNA
7636	20631	33638	0.54	1.0E-53	AJ248072.1	EST_HUMAN	IG571 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8987	21677	34826	5.91	1.0E-53	XT9536.1	NT	H.sapiens mRNA for hnRNP-core protein A1
11833	24417	37757	1.41	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IIe
11833	24417	37758	1.41	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IIe
11956	24507	37255	2.29	1.0E-53	AW245422.1	EST_HUMAN	2822943.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822943 3'
5219	25063	30651	6.18	8.0E-54	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
2027	13016	28656	2.4	8.0E-54	BE396785.1	EST_HUMAN	60127265FT NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3614031 5'
1827	14566	27278	1.77	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
5645	18533	31558	26.87	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCG1), member 8 (ABCA8), mRNA
375	13200	25845	1.27	7.0E-54	AA812537.1	EST_HUMAN	all 9c12.47 Scores: 1000 Homo sapiens cDNA clone 1377048 3' similar to contains MER30.13 MER30 repetitive element:
1822	14881	27273	1.85	7.0E-54	Y10845.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2202	14930	27667	6.38	7.0E-54	N27177.1	EST_HUMAN	yw88d12.e1 Scores: 810cweeks_2NkBP809W Homo sapiens cDNA clone IMAGE:287399 3' similar to contains LTR7.B3 LTR7 repetitive element:

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10028	22678	35982	2.08	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11047	23717	36086	1.74	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11047	23717	36087	1.74	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11261	23923		4.35	7.0E-54	AI180189.1	EST_HUMAN	gb57603.x1 Soares [feal_neer1_NB-H119W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element:]
11811	24400	37736	1.49	7.0E-54	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11811	24400	37737	1.49	7.0E-54	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
22	12850	26465	1.41	6.0E-54	AB003918.1	NT	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
376	13201	25848	6.83	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
376	13201	25847	6.83	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3277	16038	26889	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3986	16734	29368	1.91	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLON6) mRNA
4429	17165	29794	0.86	6.0E-54	AV764746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAACT10 5'
4792	17523	30145	1.78	6.0E-54	4503806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4819	17550		1.15	6.0E-54	Y08846.1	NT	H. sapiens the pseudogene, p68 lacform
11432	23199	36430	1.51	6.0E-54	AW813667.1	EST_HUMAN	RC3-ST0197-151089-011-08 ST0197 Homo sapiens cDNA
2146	14876	27811	3.78	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
178	12890		13.34	4.0E-54	AF110103.1	NT	Tupai belangeri beta-actin mRNA, partial cds
696	13703	26368	57.5	4.0E-54	AA306764.1	EST_HUMAN	EST177899 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1798	14539	27249	3.22	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1798	14538	27249	3.22	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3199	12692		1	4.0E-54	AI835066.1	EST_HUMAN	wc26d11.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
92	12918	25555	4.47	3.0E-54	AA313467.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN:
1655	14312		0.91	3.0E-54	AW515742.1	EST_HUMAN	EST166371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2574	15268	28025	0.86	3.0E-54	AI110385.1	EST_HUMAN	h887908.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2876542 3'
2530	15042		1.34	3.0E-54	AI808767.1	EST_HUMAN	DKFZP494D0731.J1 434 (synonym: h885) Homo sapiens cDNA clone DKFZp434E0731 5'
5914	18003	31631	1.74	3.0E-54	4502434	NT	IL-BT180-160396-007 BT189 Homo sapiens cDNA
7288	18971	33048	2.1	3.0E-54	AA844061.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7288	18971	33048	2.1	3.0E-54	AA844061.1	EST_HUMAN	h88208.x1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7288	18971	33048	2.1	3.0E-54	AA844061.1	EST_HUMAN	h88208.x1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10049	23627		1.83	3.0E-54	11434806	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11024	23669	36959	4.93	3.0E-54	BF345800.1	EST_HUMAN	802019408F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4165121 5'
11341	24031	37335	3.26	3.0E-54	AA383392.1	EST_HUMAN	870121.1 Soares, Iestis, NHT Homo sapiens cDNA clone IMAGE:272727 5' similar to TR-0191315
12056	24573	31119	2.98	3.0E-54	AY954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN, ;
12097	25373		2.51	3.0E-54	AW748965.1	EST_HUMAN	EST368629 IMAGE:resouces, MAGC Homo sapiens cDNA
627	13408	28040	8.86	2.0E-54	5031800	NT	RC1-870313-131169-011-b09 B10313 Homo sapiens cDNA
1344	14092	28767	0.96	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1539	14286	28972	1.37	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2541	15255	27995	1.22	2.0E-54	AW163175.1	EST_HUMAN	n78409.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1204610 similar to contains element L1 repetitive element ;
2608	15320	28062	1.65	2.0E-54	AL163210.2	EST_HUMAN	aut9203.yt Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2763764 5' similar to SW:CU11 HUMAN Q13616 CULLIN HOMOLOG 1 ;
2696	15663	28311	1.52	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010 ;
3311	16071	28721	1.18	2.0E-54	AJ278314.1	NT	wy6012.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TRQ62084 Q82084 PHOSPHOLIPASE C-NEIGHBORING ;
3536	16292		3.2	2.0E-54	AA532025.1	EST_HUMAN	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
4181	16921		2.06	2.0E-54	4502842	NT	n45609.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:995488 similar to gb-X63777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4826	17566	30178	1.02	2.0E-54	7700446	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CT16) mRNA
5388	18168	30680	1.84	2.0E-54	4759098	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5518	18314	31218	1.2	2.0E-54	BED047884.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5676	18469	31385	5.04	2.0E-54	11426937	NT	5243c11.yt NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5771	18502	31469	13.89	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5771	18502	31490	13.89	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6556	18324	32331	0.68	2.0E-54	AF008915.1	NT	Homo sapiens EV18 homolog mRNA, complete cds
6713	18628	32672	0.65	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6713	18628	32673	0.65	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
7023	19715	32772	8.8	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibrominosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9529	22182	33586	4.11	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain tyrosine receptor, complete cds
9609	22568	35753	0.76	2.0E-54	11428127	NT	Homo sapiens Janus Kinase 2 (e protein tyrosine kinase) (JAK2), mRNA
10021	22669	35885	1.01	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10021	22669	35886	1.01	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10947	18324	32331	1.57	2.0E-54	AF008915.1	NT	Homo sapiens EVIS homolog mRNA, complete cds
11727	24321		2.88	2.0E-54	7857454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
4432	17168		1.22	1.0E-54	BF316418.1	EST_HUMAN	501899230f1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128335 5'
10153	22801	39018	0.52	1.0E-54	AA412408.1	EST_HUMAN	zu10c08.1 Scores: bestis_NHT Homo sapiens cDNA clone IMAGE:731484 6'
10153	22801	39019	0.52	1.0E-54	AA412408.1	EST_HUMAN	zu10c08.1 Scores: bestis_NHT Homo sapiens cDNA clone IMAGE:731484 5'
12710	24868		2.17	1.0E-54	U077341.1	EST_HUMAN	U077341 Sugarcane cDNA library Homo sapiens cDNA clone IMAGE:731484 5'
10257	29055	39115	0.94	9.0E-55	BE081469.1	EST_HUMAN	gamma-glutamyl transpeptidase mRNA, 5 end
1292	14041		1.09	8.0E-55	Y07829.2	NT	QV2-BT0035-160-400-143-H12 B T0635 Homo sapiens cDNA
1298	14044		2.63	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11151	23818		1.67	8.0E-55	AW469714.1	EST_HUMAN	Homo sapiens RFB30 gene for RING finger protein
1059	19817	26478	0.77	7.0E-55	R09346.1	EST_HUMAN	h02802.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860907 5'
8703	21395		0.8	7.0E-55	AW103839.1	EST_HUMAN	SP-C951_BOVIN P10897 CYTOCHROME
9080	21760	34932	1.28	7.0E-55	AA086981.1	EST_HUMAN	yf26a04.1 Scores: fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127696 5' similar to TR:O00365
9116	21803	34968	2.18	7.0E-55	AA139506.1	EST_HUMAN	003065 FOS38554.1 ;
11171	23838	37120	10.32	7.0E-55	A161056.1	EST_HUMAN	al28a11.at Scores: bestis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
11171	23838	37121	10.32	7.0E-55	A161056.1	EST_HUMAN	U1138609 PLACE1 Homo sapiens cDNA clone PLACE1011578 5'
12682	25303		2.5	7.0E-55	H23395.1	EST_HUMAN	h22009.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11468	24099	37412	2.45	6.0E-55	AB040634.1	NT	h22009.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
1763	14505	27205	1.19	5.0E-55	AA704871.1	EST_HUMAN	ym37g07.1 Scores: infant brain 1N1B Homo sapiens cDNA clone IMAGE:82444 5'
1763	14505	27206	1.19	5.0E-55	AA704871.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
4720	17452	30088	1.81	5.0E-55	AW206021.1	EST_HUMAN	yf26a04.1 Scores: fetal_liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
8446	19214	32211	1.65	5.0E-55	4502240	NT	495509.s1 Scores: fetal_liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
8448	19214	32212	1.65	5.0E-55	4502240	NT	U1-H-BH-9y-g-99-0-U1 s1 NCI_CGAP_S143 Homo sapiens cDNA clone IMAGE:2723536 3'
8568	25094	32340	1.34	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (glucuronidylsulfatase punctata 1) (ARSE), mRNA
8568	25094	32341	1.34	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (glucuronidylsulfatase punctata 1) (ARSE), mRNA
6937	19872	32718	0.83	5.0E-55	7382471	NT	Homo sapiens paroxonase 2 (PON2) mRNA, and translated products
7165	19881	32955	0.7	5.0E-55	11434422	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA
7893	20588	33718	0.72	5.0E-55	11528491	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
8942	21693	34777	3.53	5.0E-55	4508302	NT	Homo sapiens BCL2-associated athanogene (BAG1), mRNA
9218	21898		1.75	5.0E-55	BE064386.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9937	22595	35785	1.77	5.0E-55	AB014511.1	NT	RC4-BT10310-1 (3300-015-10 B T0310 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA0611 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9037	22686	35787	1.77	5.0E-55	AB014811.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10122	22770	35984	2.48	5.0E-55	5453765	NT	Homo sapiens nrl (chicken) like 2 (NELL2), mRNA
12137	24626		2.78	6.0E-55	11417672	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
657	13434	28075	65.4	4.0E-55	4826923	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1421	14169	28933	1.78	4.0E-55	7651713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1421	14169	28934	1.78	4.0E-55	7651713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1504	14250		1.7	4.0E-55	BF081411.1	EST_HUMAN	752x10x101 Sacchari NSF F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.03.1.1 repetitive element;
2019	14754	27482	0.97	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2019	14754	27483	0.97	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2079	14811	27542	0.47	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (GOK) (DGKG) mRNA
2079	14811	27543	0.47	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (GOK) (DGKG) mRNA
2308	15033	27771	2.29	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2598	15310		1.21	4.0E-55	AL271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8242	20836		8.37	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11184	23859		2.3	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12057	24574		3.05	4.0E-55	BF303941.1	EST_HUMAN	8018657F2 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4120338 5'
11898	24536		1.5	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12721	24693		1.85	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
368	13164	25807	1.88	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHc.1 (ERV9)
538	13321		1.13	2.0E-55	MT0976.1	NT	Human endogenous retrovirus pHc.1 (ERV9)
634	13473	26049	13.79	2.0E-55	4507296	NT	Human endogenous retrovirus pHc.1 (ERV9)
4723	17485	30090	2.91	2.0E-55	BE179886.1	EST_HUMAN	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
7403	21513	33162	0.76	2.0E-55	AW501988.1	EST_HUMAN	U1-HF-BND-4a-f-08-03-01-11 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3078275 5'
8993	21634	34804	0.52	2.0E-55	BF224452.1	EST_HUMAN	h7h08.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
8863	21684	34608	0.52	2.0E-55	BF224452.1	EST_HUMAN	h7h08.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9098	21747		6.23	2.0E-55	AL002838.1	EST_HUMAN	sm98105.a1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.L2 THR repetitive element;
9140	21828		0.72	2.0E-55	BE007859.1	EST_HUMAN	QVQ-BN0147-280400-2713-g08 BNG147 Homo sapiens cDNA
10870	23550	36768	1.95	2.0E-55	AU116344.1	EST_HUMAN	AU116344 HEMBA1 Homo sapiens cDNA clone HEMBA100583 5'
951	12921	23558	3.01	1.0E-55	4505090	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (MBPR) mRNA
184	12987	25636	8.22	1.0E-55	U09823.1	NT	Cycloleukin curculius New Zealand white elongation factor 1 alpha (Rabelfaz) mRNA, complete cds
1127	13883	26543	3.63	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
28	12854	25470	8.58	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2173	14902		2.69	4.0E-56	BF20788.1	EST_HUMAN	601862059J1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081651 5'
2712	15416	28157	7.28	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2712	15419	28158	7.28	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2815	13297	25928	3.49	4.0E-56	AF00325.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2839	15331	28074	1.48	4.0E-56	AB32488.1	EST_HUMAN	W60708.x1 NCJ_CGAP_CG8 Homo sapiens cDNA clone IMAGE:2305101 3' similar to SW:DCOR_MUSPA
2838	15331	28075	1.48	4.0E-56	AB32488.1	EST_HUMAN	W60708.x1 NCJ_CGAP_CG8 Homo sapiens cDNA clone IMAGE:2305101 3' similar to SW:DCOR_MUSPA
6164	18941	31812	0.01	4.0E-56	AF217508.1	NT	P27119 ORNITHINE DECARBOXYLASE ;
6164	18941	31813	0.01	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10403	23049	36296	2.02	4.0E-56	AF043349.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10841	23523	36764	8.88	4.0E-56	AF043349.1	EST_HUMAN	hm5912.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2183046 3'
10841	23523	36765	8.88	4.0E-56	AF043349.1	EST_HUMAN	hm5912.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2183046 3'
1319	14058	26742	4.17	3.0E-56	8924028	NT	Homo sapiens hypothetical protein PR01304 (PRO1304), mRNA
3122	15987	28527	1.54	3.0E-56	AA325628.1	EST_HUMAN	EST28899 Cerebellum II Homo sapiens cDNA 5' end
3122	15987	28528	1.54	3.0E-56	AA325628.1	EST_HUMAN	EST28899 Cerebellum II Homo sapiens cDNA 5' end
3515	16587		1.61	3.0E-56	AF055068.1	NT	Homo sapiens IHH class 1 region
4355	17093	29728	1.43	3.0E-56	7667042	NT	Homo sapiens Down syndrome candidate region 1 (DSORT), mRNA
4360	17127	28759	4.27	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4534	17259	29902	2.34	3.0E-56	5902085	NT	Homo sapiens superfamily viralidic activity 2 (S_cerevitae homolog)-like (SKIV2L), mRNA
5598	18393	31302	2.12	3.0E-56	4759163	NT	Homo sapiens speractinectin, ewc and kazal-like domains proteoglycan (SPOCK) mRNA
5598	18393	31303	2.12	3.0E-56	4759163	NT	Homo sapiens speractinectin, ewc and kazal-like domains proteoglycan (SPOCK) mRNA
6775	19519	32547	7.03	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7223	19908	32881	1.15	3.0E-56	4604970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
7223	19908	32882	1.15	3.0E-56	4604970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
8715	21407	34550	4.88	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8715	21407	34552	0.85	3.0E-56	D83479.2	NT	Homo sapiens mRNA for KIAA0146 protein, partial cds
10378	28025	36240	1.38	3.0E-56	11434656	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10642	23333	36571	1.71	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myosin, complete cds
11284	23945	37259	6.37	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA

Page 317 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11284	23945	37240	6.37	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11673	24268	37590	1.74	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11673	24268	37591	1.74	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
12095	24597	31083	1.52	3.0E-56	11434876	NT	Homo sapiens catenin 3 (CAV3), mRNA
12095	24597	31084	1.52	3.0E-56	11434876	NT	Homo sapiens catenin 3 (CAV3), mRNA
511	13295		1.7	2.0E-56	AA169818.1	EST_HUMAN	Homo sapiens caveolin 3 (CAV3), mRNA
716	15590	28141	1.05	2.0E-56	BE004386.1	EST_HUMAN	zgs2a03.x1 Striatum neuropeptide Y (NPY) gene, exon 3
716	15590	29142	1.05	2.0E-56	BE004386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2087	15763	26399	1.18	2.0E-56	AB037635.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3623	16270	28934	1.84	2.0E-56	AV703164.1	EST_HUMAN	AV703164 ADB Homo sapiens cDNA clone ADBCG10 5'
6990	16683	32731	1.47	2.0E-56	5790038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
959	13724		1.84	1.0E-56	AF160930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3664	16417	29036	2.15	1.0E-56	AV589333.1	EST_HUMAN	hg23e11.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946462 3'
3664	16417	29037	2.15	1.0E-56	AV589333.1	EST_HUMAN	hg23e11.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946462 3'
4572	17688	30303	0.99	1.0E-56	AI006162.1	EST_HUMAN	QV-BT077-130189-079 BT077 Homo sapiens cDNA
5118	17838	30483	0.97	1.0E-56	6981002	NT	Mus musculus cytoplasmic poly(den)/ellon element binding protein (Cpeb), mRNA
6724	19558	32589	0.57	1.0E-56	AV609520.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8655	22305		0.59	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9048	22566	35800	1.71	1.0E-56	AV645987.1	EST_HUMAN	RC2-CT0163-220699-001-E02 CT0163 Homo sapiens cDNA
6111	13589		2.52	9.0E-57	AW890855.1	EST_HUMAN	QVQ-OT0033-070300-152-H03 OT0033 Homo sapiens cDNA
4180	16920	28548	1.14	9.0E-57	4758276	NT	Homo sapiens EphA4 (EPHA4) mRNA
4180	16920	28549	1.14	9.0E-57	4758276	NT	Homo sapiens EphA4 (EPHA4) mRNA
11183	23848	37134	2.17	8.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11183	23848	37135	2.17	8.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11508	24107	37420	1.46	9.0E-57	AB020391.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
290	13068	28738	3.01	8.0E-57	AV818405.1	EST_HUMAN	QV4-S10234-181169-037-405 S10234 Homo sapiens cDNA
884	13533	28303	6.36	8.0E-57	AV284599.1	EST_HUMAN	nt05610.x1 NCL_CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2759261 3' similar to gb-U05875
1805	14549	27264	1.51	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3376	18135	28791	0.98	8.0E-57	4758276	NT	z65121.7 Scores_NHT Homo sapiens cDNA clone IMAGE:757181 5'
3376	18135	28791	0.98	8.0E-57	4758276	NT	Homo sapiens EphA4 (EPHA4) mRNA
4852	17592	30205	1.3	8.0E-57	4557630	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5161	25276	30728	3.28	8.0E-57	11418185	NT	Homo sapiens acyltransferase 2, mitochondrial (ACO2), mRNA
8306	18078	32063	1.85	8.0E-57	AB020705.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds

Page 318 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6372	19141	32137	12.87	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6372	19141	32138	12.87	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7349	20030	33107	0.64	8.0E-57	7652293	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7648	20312	33423	1.7	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7648	20312	33424	1.7	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11460	17869	30487	3.29	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12459	24828	31028	2.74	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12473	24828	31028	1.69	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12820	25060		2.07	8.0E-57	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2636	15560	28093	1.71	7.0E-57	7657692	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2639	15560	28094	1.71	7.0E-57	7657692	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3244	16006	29655	0.9	7.0E-57	7242158	NT	Homo sapiens NMET (NMET), mRNA
3244	16006	29656	0.9	7.0E-57	7242158	NT	Homo sapiens NMET (NMET), mRNA
3265	16027	29677	1.09	7.0E-57	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3858	16509	29246	1.39	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3958	16509	29247	1.39	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4396	17135		0.95	7.0E-57	AF020503.1	NT	Homo sapiens FRA33 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4730	17462	30099	0.95	7.0E-57	U11059.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (Maxk)
12785	25310		2.93	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3736	18489	29125	1.57	4.0E-57	AB028968.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL4 genes, complete cds)
786	13659	26220	0.78	3.0E-57	4507706	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1308	14056		16.24	3.0E-57	AA200279.1	EST_HUMAN	nc1307.0.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2360	15111	27848	2.89	3.0E-57	AA348335.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10.1
2707	15414	28151	0.95	3.0E-57	BE676822.1	EST_HUMAN	EST6470 Hippocampus II Homo sapiens cDNA 5' end
2707	15414	28151	0.95	3.0E-57	BE676822.1	EST_HUMAN	793310.0.1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H8C.2
2707	15414	28152	0.95	3.0E-57	BE676822.1	EST_HUMAN	CE20263
3550	16305	29355	1.74	3.0E-57	AF232708.1	NT	793310.0.1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H8C.2
3685	16438		62.34	3.0E-57	AW853964.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Ch) gene, complete cds
							RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA

Page 319 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5898	18721	31860	1.24	3.0E-57	11225608	NT	Homo sapiens angiotensin converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6033	18813	31773	3.23	3.0E-57	BE796837.1	EST_HUMAN	601568980FT NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3944302 5'
8044	20738	33871	3.77	3.0E-57	W28130.1	EST_HUMAN	4268 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8070	20764	33862	2.16	3.0E-57	11645798	NT	Homo sapiens hypophyseal protein FLJ11656 (FLJ11656), mRNA
8070	20764	33863	2.16	3.0E-57	11645798	NT	Homo sapiens hypophyseal protein FLJ11656 (FLJ11656), mRNA
8179	20873	34008	0.7	3.0E-57	11427767	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
8328	21021	34167	0.73	3.0E-57	U06262.1	NT	Homo sapiens larnesyl pyrophosphate synthetase mRNA, complete cds
8757	21449	34566	4.17	3.0E-57	AU117656.1	EST_HUMAN	AU117658 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
8149	21860	35047	1.03	3.0E-57	11545798	NT	Homo sapiens hypophyseal protein FLJ11656 (FLJ11656), mRNA
8149	21860	35048	1.03	3.0E-57	11545798	NT	Homo sapiens hypophyseal protein FLJ11656 (FLJ11656), mRNA
10825	23508	36747	2.85	3.0E-57	AW248374.1	EST_HUMAN	2820473.Sprine NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2820473 5'
12101	25381	30616	8.35	3.0E-57	W23871.1	EST_HUMAN	Zb4641.T Soares_fetal_lung_NHLL18W Homo sapiens cDNA clone IMAGE:306549 5'
12460	25281		2.32	3.0E-57	AW178576.1	EST_HUMAN	RCO-HT0112-090959-001-C06 HT0112 Homo sapiens cDNA
12623	24928	31010	1.48	3.0E-57	AJ003849.1	EST_HUMAN	AJ003849 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1010-1L1
1487	14234	26919	1.39	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1487	14234	26920	1.39	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3432	16188		1.24	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3810	19580	28301	0.79	2.0E-57	BE073284.1	EST_HUMAN	MRO-BT0551-090300-103-b03 BT0551 Homo sapiens cDNA
4474	17209	26834	6.73	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5582	18379		1.84	2.0E-57	AA016131.1	EST_HUMAN	z61c05.t Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.8 L1 repetitive element
5643	18725		33.81	2.0E-57	BF116286.1	EST_HUMAN	7b6004.xt NCL_CGAP_Oy18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11 MER22 repetitive element
6067	18946	31810	0.66	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8529	21221	34363	1.08	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
9748	23267	36502	1.86	2.0E-57	AF067722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
10525	23171	36398	0.49	2.0E-57	11434330	NT	Homo sapiens KIAA1085 protein (KIAA1085), mRNA
10525	23171	36399	0.49	2.0E-57	11434330	NT	Homo sapiens KIAA1085 protein (KIAA1085), mRNA
11238	23901	37189	2.42	2.0E-57	11424084	NT	Homo sapiens hypophyseal protein FLJ20041 (FLJ20041), mRNA
11238	23901	37190	2.42	2.0E-57	11424084	NT	Homo sapiens hypophyseal protein FLJ20041 (FLJ20041), mRNA
8989	21285		3.62	1.0E-57	BE049031.1	EST_HUMAN	h032603.xt NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039082 3' similar to TR-000246 C00246 HYPOTHETICAL 9.3 KD PROTEIN
12249	24696		5.08	1.0E-57	AW470791.1	EST_HUMAN	ha33406.xt NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5591	13387	31297	0.99	9.0E-58	AA297847.1	EST_HUMAN	EST11548 Uterus Homo sapiens cDNA 5' end
12516	24855	31015	1.55	9.0E-58	BC395061.1	EST_HUMAN	601309469F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
575	13355		1.76	8.0E-58	BE868715.1	EST_HUMAN	60144549F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
639	13416	26055	4.18	8.0E-58	AJ798376.1	EST_HUMAN	U34407.X1 NCI CGAP_O243 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNKNNED NERV-H PROTEIN;
830	13418	26058	4.18	8.0E-58	AJ798376.1	EST_HUMAN	U34407.X1 NCI CGAP_O243 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNKNNED NERV-H PROTEIN;
1849	14587	27301	2.37	8.0E-58	11434921	NT	UNKNNED NERV-H PROTEIN;
1949	14597	27302	2.37	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2074	15740		2.32	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein LOC51804, mRNA
10762	20446		5.87	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
10847	23528	36773	3.6	7.0E-58	AW504109.1	EST_HUMAN	U1HF-BNO-ah-9-10-0-J171 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3075867 5'
10847	23529	36774	3.6	7.0E-58	AW504109.1	EST_HUMAN	U1HF-BNO-ah-9-10-0-J171 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3075867 5'
2251	14978	27718	1.02	6.0E-58	BE395081.1	EST_HUMAN	U1309469F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2375	15037	27837	3.78	8.0E-58	AJ130065.1	EST_HUMAN	U130689F1 NIH_MGC_44 Homo sapiens cDNA clone NT2P3037263 5'
2802	16668	28316	1.2	6.0E-58	BE242150.1	EST_HUMAN	TCAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HQSC project-TCAA Homo sapiens cDNA clone TCAAP1219
2802	16668	28317	1.2	6.0E-58	BE242150.1	EST_HUMAN	TCAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HQSC project-TCAA Homo sapiens cDNA clone TCAAP1219
6078	18557	31824	1.01	8.0E-58	AF105911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10208	22856	33072	0.79	6.0E-58	11434748	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12347	24754		1.58	6.0E-58	11525291	NT	Homo sapiens hypodermal protein FLJ20454 (FLJ20454), mRNA
293	13069	25740	3.79	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
694	13469	26116	5.41	5.0E-58	BE763984.1	EST_HUMAN	RC2-NT0057-160603-318-005 NT0057 Homo sapiens cDNA
1172	13928	26589	2.98	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1172	13928	26590	2.96	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1173	13928	26589	2.76	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1173	13928	26590	2.76	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3317	16077	28727	4.32	5.0E-58	AA689193.1	EST_HUMAN	es5907.X1 NCI CGAP_L65 Homo sapiens cDNA clone IMAGE:1603908 3'
4229	16970	28594	0.92	5.0E-58	A1636745.1	EST_HUMAN	169907.X1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2239468 3' similar to SW-PRO2_ACACA P19984 PROLIFIN II;
5541	18338		2.32	5.0E-58	11486232	NT	Homo sapiens placental-specific 1 (PLACT1), mRNA
6085	18653	31829	6.86	5.0E-58	H23072.1	EST_HUMAN	ym5107.1 Scores Infant brain 1N18 Homo sapiens cDNA clone IMAGE:52071 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6301	18074	32060	0.95	5.0E-58	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C085
6378	18148	32147	1.61	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6880	18597	32635	0.69	5.0E-58	AF061334.1	NT	Homo sapiens ribirin (NBS) mRNA, complete cds
6880	18597	32636	0.68	5.0E-58	AF061334.1	NT	Homo sapiens ribirin (NBS) mRNA, complete cds
7008	18688	32752	0.73	5.0E-58	4885400	NT	Homo sapiens holocholesterol synthase (cytochrome c heme-lyase) (HCCS) mRNA
7889	20584	33591	7.69	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10328 (FLJ10328), mRNA
8251	20945	34083	0.7	5.0E-58	A304633.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9239	21918	35089	0.68	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA5E6PL) mRNA
9239	21918	35090	0.68	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA5E6PL) mRNA
9757	22408	35514	0.88	5.0E-58	11430547	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
10023	22871	35887	1.78	5.0E-58	AL163218.2	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
10300	22947	36161	0.83	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
10300	22947	36162	0.83	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
11819	24405	37740	2.69	5.0E-58	11431078	NT	Homo sapiens chimerin (chimerin) 1 (CHN1), mRNA
12071	25305		1.81	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CEGR1), mRNA
12512	26390		1.5	5.0E-58	11426423	NT	Homo sapiens acyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12732	28001		2.67	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
364	13162	25904	4.5	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
779	13551	28212	0.88	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (L10RB), mRNA
1452	14169	26883	1.09	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2637	15349	28091	1.7	4.0E-58	U36261.1	NT	Human beta-2-microglobulin (BAM22) gene, exon 3
3319	16076	28728	1.03	4.0E-58	D16470.1	NT	Human mRNA, 3' terminal portion
3723	18476	29113	1.25	4.0E-58	5031690	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11315	23974	37275	7.06	4.0E-58	11424050	NT	Homo sapiens E18-55kDa-associated protein 5 (E18-AP5), mRNA
326	13127		2.67	3.0E-58	R17870.1	EST_HUMAN	Y10402.1 Soares infant brain (NIB) Homo sapiens cDNA clone IMAGE:31693.5'
1368	14116	26761	2.36	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3174	15937	26585	2.78	3.0E-58	BF56848.1	EST_HUMAN	802185788F1 NIH_MGC 45 Homo sapiens cDNA clone IMAGE:4308943.5'
3174	15937	26586	2.78	3.0E-58	BF56848.1	EST_HUMAN	802185788F1 NIH_MGC 45 Homo sapiens cDNA clone IMAGE:4308943.5'
6167	18944	31915	0.63	3.0E-58	BE089509.1	EST_HUMAN	Q107-B10702-170400-104-009 B10702 Homo sapiens cDNA
8352	19122	32114	1.43	3.0E-58	FO7056.1	EST_HUMAN	HSCT10081 normalized infant brain cDNA Homo sapiens cDNA clone c-1g08
8544	19309	32314	1.4	3.0E-58	AV12977.1	EST_HUMAN	AV12977 DCA Homo sapiens cDNA clone DCAAZG04.5'
919	13686	26360	11.9	2.0E-58	AF068024.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds

Page 322 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1287	14016						
6273	28065	30708	10	2.0E-58	BE208532.1	EST_HUMAN	ba0807.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69301.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X61987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5273	28065	30734	3.4	2.0E-58	BE907166.1	EST_HUMAN	601469661F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5966	16748	31709	3.4	2.0E-58	BE907166.1	EST_HUMAN	601469661F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
		31709	1.12	2.0E-58	BF513488.1	EST_HUMAN	UHH-BW1-ams-g11-Q-U1et NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071080 3'
6031	18811	31771	1.88	2.0E-58	AI124874.1	EST_HUMAN	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539874 3' similar to WP.ZK328.1 CE08065 UBQUITIN CONJUGATING ENZYME1, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6082	18841	31803	0.8	2.0E-58	RC2687.1	EST_HUMAN	y081003.f1 Soares fetal liver spleen 1NfL3 Homo sapiens cDNA clone IMAGE:196379 5'
6828	19499	32511	1.12	2.0E-58	AI291407.1	EST_HUMAN	q084601.x1 NCI_CGAP_LuB Homo sapiens cDNA clone IMAGE:1895424 3'
7056	19747	32809	2.83	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7056	19747	32810	2.83	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10641	23332	36570	21.77	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131897 5'
10895	23585	36813	2.43	2.0E-58	AV187284.1	EST_HUMAN	hm25038.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
705	13480	28128	0.86	1.0E-58	M69134.1	NT	Human complement component C3 mRNA, 3' end
1046	13805	28464	2.41	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1304	14053	28726	1.61	1.0E-58	AW967182.1	EST_HUMAN	EST139252 IMAGE sequences, MAGD Homo sapiens cDNA
1304	14053	28727	1.61	1.0E-58	AW967182.1	EST_HUMAN	EST139252 IMAGE sequences, MAGD Homo sapiens cDNA
1376	14124	28788	1.13	1.0E-58	AJ236093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and 8/9 repeat elements
2805	16510	28251	2.37	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
2834	14738	27462	1.6	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 99A (GPR99A) mRNA
3529	16322	28638	0.89	1.0E-58	4758081	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3526	16322	28639	0.88	1.0E-58	4758081	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
4913	17641	30258	1.75	1.0E-58	AI141063.1	EST_HUMAN	oz43601.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1678126 3'
6751	19543	31485	1.31	1.0E-58	BE061690.1	EST_HUMAN	RO1-B170254-280100-015-601 BT0254 Homo sapiens cDNA
6764	19508	32533	0.8	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8013	20703		0.5	1.0E-58	AW973537.1	EST_HUMAN	EST138583 IMAGE sequences, MAGM Homo sapiens cDNA
8768	21480	34609	0.66	1.0E-58	4605314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8890	21571	34714	0.91	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH9 5'
8979	21669	34818	0.66	1.0E-58	AA412397.1	EST_HUMAN	268905.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
8976	21669	34819	0.66	1.0E-58	AA412397.1	EST_HUMAN	268905.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10036	22734	35949	1.21	1.0E-58	11432594	NT	Homo sapiens discal, large (Drosophila) homolog 2 (chapsyP-110) (DLG2), mRNA

Page 323 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11780	24371		2.11	1.0E-59 X63392.1	NT	NT	H.sapiens immunoglobulin kappa light chain variable region L14
11816	24404		1.57	1.0E-59 D61405.1	NT	NT	Human MSH3 gene, exon10
2225	14953	27691	29.49	8.0E-59 4507378	NT	NT	Human sapiens TATA box binding protein (TBP) mRNA
8080	20774	33904	2.49	8.0E-59 A1781963.1	EST_HUMAN	EST_HUMAN	wh50d08.x1 NC1 CGAP_K111 Homo sapiens cDNA clone IMAGE:2384171 3'
173	15556		1.74	6.0E-59 BF035327.1	EST_HUMAN	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3682086 5'
8144	20638	33970	0.61	6.0E-59 A1750970.1	EST_HUMAN	EST_HUMAN	cn08h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn08h02 random
1748	14490	27189	1.32	5.0E-59 AW157281.1	EST_HUMAN	EST_HUMAN	au93n05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783993 3' similar to TR-075786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1748	14490	27190	1.32	5.0E-59 AW157281.1	EST_HUMAN	EST_HUMAN	au93n05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783993 3' similar to
3124	15939	28530	6.96	5.0E-59 A1807494.1	EST_HUMAN	EST_HUMAN	TR-076786 076786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
4610	17345	28978	6.55	5.0E-59 X83497.1	NT	NT	H.sapiens DNA for ZNF80-linked ERY9 long terminal repeat
6892	17659	30526	7.5	5.0E-59 AW162304.1	EST_HUMAN	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781226 3' similar to contains element TAR1 repetitive element
8705	21397	34544	1.04	5.0E-59 11421778	NT	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
9804	22357	35443	1.62	5.0E-59 AV762880.1	EST_HUMAN	EST_HUMAN	AV762889 MDS Homo sapiens cDNA clone MDSEIC12 5'
10823	23506	39745	3.78	5.0E-59 11434808	NT	NT	Homo sapiens hypodermal protein (LOC57143), mRNA
776	13548	28210	1.56	4.0E-59 D80006.1	NT	NT	Human mRNA for KIAA0184 gene, partial cds
5450	18249	31138	1.03	4.0E-59 11034810	NT	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12203	25238		1.91	4.0E-59 AF057720.1	NT	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
9	12836		6.13	3.0E-59 AV1665524.1	EST_HUMAN	EST_HUMAN	ES1377682 IMAGE resequences, MAGI Homo sapiens cDNA
219	13030	26668	4.59	3.0E-59 7692247	NT	NT	Homo sapiens KIAA0930 gene product (KIAA0980), mRNA
1705	14448	27147	8.2	3.0E-59 4505860	NT	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1705	14448	27148	8.2	3.0E-59 4505860	NT	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2125	14856	27585	5.59	3.0E-59 AB029035.1	NT	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2125	14856	27586	5.59	3.0E-59 AB029035.1	NT	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3126	16891	28534	3.77	3.0E-59 4502014	NT	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3126	16891	28535	3.77	3.0E-59 4502014	NT	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3805	16587	29188	1.45	3.0E-59 4508044	NT	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (P22) mRNA
4638	17372	30007	0.68	3.0E-59 AL163284.2	NT	NT	Homo sapiens chromosome 21 segment HS21C084
4739	17470	30107	0.92	3.0E-59 4759329	NT	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA

Page 324 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4789	17520	30143	1.57	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
4890	17713		0.97	3.0E-59	M55961.1	NT	Human probinone converting enzyme (NEC2) gene, exon 2
6126	18904	31872	2.12	3.0E-59	8624074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7259	19943	33020	1.94	3.0E-59	6464137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOBT), mRNA
7832	20527	33653	1.16	3.0E-59	X12656.1	NT	Human mRNA for dbi proto-oncogene
7832	20527	33654	1.16	3.0E-59	X12656.1	NT	Human mRNA for dbi proto-oncogene
9044	22592	35794	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
9044	22592	35795	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12327	24746		6.04	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7693	20357		0.71	2.0E-59	BF373329.1	EST_HUMAN	MR0-FT0144-250700-002-at0 F0144 Homo sapiens cDNA
9537	22190		6.32	2.0E-59	AA30974.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10425	23071		1.19	2.0E-59	BF36554.1	EST_HUMAN	RC0-NT0033-100700-032-at0 NT0038 Homo sapiens cDNA
10734	23421	36653	2.6	2.0E-59	AW410698.1	EST_HUMAN	h07N04.xt NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
10734	23421	36654	2.6	2.0E-59	AW410698.1	EST_HUMAN	h07N04.xt NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
11311	23970	37274	1.31	2.0E-59	H61604.1	EST_HUMAN	y45h09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208673 5' similar to SP-POL_FENV1 P31762 POL.POLYPROTEIN
12091	24595	31128	2.93	2.0E-59	AI031809.1	EST_HUMAN	wa36c12.xt NCI_QGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR-Q88542
12805	25293	30719	4.65	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element
159	12974		3.03	1.0E-59	BE296411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
1529	14276	28694	0.93	1.0E-59	T92522.1	EST_HUMAN	601117675F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 6'
2412	15193	27870	1.19	1.0E-59	D11456.2	NT	ye25-09.r1 Stragene lung (8937210) Homo sapiens cDNA clone IMAGE:118768 5' similar to SP-S21348
2412	15193	27871	1.19	1.0E-59	D11456.2	NT	S21348 HYPOTHETICAL PROTEIN 4--
2623	15335		2.47	1.0E-59	AA748468.1	EST_HUMAN	Homo sapiens Xdh mRNA for xanthine dehydrogenase, complete cds
7462	20135	33227	1.08	1.0E-59	AJ130694.1	NT	Q65011.s1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR-Q13537
7617	20293	33382	0.97	1.0E-59	BE266814.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7617	20293	33383	0.97	1.0E-59	BE266814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
9285	20239	33210	0.86	1.0E-59	BE266814.1	EST_HUMAN	601117675F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9504	22197	35337	0.54	1.0E-59	11419630	NT	601117675F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9504	22197	35338	0.54	1.0E-59	11428849	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10760	20195	33227	12.88	1.0E-59	AJ130694.1	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
747	13520	26178	0.85	8.0E-50	AW977845.1	EST_HUMAN	Homo sapiens mRNA for transcription factor

Page 325 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1455	14202	26886	2.65	8.0E-50	4759156	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2169	14868	27632	3.6	8.0E-50	5174656	NT	Homo sapiens differentiation-related gene 1 (nuclear-specific induction protein) (RTP) mRNA
2169	14868	27633	3.6	8.0E-50	5174656	NT	Homo sapiens differentiation-related gene 1 (nuclear-specific induction protein) (RTP) mRNA
5892	18677	31623	1.12	8.0E-50	AB029004.1	NT	Homo sapiens mRNA for KIAA081 protein, partial cds
6411	19179	32178	1.07	8.0E-50	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7696	20264	33372	1.07	8.0E-50	11420841	NT	Homo sapiens phosphatase cytidyltransferase 1, choline, beta isoform (PCYT1B), mRNA
7865	20560	33687	2.28	8.0E-50	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8837	21629	34675	2.6	8.0E-50	11428949	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
8371	21946	35118	0.98	8.0E-50	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9371	21946	35119	0.96	8.0E-50	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10473	23119	36348	0.59	8.0E-50	5433937	NT	Homo sapiens KAN binding protein 7 (KANBP7), mRNA
10736	23423	36666	6.39	8.0E-50	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10736	23423	36667	6.39	8.0E-50	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
737	13511	26169	3.61	7.0E-50	AF050566.1	NT	Homo sapiens MHG class 1 region
738	13511	26169	17.82	7.0E-50	AF050566.1	NT	Homo sapiens MHG class 1 region
798	13588	26228	0.98	7.0E-50	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2124	14855	27654	1.08	7.0E-50	AF071186.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2788	15493	28233	1.59	7.0E-50	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4158	16898	28627	2.56	7.0E-50	4505468	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9307	21974	35149	4.02	7.0E-50	H88041.1	EST_HUMAN	Y1204.R1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR repetitive element
11337	24027	37331	2.11	7.0E-50	H88041.1	EST_HUMAN	Y1204.R1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR repetitive element
2177	14906	27639	1.06	6.0E-50	BE964674.2	EST_HUMAN	801653751RT NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886069 3'
8336	21029		10.5	6.0E-50	H82456.1	EST_HUMAN	Y178005.R1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains ORF repetitive element
82	12803	25545	2.29	5.0E-50	AB07917.1	EST_HUMAN	W52507.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
82	12803	25546	2.29	5.0E-50	AB07917.1	EST_HUMAN	W52507.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2872	15738		1.27	4.0E-50	AA289037.1	EST_HUMAN	EST11408 Utens Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7253		33012	0.89	4.0E-50	BF196068.1	EST_HUMAN	h8105.X1 NCL CGAP Kid1 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW/RHOP_MOUSE
9024	21714		0.68	4.0E-50	AL163278.2	NT	Q81085 GTP-RHO BINDING PROTEIN 1 ; Homo sapiens chromosome 21 segment HS21C078
11267	23828	37219	1.29	4.0E-50	11433597	NT	Homo sapiens v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11287	23829	37220	1.29	4.0E-60	11435597	NT	Homo sapiens vraf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1852	14500	27305	4.44	3.0E-60	BE562811.1	EST_HUMAN	G01336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3600395 5'
1852	14500	27306	4.44	3.0E-60	BE562811.1	EST_HUMAN	G01336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3600395 5'
1852	14600		1.92	3.0E-60	6031190	NT	Homo sapiens prolidase (PHB) mRNA
4424	17180	29750	1.94	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region, segment 1/2
6264	18089	30788	0.57	3.0E-60	BF365143.1	EST_HUMAN	QV44NN1148-250900-423-107 NN1149 Homo sapiens cDNA
5554	18351	31260	2.12	3.0E-60	AW836195.1	EST_HUMAN	Q3L70023-200100-072-607 L70023 Homo sapiens cDNA
6850	17833	30569	1	3.0E-60	A192814.1	EST_HUMAN	g60H11.v5 NCI CGAP_K43 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:JUDP_MOUSE. P52624 URIDINE PHOSPHORYLASE ;
8301	20955	34132	4.97	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8301	20955	34133	4.97	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8482	21174	34319	0.51	3.0E-60	A1040235.1	EST_HUMAN	SW:FORM_MOUSE_Q05660 FORMIN ;
8541	21333	34477	4.32	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8550	22212	35398	0.47	3.0E-60	BF102612.1	EST_HUMAN	G01646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3830980 5'
11162	23829	37107	1.26	3.0E-60	11427120	NT	Homo sapiens CGI-152 protein (LOC57130), mRNA
11162	23829	37108	1.26	3.0E-60	11427120	NT	Homo sapiens CGI-152 protein (LOC57130), mRNA
12686	25297		2.06	3.0E-60	AA485288.1	EST_HUMAN	ab07004.1 Stralagene lung (8637210) Homo sapiens cDNA clone IMAGE:840161 5' similar to contains LTR10.1 LTR10 repetitive element ;
29	12837	25474	3.93	2.0E-60	AY006285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1404	14151	26831	7.35	2.0E-60	Z11694.1	NT	H. sapiens 410Da protein kinase related to rat ERK2
1716	14458	27155	1.29	2.0E-60	M24603.1	NT	Human bar protein mRNA, 5' end
1724	14467	27166	1.59	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2714	15421	28150	1.96	2.0E-60	AW978005.1	EST_HUMAN	EST1300114 IMAGE:rescues, MAGE Homo sapiens cDNA
3555	16321	28959	0.89	2.0E-60	4757897	NT	Homo sapiens viral murine sarcoma viral oncogene homolog B1 (BRAP) mRNA
3666	16545	29255	0.73	2.0E-60	AF231818.1	NT	Homo sapiens chromosome 21 unknown mRNA
6208	18983	31682	0.86	2.0E-60	A1701962.1	EST_HUMAN	m01112.v5 NCI CGAP_C59 Homo sapiens cDNA clone IMAGE:1076465 5' similar to contains THR11 THR repetitive element ;
5400	18109	32168	1.87	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6615	19378	32363	0.96	2.0E-60	AF151476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6750	17819	30683	2.43	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6750	17819	30584	2.43	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	19702	32767	2.73	2.0E-60	AA311169.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7010	19702	32768	2.73	2.0E-60	AA311169.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7124	18812	32890	0.59	2.0E-60	AB09124.1	EST_HUMAN	IQ2808.X1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
7632	22022		0.79	2.0E-60	BF52508.1	EST_HUMAN	Q22808 GALANIN RECEPTOR
7924	20596	33729	0.84	2.0E-60	X65997.1	EST_HUMAN	U1-HBV1-enuc-42-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone CAM_EST15
8765	21486	34608	3.01	2.0E-60	L36033.1	NT	HS1B6EST human adult testis Homo sapiens cDNA clone CAM_EST15
8876	22528	35724	2.29	2.0E-60	11691659	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8876	22528	35724	2.29	2.0E-60	11691659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
8876	22528	35725	2.29	2.0E-60	11691659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
11449	23216	36448	1.53	2.0E-60	11434728	NT	Homo sapiens ribosomal protein S6 kinase, 90KD, polypeptide 5 (RPS6KAB), mRNA
11809	24398	37732	1.8	2.0E-60	BF530674.1	EST_HUMAN	602071973F1 NCL CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4214893 5'
11809	24398	37733	1.8	2.0E-60	BF530674.1	EST_HUMAN	602071973F1 NCL CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4214893 5'
12364	24767		3.02	2.0E-60	11418192	NT	Homo sapiens non-Histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12494	25228		1.93	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12496	24861		2.34	2.0E-60	11418068	NT	Homo sapiens similar to HSPC22 protein (H. sapiens) (LOC83504), mRNA
12510	24862		1.77	2.0E-60	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
500	13263	25925	1.13	1.0E-60	BE178566.1	EST_HUMAN	PM3-HT0605-27020-001-e06 HT0605 Homo sapiens cDNA
3682	16632	29271	1.16	1.0E-60	AI143389	EST_HUMAN	AI143389 Y78A41 Homo sapiens cDNA clone Y78A41001854 5'
4901	17628	30246	1.2	1.0E-60	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C065
7649	20543	33671	0.91	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141789-011-h06 BT0311 Homo sapiens cDNA
8953	21345		3.46	1.0E-60	AA240411.1	EST_HUMAN	nc0412.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1
8953	21345		3.46	1.0E-60	AA240411.1	EST_HUMAN	repetitive element
8981	21373	34517	1.41	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1077	13835	25463	2.21	9.0E-61	AI119344.1	EST_HUMAN	AI119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005563 5'
2876	15365	26129	1.16	8.0E-61	AW006478.1	EST_HUMAN	W05610.X1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2876	15365	26127	1.16	8.0E-61	AW006478.1	EST_HUMAN	W05610.X1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2961	15717		1.53	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
7795	20491	33614	1.05	8.0E-61	AA593968.1	EST_HUMAN	nc05906.x1 NCL CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1083218 3'
124	12847	25593	1.97	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
124	12847	25594	1.97	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	12841	25593	2.38	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	12841	25594	2.38	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA

Page 328 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6034	12941	25583	1.04	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
6034	12941	25584	1.04	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
250	13067	25705	2.95	6.0E-61	BE409310.1	EST_HUMAN	601300038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
763	13505	26226	1.62	6.0E-61	BE409310.1	EST_HUMAN	601300038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1288	14047	26719	1.15	6.0E-61	AF108880.1	NT	Homo sapiens PR02014 mRNA, complete cds
1628	14372	27061	0.97	6.0E-61	BE237400.1	EST_HUMAN	601109236F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1643	14369	27078	2.83	6.0E-61	AA596033.1	EST_HUMAN	m85606.s1 NCI_OGAP_Lart Homo sapiens cDNA clone IMAGE:1088867 3'
2123	14854	27583	1.59	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3301	16053	28711	0.37	6.0E-61	AU130680.1	EST_HUMAN	AU130680 NT26P3 Homo sapiens cDNA clone NT26P3001263 5'
6941	18723	31052	3.37	6.0E-61	S76249.1	NT	Ig-beta/IG29-CD78b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7242	19927	33003	1.92	6.0E-61	U24488.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7518	20159	33282	1.87	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, complete cds
11474	24075	37384	1.35	6.0E-61	AF090386.1	NT	Homo sapiens napsin A mRNA, complete cds
11474	24075	37385	1.35	6.0E-61	AF090386.1	NT	Homo sapiens napsin A mRNA, complete cds
12265	13565	26226	1.02	6.0E-61	BE409310.1	EST_HUMAN	601300038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
350	13149	25769	1.73	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1674	14419	27112	2.22	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3032	15798	28444	2.56	5.0E-61	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
3193	15968	28608	3.27	5.0E-61	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
3983	18712	34983	1.78	6.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4941	13149	25769	1.07	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
6080	17769	30416	3.38	5.0E-61	4502286	NT	Homo sapiens ATPase, Cat+ transporting, plasma membrane 1 (ATP2B1) mRNA
6725	18517	31438	0.87	4.0E-61	7861637	NT	Homo sapiens DKFZP668023 protein (DKFZP668023) mRNA
12098	24582	3	3.61	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
8320	21013	34161	0.89	3.0E-61	AF160180.1	EST_HUMAN	AF160180 Human mRNA from cdc4+ stem cells Homo sapiens cDNA clone C8DAGB04
8596	21288	34427	0.64	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
6596	21268	34428	0.64	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
485	13271	25806	1.52	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1190	13942	26807	0.82	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-050400-147-401 HT0513 Homo sapiens cDNA
1190	13942	26808	0.82	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-050400-147-401 HT0513 Homo sapiens cDNA
1650	14406	27097	1	2.0E-61	N53039.1	EST_HUMAN	qv53411.s1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:249453 3' similar to dbL25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2647	15357		1.04	2.0E-61	N39397.1	EST_HUMAN	Y03311.1 Scavenger melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270189 5'
6332	19102	32090	0.98	2.0E-61	11428168	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (11017180) (ATP6P1A), mRNA
8913	21604	34748	0.98	2.0E-61	AV69437.1	EST_HUMAN	AV69437 GKRC Homo sapiens cDNA clone GKCELG06 5'
9492	22012		0.89	2.0E-61	AB011108.1	EST	Homo sapiens mRNA for KIAA0535 protein, partial cds
8822	22473	35576	1.67	2.0E-61	AW500258.1	EST_HUMAN	UHF-BNO-skl-4-120-U1.1 NIH_MGCC 50 Homo sapiens cDNA clone IMAGE:3078774 5'
10150	22708	35014	2.3	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (3501) (RPO39), mRNA
10789	23462		1.81	2.0E-61	11419728	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
756	13528	28188	1.11	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1851	14580	27304	3.71	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2183	14922	27656	1.42	1.0E-61	AW627281.1	EST_HUMAN	nt11009.y1 NC1_CGAP_L16 Homo sapiens cDNA clone IMAGE:2683399 5' similar to contains element MSR1 repetitive element:
2839	15607	28257	1.47	1.0E-61	BE386363.1	EST_HUMAN	601273513F1 NIH_MGCC 20 Homo sapiens cDNA clone IMAGE:3614667 5'
3369	16128	28793	0.86	1.0E-61	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3715	16466	29106	1.2	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-p08 HT0577 Homo sapiens cDNA
4407	17144	29773	0.81	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4407	17144	29774	0.81	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4804	17535	30157	8.11	1.0E-61	AW288181.1	EST_HUMAN	UHH-BWO-qit-5-08-C-U1.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4804	17535	30158	8.11	1.0E-61	AW288181.1	EST_HUMAN	UHH-BWO-qit-5-08-C-U1.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4805	17632	30247	0.75	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5309	18114	30772	1.82	1.0E-61	M76423.1	NT	H sapiens carbonic anhydrase VII (CA VII) gene, exons 4, 5, 6, and 7, and complete cds
5503	18398	31310	0.79	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
5753	19594	31511	1.29	1.0E-61	11416991	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
6800	19461	32482	7.11	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds
6981	19584	32732	0.67	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7091	19780	32845	1.42	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7091	19780	32846	1.42	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8033	20726	33961	3	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8212	20906	34041	3.06	1.0E-61	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9162	21852		2.7	1.0E-61	AW695728.1	EST_HUMAN	MRG-BNG070-040400-010-C01 BNG070 Homo sapiens cDNA
9257	21636	35110	7.73	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
9928	22676	35776	5.24	1.0E-61	11428992	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10531	23228	39462	2.84	1.0E-61	11426578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10555	23535	36780	1.49	1.0E-61	AB044550.1	NT	Homo sapiens P10Kcl19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
11006	23678	36635	1.93	1.0E-61	AB007630.1	NT	Homo sapiens mRNA for CSR2, complete cds
12007	25273	30726	3.02	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12007	25273	30727	3.02	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12559	24558	30988	11.56	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10255	22303	36113	1.45	9.0E-62	BE04386.1	EST_HUMAN	RC4-B10310-10300-015-10 B10310 Homo sapiens cDNA
4614	17249	28855	1.1	8.0E-62	AA80420.1	EST_HUMAN	cd68h1.1 at NCJ_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
1085	13643	29501	1.62	7.0E-62	AV714334.1	EST_HUMAN	P4714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
3497	16263	28907	0.74	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
5525	16615	31547	0.64	7.0E-62	11427963	NT	Homo sapiens hypophthalic protein (FLJ20281), mRNA
11323	24014	37317	7.1	7.0E-62	AI206581.1	EST_HUMAN	q556a0.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839180 3' similar to TR:O15103
2959	15764	142	1.42	6.0E-62	U09410.1	NT	O15103 HYPOTHETICAL-27.3 KD PROTEIN. ;
3379	16138	141	4.1	8.0E-62	11418255	NT	Homo zinc finger protein ZNF131 mRNA, partial cds
7525	20196	33288	3.03	6.0E-62	A1762801.1	EST_HUMAN	Homo sapiens CGL-55 protein (CGL55), mRNA
7525	20196	33290	3.03	6.0E-62	A1762801.1	EST_HUMAN	W04402.x1 NCJ_OGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
7984	20579	33981	0.72	6.0E-62	AW501124.1	EST_HUMAN	U1HF-BP0p-alt-4-09-U1r1 NIH_MGC 51 Homo sapiens cDNA clone IMAGE:3072833 5'
8155	20548	33981	1.45	6.0E-62	11431139	NT	Homo sapiens CGL-18 protein (LOC51009), mRNA
8254	21933	35106	3.27	6.0E-62	AW614593.1	EST_HUMAN	MR3-ST0203-130100-025-09 ST0203 Homo sapiens cDNA
407	13162	25840	2.8	5.0E-62	AI69528.1	EST_HUMAN	W057607.x1 NCJ_OGAP_LU28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:CG96_HUMAN
2406	15127	27693	4.25	6.0E-62	AJ271735.1	NT	Q05879 GOLGIN-98, contains element MER22 repetitive element ;
2406	15127	27694	4.25	6.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2558	15312	28048	1.35	5.0E-62	U36487.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2668	16312	28048	1.35	5.0E-62	U36487.1	NT	Human xanthine dehydrogenase/murase mRNA, complete cds
3413	16171	28820	2.92	6.0E-62	4506758	NT	Homo xanthine dehydrogenase/murase mRNA, complete cds
4293	17032	29550	2.6	5.0E-62	AA431093.1	EST_HUMAN	zw76a08.61 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782244 3' similar to SW:NRDC_RAT
8447	21139	34376	0.55	5.0E-62	4506758	NT	P47245 NARDILYSIN ;
9417	22095	35267	0.45	5.0E-62	AW410867.1	EST_HUMAN	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
11231	23894	37180	2.85	6.0E-62	11425574	NT	Homo sapiens cDNA clone IMAGE:2961616 5'
11231	23894	37181	2.85	6.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA

Page 331 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
820	13591	26288	1.95	4.0E-02	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
820	13591	26289	1.95	4.0E-02	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
821	13591	26288	2.86	4.0E-02	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
821	13591	26289	2.86	4.0E-02	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2459	15177	27916	1.78	4.0E-02	AB27900.1	EST_HUMAN	wf12d08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57139.maf1 HISTONE H2B.2 (HUMAN);
2459	15177	27917	1.78	4.0E-02	AB27900.1	EST_HUMAN	wf12d08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57139.maf1 HISTONE H2B.2 (HUMAN);
3394	16153		6.34	4.0E-02	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5833	18622	31655	1.84	4.0E-02	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6204	18979	31658	1.9	4.0E-02	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facete related) (USP9X), mRNA
7071	18762	32826	1.84	4.0E-02	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7534	20204	33289	2.48	4.0E-02	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7534	20204	33300	2.48	4.0E-02	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8071	20785	33804	1.03	4.0E-02	11428973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
8745	21437	34384	4.97	4.0E-02	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10394	23614	36864	4.45	4.0E-02	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
10394	23614	36865	4.45	4.0E-02	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11895	24533	37270	2.81	4.0E-02	11418098	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12590	24947	30684	1.34	4.0E-02	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12646	24942	30691	16.72	4.0E-02	11417692	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12646	24942	30692	16.72	4.0E-02	11417692	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12692	24976	30693	2.72	4.0E-02	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
72	12869	25335	0.89	3.0E-02	4657784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3041	15907	28452	1.71	3.0E-02	AB040609.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3041	15907	28453	1.71	3.0E-02	AB040609.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3696	16439	25081	5.41	3.0E-02	X52895.1	NT	Human cyclophilin-related processed pseudogene

Page 332 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8438	21130	34287	5.82	3.0E-62	A693733.1	EST_HUMAN	wr3304.ct.NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:228903 3' similar to contains THR12
1209	13960	26927	2.36	2.0E-62	AL163284.2	NT	THR repetitive element;
8873	21366	34511	4.83	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8873	21365	34512	4.88	2.0E-62	BF329911.1	EST_HUMAN	RCA-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10072	22720		3.8	2.0E-62	AF224699.1	NT	RCA-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11689	24284		4.81	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1021	13781	26443	1.87	1.0E-62	AF248540.1	NT	QVA-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1536	14293	28970	11.01	1.0E-62	L78810.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1791	14531	27239	1.04	1.0E-62	AA625207.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2015	16881	28328	0.99	1.0E-62	AA139044.1	EST_HUMAN	atf0e1t1.r1 Soares_NIHMPV_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP-K01H12.1
4317	17066		0.71	1.0E-62	BE188413.1	EST_HUMAN	DKFZ5956F104.11.569 (synonym: hlkcd2) Homo sapiens cDNA clone DKFZp566F104.5
4480	17226	28895	1.57	1.0E-62	8923201	NT	CDC3453;
5071	17790	30405	0.9	1.0E-62	L23503.1	NT	Human gliptaglin-like peptide-1 receptor (GLP-1) mRNA, complete cds
							Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
							Homo sapiens X2a region new ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDIM protein (CDM), adrenoleukodystrophy protein >
6196	18972	31948	0.86	1.0E-62	U52111.2	NT	Homo sapiens X2a region new ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDIM protein (CDM), adrenoleukodystrophy protein >
7034	19726	32782	0.91	1.0E-62	AA400060.1	EST_HUMAN	ab05902.s1 Stralagens fetal retina g37202 Homo sapiens cDNA clone IMAGE:839906 3'
7045	19736	32796	2.94	1.0E-62	AA722878.1	EST_HUMAN	zq389f10.s1 Soares_fetal_hear_NBH119W Homo sapiens cDNA clone IMAGE:409771 3'
7045	19736	32797	2.94	1.0E-62	AA722878.1	EST_HUMAN	zq389f10.s1 Soares_fetal_hear_NBH119W Homo sapiens cDNA clone IMAGE:409771 3'
8655	21347	34491	0.5	1.0E-62	AA200050.1	EST_HUMAN	zq389c07.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705660 5'
8956	21647	34797	2.13	1.0E-62	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8956	21647	34798	2.13	1.0E-62	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8969	21699	34838	2.02	1.0E-62	X16533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
8969	21699	34839	2.02	1.0E-62	X16533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9457	22027	35177	3.54	1.0E-62	AA489170.1	EST_HUMAN	aa3300.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:816055 3'
11339	24029	37353	2.01	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 6 HincIII fragment, SC6A14DB
24450			1.52	1.0E-62	11424055	NT	Homo sapiens eosinophil component Rfp-45 (LOC55615), mRNA
12474	24638	37762	1.52	1.0E-62	11424055	NT	Homo sapiens eosinophil component Rfp-45 (LOC55615), mRNA
12673	24966	36980	2.25	1.0E-62	11416322	NT	Homo sapiens cadherin EGF-LAG seven-pass G-type receptor 1 (CELSR1), mRNA
329	13130	25766	2.99	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2345			1.53	9.0E-63	AW16406.1	EST_HUMAN	QVA-S10234-181199-037-005 S10234 Homo sapiens cDNA
15068			2.59	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (Tfujilwara) Homo sapiens cDNA clone GEN-593C10 5'

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4020	18766	28395	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4020	18766	28396	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5164	17865	37798	3.05	9.0E-63	11418195	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
5379	18179	30869	1.63	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7082	19772	32837	3.86	9.0E-63	11426968	NT	Homo sapiens nucleophin 80d (NUP83), mRNA
7724	20387	33501	0.91	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isozyme 3 (PDK3) mRNA
8224	20918	34055	1.38	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
10816	23496	39736	2.03	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10816	23496	39737	2.03	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
2543	15066	27603	1.32	8.0E-63	4557734	NT	Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2373	16095	27834	2.06	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3454	18210	28891	3.02	8.0E-63	AF198348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3454	18210	28892	3.02	8.0E-63	AF198348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4234	16876	29600	3.31	8.0E-63	AL163266.2	NT	Homo sapiens chromosome 21 segment HS21C068
908	13875		2.09	7.0E-63	AI872137.1	EST_HUMAN	Wnt5g10.71 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:2439008 3'
5255	18081		48.05	6.0E-63	AA420803.1	EST_HUMAN	ncs3102.71 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00381 80S
8773	21465	34612	1.97	5.0E-63	11528464	NT	RIBOSOMAL PROTEIN (HUMAN);
3315	16078	28728	0.84	4.0E-63	AL163276.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3788	16540	29174	1.16	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3788	16540	29175	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6353	19123	32115	3.64	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6353	19123	32116	3.64	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-160100-072-009 BT0595 Homo sapiens cDNA
11077	23747	37021	2.3	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-160100-072-009 BT0595 Homo sapiens cDNA
11077	23747	37022	2.3	4.0E-63	AW134709.1	EST_HUMAN	U1H-B11-ab4-a-02-a-U1.1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
11846	24430	37771	4.32	4.0E-63	AA392834.1	EST_HUMAN	U1H-B11-ab4-a-02-a-U1.1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1928	14864	27377	2.82	3.0E-63	AB018260.1	NT	EST72807 Ovary II Homo sapiens cDNA 5' end similar to zinc finger protein family
2782	15487	28225	2.26	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2824	13987	28636	11.81	3.0E-63	6005693	NT	Human Mel-RNA-i gene 1
6382	19151	32150	32.78	3.0E-63	11545810	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
9805	22258	35444	1.15	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC393928), mRNA
9805	22258	35445	1.15	3.0E-63	BE876158.1	EST_HUMAN	601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888283 5'
9805	22258	35446	1.15	3.0E-63	BE876158.1	EST_HUMAN	601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888283 5'
186	12080	28699	1.08	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
163	13006	25847	1.68	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
485	13270		2.34	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8KD) (GLCLC) mRNA
807	13378	28244	6.57	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1659	14306	28964	1.43	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1559	14306	28965	1.43	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1760	14502	27203	1.1	2.0E-63	BE410739.1	EST_HUMAN	601301627/NIH_MGC_21 Homo sapiens cDNA clone IMAGE3638103 5'
3154	15917	28563	3.44	2.0E-63	4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3279	16040	28650	2.02	2.0E-63	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3885	16635	29274	3.74	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4813	17544	30199	1	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5098	17818	30435	0.98	2.0E-63	8912617	NT	Homo sapiens glutamyl-peptidase cyclotransferase (glutaminyl cyclase) (GPCT), mRNA
5181	25062	30505	1.25	2.0E-63	11419429	NT	Homo sapiens similar to extracellular pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
5794	18585	31512	2.96	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c06 FT0170 Homo sapiens cDNA
5794	18585	31513	2.96	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6033	18571	31637	0.84	2.0E-63	11421840	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6053	18571	31658	0.84	2.0E-63	11421840	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV51A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S3/13S3>
6802	19266	32379	1.67	2.0E-63	U69059.1	NT	Homo sapiens MIST mRNA, partial cds
6849	19411	32425	0.88	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6849	19411	32426	0.88	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6975	19456	32477	1.45	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934), mRNA
6975	19456	32478	1.45	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934), mRNA
7878	20342	33454	0.57	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
							Homo sapiens similar to serine domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
7713	20377	33490	0.56	2.0E-63	11421514	NT	Homo sapiens chromosome 21 segment HS21C010
8431	21124	34282	3.96	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8952	21643	34791	1.35	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8952	21643	34792	1.35	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9839	22490	35691	1.12	2.0E-03	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10647	23338	38577	6.43	2.0E-03	N78945.1	EST_HUMAN	Zb18005.s1 Sceres_feld_Lung_NHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:U17006.405 RIBOSOMAL PROTEIN S4 (HUMAN);
10672	23363	38604	2.86	2.0E-03	AF09810.1	NT	Homo sapiens neurodin III alpha gene, partial cds
10672	23363	38605	2.86	2.0E-03	AF09810.1	NT	Homo sapiens neurodin III alpha gene, partial cds
12098	25177	30807	6.97	2.0E-03	11418185	NT	Homo sapiens acylase 2, mitochondrial (AC02), mRNA
1502	14248	26934	1.28	1.0E-03	F08495.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1502	14248	26935	1.28	1.0E-03	F08495.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1502	14248	26935	1.28	1.0E-03	F08495.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4308	17047	29872	2.82	1.0E-03	F08495.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4308	17047	29873	2.82	1.0E-03	F08495.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5298	18074	30703	0.8	1.0E-03	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5298	18074	30703	0.8	1.0E-03	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6683	18476	31364	1.4	1.0E-03	AW582268.1	EST_HUMAN	QY0-ST0215-060100-083-b09 ST0216 Homo sapiens cDNA
6256	18071	32055	0.68	1.0E-03	AW451950.1	EST_HUMAN	U1-H-B19-alkh-02-Q-U1.s1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6256	18071	32056	0.68	1.0E-03	AW451950.1	EST_HUMAN	U1-H-B19-alkh-02-Q-U1.s1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8371	21084		2.88	1.0E-03	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12737	25280		4.04	1.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1024	13784	33596	4.35	9.0E-04	AI478189.1	EST_HUMAN	tm50007.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161628 3'
1024	13784	33596	4.35	9.0E-04	AI478189.1	EST_HUMAN	tm50007.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161628 3'
6048	18828	31792	3.88	8.0E-04	BE805765.1	EST_HUMAN	601155232FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
11916	24479		7.34	8.0E-04	11418177	NT	601155232FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
11916	24479		7.34	8.0E-04	11418177	NT	601155232FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
3520	16276		1.13	7.0E-04	BE394321.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4893	17417	30052	2.73	7.0E-04	4507490	NT	Y08802.7 Stragazine lung (R373210) Homo sapiens cDNA clone IMAGE:79179 5'
4893	17417	30053	2.73	7.0E-04	4507490	NT	601131455FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3653204 5'
4893	17417	30053	2.73	7.0E-04	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
9933	22881	35779	3.43	7.0E-04	Y07848.1	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
1716	14459	27156	1.63	6.0E-04	AI651892.1	EST_HUMAN	Homo sapiens EWS, gene22, np22 and bam22 genes
1716	14459	27156	1.63	6.0E-04	AI651892.1	EST_HUMAN	wb51607.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3120	15885	28524	4.39	6.0E-04	AI651992.1	EST_HUMAN	wb51607.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3120	15885	28524	4.39	6.0E-04	AI651992.1	EST_HUMAN	GLUCURONIDASE PRECURSOR (HUMAN);
5534	18332	31237	2.46	6.0E-04	Y18933.1	NT	wy13603.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2529438 3'
5534	18332	31237	2.46	6.0E-04	Y18933.1	NT	wy13603.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2529438 3'
5534	18332	31238	2.46	6.0E-04	Y18933.1	NT	Homo sapiens MGP-1 gene and enhancer region
5555	18362	31281	4.08	6.0E-04	M13975.1	NT	Homo sapiens MGP-1 gene and enhancer region
5555	18362	31281	4.08	6.0E-04	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

Page 336 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5564	18391	31269	1.26	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705). mRNA
5739	18531	31453	0.62	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR). mRNA
5739	18531	31454	0.62	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR). mRNA
7135	19823	32859	2.34	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1). mRNA
7135	19823	32860	2.34	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1). mRNA
9226	21905	35077	6.76	6.0E-64	11420555	NT	Homo sapiens acyl-CoA synthetase (LOC55902). mRNA
9403	22068	35240	2.09	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK). mRNA, complete cds
9618	22271	35458	2.78	6.0E-64	S76475.1	NT	hK (human, brain, mRNA, 2716 nt)
10559	23360	36600	6.01	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3). mRNA
10569	23360	36601	6.01	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3). mRNA
10941	15895	28524	1.84	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCI_QCAP_Bm23 Homo sapiens cDNA clone IMAGE:2529435 3'
10941	15895	28525	1.84	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCI_QCAP_Bm23 Homo sapiens cDNA clone IMAGE:2529435 3'
10941	15895	28526	1.84	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCI_QCAP_Bm23 Homo sapiens cDNA clone IMAGE:2529435 3'
12116	24608	31059	4.97	6.0E-64	AF231919.1	NT	Homo sapiens interleukin 10 receptor, beta (L10RB). mRNA
801	13573	26235	2.85	6.0E-64	AF231919.1	NT	Homo sapiens interleukin 10 receptor, beta (L10RB). mRNA
801	13573	26236	2.85	6.0E-64	AF231919.1	NT	Homo sapiens interleukin 10 receptor, beta (L10RB). mRNA
1315	14064	26738	1.84	6.0E-64	AB020710.1	NT	Homo sapiens chromosome 21 unknown mRNA
1401	14148	26827	1.3	6.0E-64	L40933.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1401	14148	26828	1.3	6.0E-64	L40933.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1706	14449	27149	1.37	6.0E-64	U69358.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMPRP) gene, complete cds
2829	14210	26937	4.85	6.0E-64	7662205	NT	Human (3)mb protein homolog mRNA, complete cds
2829	14210	26938	4.85	6.0E-64	7662205	NT	Human (3)mb protein homolog mRNA, complete cds
3940	16980	29828	6.71	6.0E-64	AF017433.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
4085	16980	29455	1.05	6.0E-64	AB020710.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
7716	20390	33493	0.58	4.0E-64	BE794807.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
10715	23404	36644	2.23	4.0E-64	AW813783.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
10715	23404	36645	2.23	4.0E-64	AW813783.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
2195	14924	27656	5.41	3.0E-64	C18953.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
3249	16011	28662	0.89	3.0E-64	BE794807.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
3436	16192	28841	2.22	3.0E-64	AW117174.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
3436	16192	28842	2.22	3.0E-64	AW117174.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
5990	18771	31734	1.21	3.0E-64	Z8673.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
6401	19170	32169	3.34	3.0E-64	BF370000.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618). mRNA
8365	21056	34198	1.93	3.0E-64	AF248953.1	NT	Homo sapiens gdi3 matrix protein GMI130 (GOLGA2) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8365	21058	34199	1.93	3.0E-64	AF248953.1	NT	Homo sapiens pdgfr matrix protein GM130 (GOLGA2) mRNA, complete cds
8393	21068	34220	3.69	3.0E-64	BE206521.1	EST_HUMAN	b57212.1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ
8393	21068	34220	3.69	3.0E-64	BE206521.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
8393	21068	34221	3.69	3.0E-64	BE206521.1	EST_HUMAN	b57212.1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ
9327	21994	33165	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9327	21994	33166	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9414	22092	35293	0.6	3.0E-64	AW977384.1	EST_HUMAN	EST1339493 IMAGE resequences, MAGO Homo sapiens cDNA
9414	22092	35294	0.6	3.0E-64	AW977384.1	EST_HUMAN	EST1339493 IMAGE resequences, MAGO Homo sapiens cDNA
11691	24286	37608	1.8	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1066	13824	28484	1.64	2.0E-64	AA609940.1	EST_HUMAN	af09808.s1 Scores: _bestg_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1377	14125	28799	1.54	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (eHBP) mRNA
2528	15244		1.82	2.0E-64	AI927030.1	EST_HUMAN	wc37601.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2533	15248	27687	2.05	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2533	15248	27688	2.05	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3137	15901	28546	1.42	2.0E-64	4604068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3767	16519	28157	0.78	2.0E-64	AV058145.1	EST_HUMAN	EST1370215 IMAGE resequences, MAGO Homo sapiens cDNA
3767	16519	28158	0.78	2.0E-64	AV058145.1	EST_HUMAN	EST1370215 IMAGE resequences, MAGO Homo sapiens cDNA
5916	18701	31635	2.78	2.0E-64	AU124397.1	EST_HUMAN	AUT124397 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6148	18925	31896	1.47	2.0E-64	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
6394	19163	32164	5.21	2.0E-64	BF686337.1	EST_HUMAN	60212347.4f1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4260395 5'
6497	19263	32264	1.16	2.0E-64	AI078987.1	EST_HUMAN	cc28603.x1 Scores: total_fetus_Nb2HF8_9v Homo sapiens cDNA clone IMAGE:1676717 3'
6801	19564	32376	4.54	2.0E-64	M77185.1	NT	H. sapiens dopamine receptor D5 pseudogene 1, partial cds
7707	20371	33484	0.7	2.0E-64	11431054	NT	H. sapiens dopamine receptor D5 pseudogene 1, partial cds
7732	20395	33510	0.65	2.0E-64	AW606785.1	EST_HUMAN	QVY-H10413-010200-059-H12 HT0413 Homo sapiens cDNA
8567	21269	34395	0.73	2.0E-64	11434003	NT	Homo sapiens albumin 2-binding protein 1 (A2BP1), mRNA
8567	21269	34396	0.73	2.0E-64	11434003	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCPT), mRNA
9038	21729	34882	0.86	2.0E-64	11423508	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCPT), mRNA
9130	21818	34984	0.97	2.0E-64	AU132570.1	EST_HUMAN	AUT132570 NT2RP4 Homo sapiens cDNA clone NT2RP400109 5'
9879	22529	35726	0.89	2.0E-64	T06397.1	EST_HUMAN	EST04288 Fetal brain, Stralagene (calb936206) Homo sapiens cDNA clone HFD588
9879	22529	35727	0.89	2.0E-64	T06397.1	EST_HUMAN	EST04288 Fetal brain, Stralagene (calb936206) Homo sapiens cDNA clone HFD588
10662	23563	35662	3.72	2.0E-64	BF628114.1	EST_HUMAN	602042682f1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'

Page 338 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10381	23656	36909	5.97	2.0E-64	A1922811.1	EST_HUMAN	wn181b06.x1 NCI_CGAP_LUT Homo sapiens cDNA clone IMAGE:2452211 3'
10381	23656	36910	5.97	2.0E-64	A1922811.1	EST_HUMAN	wn181b06.x1 NCI_CGAP_LUT Homo sapiens cDNA clone IMAGE:2452211 3'
11198	23863	37149	1.78	2.0E-64	AW1864773.1	EST_HUMAN	PV2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
12039	24662	31114	1.65	2.0E-64	8987387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
12468	24834		4.85	2.0E-64	HS5162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
251	13060	25698	2.84	1.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
1772	14574	27214	10.45	1.0E-64	A1929419.1	EST_HUMAN	au60d01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb.L21698 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3010	15776	28428	0.79	1.0E-64	4507334	NT	Homo sapiens synapobin 1 (SYNJ1), mRNA
3501	19257	28912	5.74	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel α -
3572	19327	28974	1.27	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3772	19327	28976	1.27	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3881	19631	29270	0.79	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11025 (FLJ11026), mRNA
8664	22612	33816	1.07	1.0E-64	AA042975.1	EST_HUMAN	ZK53108.s1 Soares_pregnant uterus_NHRPU Homo sapiens cDNA clone IMAGE:486657 3'
12012	24546		1.81	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2274	15000	27738	1.53	8.0E-65	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
2274	15000	27739	1.53	9.0E-65	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
11523	24123		10.43	9.0E-65	BC330878.1	EST_HUMAN	QV4-B10257-081169-017-e03 B10257 Homo sapiens cDNA
11493	24094	37405	10.87	8.0E-65	A1929244.1	EST_HUMAN	au168h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW-RL21_HUMAN P46778-60S RIBOSOMAL PROTEIN L21 ;
10056	22703	35921	2.01	7.0E-65	BE081663.1	EST_HUMAN	QV2-B10635-240400-102-e02 B10635 Homo sapiens cDNA
11807	24397	37731	1.27	7.0E-66	Z21378.1	EST_HUMAN	HSAAEAANO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam tes346 (b)
1034	13794	28454	3.59	6.0E-65	AV721988.1	EST_HUMAN	AV721988 HTB Homo sapiens cDNA clone HTB8ZC08 5'
1915	14652		4.73	6.0E-65	AA550929.1	EST_HUMAN	rib6101.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:999379 similar to gb.K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6475	19242	32242	0.52	8.0E-65	AA503892.1	EST_HUMAN	inh37b07.s1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
8845	21337	34481	2.3	6.0E-65	AW083282.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Cox21 Homo sapiens cDNA clone IMAGE:2503545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF's ; contains L1 b2 L1 repetitive element ;
8909	21600	34742	3.46	6.0E-65	AA427878.1	EST_HUMAN	z633b08.s1 Soares_total_fetus_Nb2Hf8_gw Homo sapiens cDNA clone IMAGE:773747 3'
8909	21600	34743	3.46	6.0E-65	AA427878.1	EST_HUMAN	z633b08.s1 Soares_total_fetus_Nb2Hf8_gw Homo sapiens cDNA clone IMAGE:773747 3'
8973	21693	34814	0.81	8.0E-65	AA085314.1	EST_HUMAN	qf18d05.x1 NCI_CGAP_Bnc25 Homo sapiens cDNA clone IMAGE:1750425 3'

Page 339 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8873	21683	34815	0.81	6.0E-65	AI085314.1	EST_HUMAN	4f1805.x1 NCL CGAP_Bm26 Homo sapiens cDNA clone IMAGE:1750425 3'
10783	23466	38707	3.82	6.0E-65	BE567816.1	EST_HUMAN	60134048BF1 NH_MGC_53 Homo sapiens cDNA clone IMAGE:3692877 5'
10968	23544	36897	1.52	6.0E-65	BF340825.1	EST_HUMAN	60203721F1 NCL CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4186877 5'
11480	24081	37382	1.86	6.0E-65	AL103210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1331	14080	26734	1.6	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product [KIAA0156], mRNA
1331	14080	26735	1.6	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product [KIAA0156], mRNA
2151	14881	27615	1.6	5.0E-65	AB033788.1	NT	Homo sapiens HPAD-cobonyl0 mRNA for peptidylarginine deaminase type I, complete cds
3260	18012	28963	1.6	6.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3260	18012	28964	1.6	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10364	23011	36228	1.01	5.0E-65	AF009568.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
188	13001	26542	2.02	4.0E-65	AL120419.1	EST_HUMAN	DKFZ761G108_x1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZ761G108 5'
726	13502	26156	1.37	4.0E-65	AI266468.1	EST_HUMAN	qtn46d01.x1 Soares_placenta_80dweeks_2NblpP81c9W Homo sapiens cDNA clone IMAGE:1891800 3'
726	13502	26157	1.37	4.0E-65	AI266468.1	EST_HUMAN	qtn46d01.x1 Soares_placenta_80dweeks_2NblpP81c9W Homo sapiens cDNA clone IMAGE:1891800 3'
1059	13814	28475	1.38	4.0E-65	4828735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1469	14216	26903	11.08	4.0E-65	45066536	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2336	15060	27790	0.91	4.0E-65	BE221469.1	EST_HUMAN	hu256d04.x1 NCL CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2336	15060	27797	0.91	4.0E-65	BE221469.1	EST_HUMAN	hu256d04.x1 NCL CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
3930	16580	29321	1.08	4.0E-65	AIW993185.1	EST_HUMAN	RC2-BJ0033-16020-015-a03 BN0033 Homo sapiens cDNA
5124	17642	30459	1.03	4.0E-65	9055268	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDLT), mRNA
5124	17642	30460	1.03	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDLT), mRNA
6063	18842	31804	4.6	4.0E-65	AB033063.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6063	18842	31806	4.6	4.0E-65	AB033063.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6983	19678	32723	0.55	4.0E-65	AI008372.1	NT	Homo sapiens oxygen binding protein-related protein 3 (ORP3) mRNA, complete cds
7017	19709	32795	0.97	4.0E-65	AI008372.1	NT	Homo sapiens oxygen binding protein-related protein 3 (ORP3) mRNA, complete cds
7119	19807	32873	2.52	4.0E-65	11645780	NT	Human clathrin 27 gene, exons 10 and 11, and L1 and Alu repeats
7449	20124	33215	0.97	4.0E-65	U40372.1	NT	Homo sapiens hypoxanthine phosphoribosyltransferase (HSPDR1C3A) mRNA
7448	20124	33216	0.97	4.0E-65	U40372.1	NT	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7448	20124	33216	0.97	4.0E-65	U40372.1	NT	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7741	20437	33558	1.86	4.0E-65	5463765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
7741	20437	33559	1.86	4.0E-65	5463765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9044	21734	34898	0.63	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10480	23126		2.04	4.0E-65	AJ277568.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10874	23554	36801	1.97	4.0E-65	AV738764.1	EST_HUMAN	AV738764 GB Homo sapiens cDNA clone BC005035 5'
11041	23712	36982	3.68	4.0E-65	AF118946.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12319	13814	28475	1.46	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1210	15522		3.8	3.0E-65	X78932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1551	14297	26984	0.91	3.0E-65	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
							ov2303.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
1816	14556	27271	0.93	3.0E-65	AI000592.1	EST_HUMAN	MSR1 repetitive element
3271	15032	28693	0.76	3.0E-65	4504693	NT	Homo sapiens lamitin, beta 1 (LAMB1), mRNA
							ov2303.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3709	16462	29101	0.69	3.0E-65	AI000592.1	EST_HUMAN	MSR1 repetitive element
4602	17337	29666	1.91	3.0E-65	5912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
9669	22817	35520	1.44	3.0E-65	BE787368.1	EST_HUMAN	601476685F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3892405 5'
11363	23174	38402	11.12	3.0E-68	AA430006.1	EST_HUMAN	z6560511 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3389	16157	28508	5.75	2.0E-68	BF680284.1	EST_HUMAN	602160062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295666 5'
6442	10210		2.46	2.0E-68	BE263373.1	EST_HUMAN	601180883F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3634741 5'
7032	19724	32760	32.07	2.0E-66	BF676022.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
8744	21436	34582	1.00	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
8744	21436	34583	1.06	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10552	23248	38485	2	2.0E-65	11419247	NT	Homo sapiens SWISINP related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SNARCD3), mRNA
							EST1178755 Caden carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
11890	24515		3.95	2.0E-65	AA307604.1	EST_HUMAN	601854033F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4073766 5'
12431	25156		2.2	2.0E-65	BF246086.1	EST_HUMAN	601760348F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
89	12915		1.89	1.0E-65	BF125544.1	EST_HUMAN	601760348F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
526	13310	25943	1.44	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homolog (RABEX6), mRNA
2033	14768	27498	1.29	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA11613 protein, partial cds
3365	16124	28764	0.81	1.0E-65	BE466681.1	EST_HUMAN	h224a03.x1 NCJ CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
3690	16728	29362	2.47	1.0E-65	4504032	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
3980	16728	29363	2.47	1.0E-65	4504032	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
4183	16923	29551	2.01	1.0E-65	AW028940.1	EST_HUMAN	ws060409.x1 NCJ CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543182 3'
4183	16923	29552	2.01	1.0E-65	AW028940.1	EST_HUMAN	ws060409.x1 NCJ CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543182 3'
8152	20846	33977	2.04	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042412 ST0298 Homo sapiens cDNA
8152	20846	33978	2.04	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042412 ST0298 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4332	17071	29700	1.15	9.0E-66	AB24853.1	EST_HUMAN	W15707.41 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WIPF1/EG9.4A
8333	21026		0.49	9.0E-66	BE178953.1	EST_HUMAN	CE18595:
11108	23778	37052	3.14	6.0E-66	X69181.1	NT	H-sapiens mRNA for ribosomal protein L31
1348	14094	28769	1.45	5.0E-66	BE004410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
5045	17765	30382	0.74	6.0E-66	BE898644.1	EST_HUMAN	801881502F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5048	17765	30383	0.74	6.0E-66	BE898644.1	EST_HUMAN	801881502F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
8194	21884	36028	18.11	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
773	13545	26206	0.98	4.0E-66	8679819	NT	Homo sapiens fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1729	14471	27170	1.14	4.0E-66	AW897788.1	EST_HUMAN	RC1-NN0053-100500-022-402 NN0053 Homo sapiens cDNA
2278	15004	27744	1.83	4.0E-66	X69211.1	NT	H-sapiens DNA for endogenous retroviral like element
2477	15185		3.02	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4733	17465		10.89	4.0E-66	9935487	NT	Human endogenous retrovirus, complete genome
5463	18282	31153	3.73	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5657	18452	31366	1.15	4.0E-66	AW939119.1	EST_HUMAN	QV14-DT0069-110200-057-g10 DT0069 Homo sapiens cDNA
6757	17926	30361	4.83	4.0E-66	AW896473.1	EST_HUMAN	EST377546 IMAGE resequences, MAGI Homo sapiens cDNA
7031	19723	32779	7.93	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
7529	18282	31153	0.72	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
7876	20671	33794	5.63	4.0E-66	11421638	NT	Homo sapiens hypobithiolase protein FLJ20119 (FLJ20116), mRNA
8034	20729	33962	0.73	4.0E-66	X67147.1	NT	Human endogenous retrovirus PHE1 (ERV9)
10556	23282	36489	1.97	4.0E-66	BF507493.1	EST_HUMAN	UJ-HBW1-anti-a-10-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
11351	24041	37344	1.28	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0988 protein, partial cds
1407	14154	26835	10.96	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1407	14154	26836	10.96	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1875	14711	27429	1.16	3.0E-66	N55323.1	EST_HUMAN	yz27g12.1 Soares, multiple sclerosis, 2NHHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to
1875	14711	27429	1.16	3.0E-66	N55323.1	EST_HUMAN	yz27g12.1 Soares, multiple sclerosis, 2NHHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to
1875	14711	27430	1.16	3.0E-66	N55323.1	EST_HUMAN	yz27g12.1 Soares, multiple sclerosis, 2NHHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to

Page 343 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1975	14711	27431	1.16	3.0E-66	NT	EST_HUMAN	Y27121.1 Soares_multiple_sclerosis_2NHMSP Homo sapiens cDNA clone IMAGE284326 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR-B56612.
2711	15418	28156	3.54	3.0E-66	11141880	NT	Homo sapiens TGF-beta1-induced transcription factor 2 (TGIF2), mRNA
3115	15880	28520	6.3	3.0E-66	7692223	NT	Homo sapiens KIA00409 gene product (KIA00409), mRNA
5390	18180	30870	1.14	3.0E-66	AB020690.1	NT	Homo sapiens mRNA for KIA00892 protein, partial cds
5490	18269	31186	0.73	3.0E-66	MT13976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5696	18479	31397	1.92	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6896	18479	31398	1.92	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8425	22103	35275	0.62	3.0E-66	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9619	22272	35439	0.52	3.0E-66	11417118	NT	Homo sapiens KIA00433 protein (KIA00433), mRNA
9873	22621	36928	0.8	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10420	23066	36287	0.97	3.0E-66	AF159650.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MOBPE) mRNA, complete cds
11494	24095	37406	6.18	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (566), alpha isoform (PPP2R6A) mRNA
11806	24396	37730	1.57	3.0E-66	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
50	12879	25505	2.15	2.0E-66	7957334	NT	Homo sapiens Mashapen/NIK-related kinase (MINK), mRNA
60	12879	25506	2.15	2.0E-66	7957334	NT	Homo sapiens Mashapen/NIK-related kinase (MINK), mRNA
413	12824	25437	1.76	2.0E-66	45065524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
413	12824	25437	1.76	2.0E-66	45065524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1819	14555	27272	2.05	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3510	10266	28920	0.77	2.0E-66	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3747	15500	29134	0.68	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4044	16769	29417	0.9	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4607	17342	29973	9.46	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4607	17342	29974	9.46	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5726	18518	31439	1.3	2.0E-66	AV968554.1	EST_HUMAN	EST380830 IMAGE sequences, MAGI Homo sapiens cDNA
5726	18518	31440	1.3	2.0E-66	AV968554.1	EST_HUMAN	EST380830 IMAGE sequences, MAGI Homo sapiens cDNA
8746	21438	34985	2.26	2.0E-66	N45480.1	EST_HUMAN	y59602.1 Soares_multiple_sclerosis_2NHMSP Homo sapiens cDNA clone IMAGE277826 5'
12326	25370		2.37	2.0E-66	11418318	NT	Homo sapiens C-2 and S-phase expressed 1 (GTSE1), mRNA
1678	14422		1.15	1.0E-66	BE687173.1	EST_HUMAN	8015083/81 NIH_MGC_71 Homo sapiens cDNA clone IMAGE3909931 5'
2655	15662	28309	1.36	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	15682	28310	1.38	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4352	15682	28309	3.81	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4352	15682	28310	3.81	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5297	18102	30761	5.98	1.0E-66	BE573088.1	EST_HUMAN	602182988F1 NIH_NGCG 5' Homo sapiens cDNA clone IMAGE:4294161 5'
5692	18488	31406	0.77	1.0E-66	BE785232.1	EST_HUMAN	IL2-NT0101-2807003-116E04 NT0101 Homo sapiens cDNA
5692	18488	31407	0.77	1.0E-66	BE785232.1	EST_HUMAN	IL2-NT0101-2807003-116E04 NT0101 Homo sapiens cDNA
6839	19501	32526	1.57	1.0E-66	BF32823.1	EST_HUMAN	cg8040.4 x1 NGL CGAP GGB1 Homo sapiens cDNA clone IMAGE:827262 3'
8357	21050	34189	1.19	1.0E-66	AA68858.1	EST_HUMAN	cg8040.4 x1 NGL CGAP GGB1 Homo sapiens cDNA clone IMAGE:827262 3'
8628	21063	35164	0.84	1.0E-66	AA018828.1	EST_HUMAN	z85761.2.1 Soares retina N2B-HR Homo sapiens cDNA clone NPCBVA05 5'
10270	22918	38129	0.92	1.0E-66	AV748748.1	EST_HUMAN	AV748748 NPC Homo sapiens cDNA clone NPCBVA05 5'
10270	22918	38130	0.92	1.0E-66	AV748748.1	EST_HUMAN	AV748748 NPC Homo sapiens cDNA clone NPCBVA05 5'
10882	23542	36789	2.48	1.0E-66	AF11167.2	NT	Homo sapiens lun dimerization protein gene, partial cds: cfas gene, complete cds, and unknown gene
11509	24109	37422	1.8	1.0E-66	AW68744.1	EST_HUMAN	EST380820 IMAGE: sequences, MAGJ Homo sapiens cDNA
12113	24606		2.51	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
371	13189	25841	1.52	7.0E-67	AW16232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1361	14109	26784	2.89	7.0E-67	AA383418.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN):
1547	14293	26978	1.38	7.0E-67	W85947.1	EST_HUMAN	EST06812 Testis 1 Homo sapiens cDNA 5' and similar to similar to C. elegans hypodermal protein, coamid
1547	14293	26980	1.38	7.0E-67	W85947.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
2028	14761	27489	2.06	7.0E-67	7657243	NT	ZK353
2028	14761	27489	2.06	7.0E-67	7657243	NT	ZK353
2813	13106	25841	3.4	7.0E-67	AW16232.1	EST_HUMAN	zh56065.f1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
5989	18770	31733	0.78	7.0E-67	10190685	NT	zh56065.f1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
6177	18954	31927	2.02	7.0E-67	11425572	NT	Homo sapiens histidyl 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6177	18954	31928	2.02	7.0E-67	11425572	NT	Homo sapiens histidyl 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6523	19385	32389	1.29	7.0E-67	4885084	NT	Homo sapiens histidyl 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
7531	20201	33286	1	7.0E-67	11416212	NT	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
7631	20201	33287	1	7.0E-67	11416212	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN):
8222	20916	34052	0.69	7.0E-67	4557732	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
8830	21522	34669	0.68	7.0E-67	10835044	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
							Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
							Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein
							1A (110116KD) (AT1P6M1A), mRNA
							Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
							Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
							Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
							Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11266	23918		1.56	7.0E-67	11434579	NT	Homo sapiens fucosyltransferase 8 (alpha 1,8) fucosyltransferase (FUT8), mRNA
11677	24272	37594	6.37	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11688	24465	37803	2.24	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11698	24466	37804	2.24	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12555	24769	31001	1.58	7.0E-67	AB011392.1	NT	Homo sapiens gene for A1-8, complete cds
543	13329	25960	2.12	6.0E-67	X88968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
778	13350	26211	0.92	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for Transmembrane receptor protein
1250	13699	26068	1.28	6.0E-67	Y14320.1	NT	Homo sapiens PMF59 gene, exons 3,4,5,6 & 7
3166	16929	28578	1.17	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3431	16187	28835	1.64	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3431	16187	28836	1.64	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4108	16849	29474	0.7	6.0E-67	AL463201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4108	16849	29475	0.7	6.0E-67	AL463201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4657	17391	30026	5.01	6.0E-67	7857020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
5101	17635	30026	5.01	6.0E-67	7857020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
3215	15978	28629	1.91	5.0E-67	AF00680.1	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
10905	23585		1.06	6.0E-67	BE010038.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV73SA2 to TCRBV12S2 region
1303	14094	28728	0.93	4.0E-67	R00819.1	EST_HUMAN	Yr02411.r1 Soares adult brain N2b4HB557 Homo sapiens cDNA
7920	20615	33743	0.82	4.0E-67	AI735032.1	EST_HUMAN	Q22605.v8 NCL CGAP Kid3 Homo sapiens cDNA clone IMAGE:167253 5'
8281	20975		1.24	4.0E-67	BF357321.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
10998	28669		1.39	4.0E-67	AA714284.1	EST_HUMAN	R00819.s1 NCL CGAP SST1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR-O10385 O10385
2816	13396	26031	1.95	3.0E-67	AA333788.1	EST_HUMAN	PRO-POL-DUTHPASE POLYPROTEIN ;
3446	18202	28852	0.98	3.0E-67	BE064410.1	EST_HUMAN	EST37803 Embryo 9 week Homo sapiens cDNA 5' and
4646	17380	30012	2.87	3.0E-67	AW869156.1	EST_HUMAN	RC4-BT03T1-141168-011-406 BT03T1 Homo sapiens cDNA
8081	28778	33905	1.53	3.0E-67	BF198068.1	EST_HUMAN	MR3-SN00088-00000-008-007 SN0088 Homo sapiens cDNA
11224	23887		14.39	3.0E-67	AA328784.1	EST_HUMAN	h81165.x1 NCL CGAP Kid41 Homo sapiens cDNA clone IMAGE:3134613 3' similar to SW:RHP_MOUSE
183	12968	25835	0.81	2.0E-67	BE348364.1	EST_HUMAN	Q61065 GTP-RHO BINDING PROTEIN 1 ;
825	13595	26265	7.3	2.0E-67	AW816405.1	EST_HUMAN	cm1807.s1 Soares NFL T GRC_S1 Homo sapiens cDNA clone IMAGE:1641365 3'
1083	13841		1.75	2.0E-67	AF167460.1	NT	h16f030.x1 NCL CGAP L224 Homo sapiens cDNA clone IMAGE:1681196 3' similar to WP:F23H11.9 CE09617 ;
							QV4-ST0234-181199-037-008 ST0234 Homo sapiens cDNA
							Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

Page 348 of 538
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1877	14814	27325	1.36	2.0E-67	BE303037.1	EST_HUMAN	baf72d03.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905978 5' similar to TR:094892 094892 KIA00788 PROTEIN. ;
1877	14814	27326	1.38	2.0E-67	BE303037.1	EST_HUMAN	baf72d03.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905978 5' similar to TR:094892 094892 KIA00788 PROTEIN. ;
2235	14863	27702	1.3	2.0E-67	11422946	NT	Homo sapiens hypophyseal protein dJ462023.2 (DJ462023.2) mRNA
2235	14863	27703	1.3	2.0E-67	11422946	NT	Homo sapiens hypophyseal protein dJ462023.2 (DJ462023.2) mRNA
2384	15105	27845	1.08	2.0E-67	A309561.1	NT	Homo sapiens K5A5 zinc finger protein ZFGR mRNA, complete cds
2432	15153	27887	1.28	2.0E-67	4788798	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3460	18218	28870	3.8	2.0E-67	AA625755.1	EST_HUMAN	zu91.g01.61 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
3684	18732	28368	3.03	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5981	18782	31726	0.6	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6034	18814	31774	5.54	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4061893 5'
6203	18878	31958	2.46	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6203	18878	31957	2.46	2.0E-67	AL120542.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8456	21148	34290	0.82	2.0E-67	AA334609.1	EST_HUMAN	DKFZ761A229.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ761A229 5'
8456	21148	34291	0.82	2.0E-67	AA334609.1	EST_HUMAN	EST38950 Embryo, 9 week Homo sapiens cDNA 5' and similar to similar to cerebellin
8895	21588	34724	1.21	2.0E-67	AW602835.1	EST_HUMAN	EST38950 Embryo, 9 week Homo sapiens cDNA 5' and similar to similar to cerebellin
8895	21588	34726	1.21	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0666-170100-011-c07 BT0666 Homo sapiens cDNA
8908	22251	35447	0.83	2.0E-67	AV791333.1	EST_HUMAN	AV791333 HTF Homo sapiens cDNA clone HTFAR003 5'
9498	22876	35248	0.97	2.0E-67	AV791333.1	EST_HUMAN	UJH.BJ2-sh-c-10-0.U1et NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10070	23546	36889	3.72	2.0E-67	BF034485.1	EST_HUMAN	601445262F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858975 5'
10988	25433		4.67	2.0E-67	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11183	23868	37145	2.11	2.0E-67	BE289714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11434	23201	35433	1.86	2.0E-67	BF377160.1	EST_HUMAN	PM2-TN0703-040900-c01-c02 TN0703 Homo sapiens cDNA
12235	25231	30818	1.35	2.0E-67	11418188	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P7), mRNA
12527	24874	31018	2.05	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
248	13055	25695	9.34	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
692	13467	28114	1.01	1.0E-67	AA702784.1	EST_HUMAN	2505054.s1 Soares_fetal_liver_spleen_1NFLS_51 Homo sapiens cDNA clone IMAGE:448015 3'
11845	24429	37770	8.58	1.0E-67	AI654867.1	EST_HUMAN	w06612.1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2310550 3'
2174	14903	27638	-2.13	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852254 5'
3851	16601	29238	4.96	8.0E-08	AA209456.1	EST_HUMAN	208210.1.r1 Stralagene INT neuron (8697233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SV:SAV_SULAC Q07590 SAV PROTEIN. ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3951	16001	29239	4.98	8.0E-68	AA209456.1	EST_HUMAN	z822b10.r1 Striatagene N1T1 neuron (#637223) Homo sapiens cDNA clone IMAGE:648163 5' similar to
8000	20695	33822	0.55	7.0E-68	AB10505.1	EST_HUMAN	SW/SAV_SULAC_Q07590 SAV PROTEIN. ;
7737	20402	33518	0.58	6.0E-68	AB014820.1	NT	WB80e3.x1 NO1 CGAP P128 Homo sapiens cDNA clone IMAGE:2312880 3'
10347	22894	36213	2.47	6.0E-68	11422085	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
11097	23767	37042	1.61	6.0E-68	AF133901.1	NT	Homo sapiens trefaldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12829	24875		1.78	6.0E-68	BE12564.1	EST_HUMAN	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
12772	25026	30693	1.4	6.0E-68	BF310675.1	EST_HUMAN	601449207F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
800	13572	26233	5.05	5.0E-68	AF231918.1	NT	601894835F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
800	13572	26234	5.05	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2783	15488	26228	1.38	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3144	16508	28553	3.23	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4457	17183	28819	0.73	5.0E-68	AL157645.1	EST_HUMAN	Homo sapiens mRNA for KIAA1431 protein, partial cds
6927	18399	32402	0.61	5.0E-68	7019512	NT	DKFZp47D207.r1 847 (synonym: hibr1) Homo sapiens cDNA clone DKFZp47D207 5'
6927	18399	32403	0.61	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab33)-like 1 (RAB33L1), mRNA
4918	17646		0.87	4.0E-68	P04408	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
5098	17817	30434	0.87	4.0E-68	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5974	18651	31602	0.7	4.0E-68	AF157083.1	NT	Homo sapiens sardin (SEDL) gene, exon 4
6976	19692	32639	6.51	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6976	19692	32639	6.51	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7582	20250	33538	0.88	4.0E-68	7861683	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8928	21629	34771	6.05	4.0E-68	D83479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8938	21629	34772	5.05	4.0E-68	D83479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9077	21765	34929	3.08	4.0E-68	AB040918.1	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTPAA1), mRNA
1025	23605	36854	1.68	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTPAA1), mRNA
1025	23605	36855	1.68	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTPAA1), mRNA
11115	23765	37051	1.28	4.0E-68	AB040948.1	NT	Homo sapiens mRNA for KIAA1515 protein, partial cds
11828	24442	37749	1.39	4.0E-68	AJ261780.1	NT	Homo sapiens MESPS5, GNAS1 antisense (partial) and XLapins (partial) genes
11884	24448	37789	12.15	4.0E-68	4759287	NT	Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA
11884	24448	37789	12.15	4.0E-68	4759287	NT	Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA
3653	18408	20045	5.37	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9357	20428		5.82	3.0E-68	A1342323.1	EST_HUMAN	q838102.x1 Soares_fetal_jung_NHL18W Homo sapiens cDNA clone IMAGE:1650391 3' similar to contains THR42 THR repetitive element ;

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10369	23045	36261	1.23	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023C09
2865	17863		15.31	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4833	17368	30004	1.38	2.0E-68	AB008981.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6776	19520		9.54	2.0E-68	R45088.1	EST_HUMAN	y536p4.1t Soares infant brain N18B Homo sapiens cDNA clone IMAGE:34865 3'
6993	19448	32462	5.39	2.0E-68	BF035316.1	EST_HUMAN	801465814F1 NIH_MGC 86 Homo sapiens cDNA clone IMAGE:3662034 5'
7270	19654	33030	0.73	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT10544-180900-273-A01 C10534 Homo sapiens cDNA
8848	21530	34695	0.63	2.0E-68	Q05659	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
10303	23151	36376	0.75	2.0E-68	N78483.1	EST_HUMAN	x276407.1t Soares multiple sclerosis_ZNBMSP Homo sapiens cDNA clone IMAGE:289185 5'
11210	23873	37160	1.66	2.0E-68	BF330394.1	EST_HUMAN	QY0-B10074-130666-014-g04 B10074 Homo sapiens cDNA
77	12603	25541	1	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
289	13095	25737	13	1.0E-68	AW816403.1	EST_HUMAN	Homo sapiens mRNA for KIA0577 protein, complete cds
2248	14977	27115	1.03	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIA0577 protein, complete cds
2249	14977	27116	1.03	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIA0577 protein, complete cds
3591	16739	28373	0.85	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3532344 5'
4959	17694	30302	0.92	1.0E-68	AA897343.1	EST_HUMAN	alc12.1t Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
6239	18045	30874	1.37	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KIA0869), mRNA
7576	20245	33330	1	1.0E-68	11436716	NT	Homo sapiens cathepsin(LUMO)-specific protease (SEN11), mRNA
10373	23019	36235	0.6	1.0E-68	AA429338.1	EST_HUMAN	x274602.1t Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781923 5'
10755	23441	36695	1.85	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10766	23441	36696	1.85	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10319	23502	36741	3.5	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds
11148	23815	37058	1.71	1.0E-68	11433277	NT	Homo sapiens myosin C (MYO1C), mRNA
11228	23869	37176	1.62	1.0E-68	AF043126.1	NT	Homo sapiens interleukin-7 receptor precursor (IL7R) gene, exons 7 and 8 and complete cds
11270	23931	37223	1.26	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 4-5
11270	23931	37224	1.26	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 4-5
11866	24281	37564	1.48	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC81632), mRNA
11666	24281	37565	1.48	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC81632), mRNA
12511	12903	25541	2.86	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12719	26322	30712	2.11	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
19	12847	26460	1.16	9.0E-69	6031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
19	12847	25491	1.19	9.0E-69	6031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1005	13766	26426	1.41	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1005	13766	26427	1.41	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2275	15001	27740	1.15	9.0E-69	4759278	NT	Homo sapiens EphA4 (EPHA4) mRNA

Page 349 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2275	15001	27741	1.15	9.0E-69	4758279	NT	Homo sapiens EPAA4 (EPHA4) mRNA
4109	18852	28478	0.71	9.0E-69	4757857	NT	Homo sapiens v-ref murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
10805	23488		6.5	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA100066 5'
3381	18140		1.09	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
8259	18033	32008	8.49	7.0E-69	8958912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
7762	20458	33581	9.09	6.0E-69	A192764.1	EST_HUMAN	q62n01.x1 Scarsa, fetal, lung, NHL-19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to cBL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
7762	20458	33582	9.09	6.0E-69	A192764.1	EST_HUMAN	q62n01.x1 Scarsa, fetal, lung, NHL-19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to cBL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8873	21584	34709	1.07	5.0E-69	A026039.1	EST_HUMAN	q6L1566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
507	13291		1.76	4.0E-69	A073930.1	EST_HUMAN	wm28n11.x1 NCI CGAP U18 Homo sapiens cDNA clone IMAGE:2437125 3'
5974	25073	31384	1.42	4.0E-69	BE561063.1	EST_HUMAN	801344706FT NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677841 5'
5763	18545	31467	5.26	4.0E-69	A1764973.1	EST_HUMAN	wh57608.x1 NCI CGAP KdH1 Homo sapiens cDNA clone IMAGE:2384619 3' similar to TR:O55137
6531	19297	32301	2.71	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE ;
6531	19297	32302	2.71	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8812	21604	34651	0.52	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
377	19202	26848	3.69	3.0E-69	BE258012.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
598	13376	26008	2.32	3.0E-69	AF221712.1	NT	80110371FT NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-Interacting Zinc finger protein mRNA, partial cds
1548	14284		3.19	3.0E-69	T80514.1	EST_HUMAN	y08a02.1 Scores infant brain *NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48536
5183	17894	37787	3.84	3.0E-69	11418185	NT	A48936 SPEGF III-EFG REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
							Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
6705	19820		0.67	3.0E-69	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(p)-deoxyribonucleoside (dNT-2 gene), exons 1-5
6759	17928	30553	0.74	3.0E-69	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
7272	19956	33032	0.68	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor encoding mitochondrial protein, complete cds
7320	20023	33082	1.83	3.0E-69	J62351.1	NT	Homo sapiens arm-repeat protein NFPA/Pisaurin (CTNND2) mRNA, partial cds
7451	20127	33219	0.32	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein TBBP mRNA, complete cds
8270	20994	34108	0.88	3.0E-69	AW138646.1	EST_HUMAN	U1H-BIT-low-gd1-Q-U1st NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8666	21338		0.85	3.0E-69	AA376399.1	EST_HUMAN	EST86607 HSC172 cells II Homo sapiens cDNA 5' and similar to ribosomal protein S18
9313	21980	35152	1.01	3.0E-69	X13223.1	NT	H sapiens mRNA for N-acetylglucosaminide-(ura 1-4)-galactosyltransferase

Page 350 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9433	22111	35286	2.03	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
8729	22380	35592	0.75	3.0E-69	5730039	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10538	23235	35488	1.44	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10745	23432		7.81	3.0E-69	AA376359.1	EST_HUMAN	EST19807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
12024	24552		5.17	3.0E-69	11419157	NT	Homo sapiens HSC62.2, protein (HSC62.2), mRNA
125	13180	25827	1.64	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
125	13180	25828	1.64	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
395	13180	25827	10.33	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
395	13180	25828	10.33	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1878	14615	27327	2.08	2.0E-69	BE267867.1	EST_HUMAN	60110844AF1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3350074 5'
2848	15618		3.18	2.0E-69	AA431157.1	EST_HUMAN	2x71g02.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE751682 5'
8452	21144	34284	1.08	2.0E-69	AA114270.1	EST_HUMAN	zn29g01.1 Stragelena pancreas (9837208) Homo sapiens cDNA clone IMAGE527088 5'
1698	14441	27139	1.88	1.0E-69	AF033788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
4662	17687		0.74	1.0E-69	BE409084.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3635781 5'
5959	18741	31700	0.87	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3958532 5'
5959	18741	31701	0.87	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3958532 5'
5503	18273	32274	4.37	1.0E-69	AW363989.1	EST_HUMAN	QV05-TT0010-031189-045-c07 T10010 Homo sapiens cDNA
6721	19636	32678	1.28	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6737	19671	32603	3.01	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6737	19671	32604	3.01	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6782	19528	32584	1.14	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE3610814 5'
6782	19528	32555	1.14	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE3610814 5'
10073	22721	35937	4.91	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10073	22721	35938	4.91	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10168	22810	35934	1.38	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10314	22951	36177	0.57	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE4181325 5'
10782	23465		10.62	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8), mRNA
11664	24512	37261	1.74	1.0E-69	BF125387.1	EST_HUMAN	601702902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE4025785 5'
12866	24769		4.45	1.0E-69	AB009894.1	EST_HUMAN	W64609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	15591	27791	2.08	8.0E-70	AA230303.1	EST_HUMAN	nc13d1.2.1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4340	17079	29708	1.83	8.0E-70	L71566.1	NT	Homo sapiens DGS4 mRNA, 3' end
1808	14546	27260	1.01	7.0E-70	A1497807.1	EST_HUMAN	U08907.X1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1806	14546	27261	1.01	7.0E-70	A1497807.1	EST_HUMAN	U08907.X1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1823	14680	27371	1.68	7.0E-70	AA232355.1	EST_HUMAN	z16104.11 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2056	14788		2.92	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4199	16840	29566	3.67	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5395	18165	30888	4.88	7.0E-70	AB032363.1	NT	Homo sapiens MIST mRNA, partial cds
5395	18165	30889	4.88	7.0E-70	AB032363.1	NT	Homo sapiens MIST mRNA, partial cds
6828	19487	32509	2.16	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8330	21023	34169	2.2	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8622	21314	34457	3.58	7.0E-70	M74069.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8622	21314	34458	3.58	7.0E-70	M74069.1	NT	Human displacement protein (GCAAT) mRNA
9055	21744	34902	3.8	7.0E-70	X89441.1	NT	Human PBX3 mRNA
9055	21744	34903	3.8	7.0E-70	X89441.1	NT	Human PBX3 mRNA
9335	20408	33522	3.43	7.0E-70	AF163715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9361	20431	33951	2.69	7.0E-70	11525684	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2) mRNA
9381	20431	33952	2.69	7.0E-70	11525684	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2) mRNA
9856	22209	35594	0.57	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8KD) (GLCLC) mRNA
10196	22844	36058	0.62	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10196	22844	36059	0.62	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11010	23682	36941	1.54	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4) mRNA
11010	23682	36942	1.54	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4) mRNA
11597	24196	37515	1.95	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA) mRNA
11597	24196	37516	1.65	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA) mRNA
851	13821	26291	1.77	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease notch-II, Alzheimer disease) (APP), mRNA
2133	14893	27593	1.21	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2513	15230	27970	1.22	6.0E-70	8923369	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907) mRNA
2555	16598	28003	2.18	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792) mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2555	15598	28004	2.18	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11974	24519		2.75	5.0E-70	BE106034.1	EST_HUMAN	MR3-H70487-150200-118-406 HT0487 Homo sapiens cDNA
6856	19417	32431	1.03	4.0E-70	T06037.1	EST_HUMAN	EST103528 Fetal brain, Striatum (ca193528) Homo sapiens cDNA
6856	18613	32653	1.78	4.0E-70	AW793226.1	EST_HUMAN	CM44-JM0003-010300-105-508 UM0003 Homo sapiens cDNA
6856	18613	32654	1.78	4.0E-70	AW793226.1	EST_HUMAN	CM44-JM0003-010300-105-508 UM0003 Homo sapiens cDNA
1354	14330	27016	1.23	3.0E-70	BE071766.1	EST_HUMAN	RCO-BT0522-071289-011-at12 BT0522 Homo sapiens cDNA
1854	14330	27017	1.23	3.0E-70	BE071766.1	EST_HUMAN	RCO-BT0522-071289-011-at12 BT0522 Homo sapiens cDNA
5532	18330	31234	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5532	18330	31235	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5555	18642	31591	1.8	3.0E-70	A1831976.1	EST_HUMAN	wf65d03.x1 NGL CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2385005 3'
6260	19053	32031	1.85	3.0E-70	BF685233.1	EST_HUMAN	602141601FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6260	19053	32032	1.65	3.0E-70	BF685233.1	EST_HUMAN	602141601FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10008	22656	35869	0.58	3.0E-70	BE502973.1	EST_HUMAN	h281102.x1 NGL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
37	12865	25484	1.2	2.0E-70	AF012672.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
673	13449	26089	14.09	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
673	13449	26089	14.09	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
689	13464	26113	1.7	2.0E-70	A1248899.1	EST_HUMAN	gxs1101.x1 NGL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1000	13760	26421	1.58	2.0E-70	59226580	NT	Homo sapiens hypodermal protein FLJ20758 (FLJ20758), mRNA
1161	13915	26578	3.05	2.0E-70	7651983	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
1161	13915	26579	3.05	2.0E-70	7651983	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
1736	14478	27177	1.66	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2318	15043		5.32	2.0E-70	AA054010.1	EST_HUMAN	Z48904.r1 Soares retina N2k4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3615	18368	29011	0.78	2.0E-70	H37988.1	EST_HUMAN	P03345 GAG POL YPROTEIN ;
4027	16772	29404	5.09	2.0E-70	M69181.1	NT	yp85d04.r1 Soares fetal liver spleen TNF5 Homo sapiens cDNA clone IMAGE:191599 5'
5428	18227	30839	8.7	2.0E-70	X72682.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5428	18227	30840	8.7	2.0E-70	X72682.1	NT	H. sapiens gene for schwannin (CS9)
6111	18938	31657	1.27	2.0E-70	AF310105.1	NT	H. sapiens gene for schwannin (CS8)
6538	19303	32307	1.75	2.0E-70	DT2825.1	NT	Homo sapiens MALP1 mRNA, complete cds
6538	19303	32307	1.75	2.0E-70	DT2825.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6569	19333	32342	12.14	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6569	19333	32343	12.14	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds

Page 353 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6897	17973	30530	1.88	2.0E-70	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
7303	19886	33062	0.76	2.0E-70	AF289207.1	NT	Homo sapiens cysteine-RNA synthetase mRNA, complete cds, alternatively spliced
7819	20514	33839	9.02	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8121	20816	33951	0.5	2.0E-70	11423599	NT	Homo sapiens myo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
8558	21250		0.8	2.0E-70	H47959.1	EST_HUMAN	Yp79p02.7 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:193882 5'
9097	21756	34918	0.96	2.0E-70	11529355	NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
10038	22696	35904	1.46	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10500	23146	36373	0.47	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
11003	23677	36933	3.75	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11005	23677	36934	3.75	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11639	24236	37559	7.32	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (EIF3S6) mRNA
12553	24767	31058	3.06	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12553	24767	31059	3.06	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3386	16147		2.63	1.0E-70	4607476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9180	21850		0.69	1.0E-70	W85785.1	EST_HUMAN	Zf55p05.1t Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418024 5'
9658	22349		0.65	1.0E-70	AA442292.1	EST_HUMAN	Zf54p03.1t Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
10852	23532	36777	7.13	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
5854	18641	31579	7.05	9.0E-71	A143870.1	EST_HUMAN	q6401.1t Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6854	18641	31680	7.05	9.0E-71	A143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE. ;
6832	19858	32714	2.23	9.0E-71	A1954903.1	EST_HUMAN	q6401.1t Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
11508	19868	32714	4.79	9.0E-71	A1954903.1	EST_HUMAN	W852p05.1t NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
8969	21638		5.03	8.0E-71	AA171451.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
7275	19859	33036	8.9	7.0E-71	AA442292.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
8578	21270	34408	1.02	7.0E-71	AA705437.1	EST_HUMAN	ZP211.1t1 Stratagene neurocithellium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to
11302	23961	37282	2.07	7.0E-71	AL163210.2	NT	TR:G1143061 G1143061 STRAIN XA34 POL. ;
2207	14835	27673	5.87	6.0E-71	AF065322.1	NT	z66106.1t Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
							z6106.1t Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4101	18844	29472	1.36	5.0E-71	AW816405.1	EST_HUMAN	QV410234-181190-037-005 ST0234 Homo sapiens cDNA
5790	19581	31508	2.23	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6564	19329	32336	1.42	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
6821	19492	32504	1.43	5.0E-71	7862209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6878	17954	30550	0.62	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
6878	17954	30551	0.62	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7046	19737	32798	0.76	5.0E-71	AB033106.1	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7410	20087	33171	1.47	5.0E-71	M58106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7607	20273	33361	0.75	5.0E-71	11529445	NT	Homo sapiens MAGUK protein p57, Protein Associated with Lys 2 (LOC51678), mRNA
7634	20289	33408	22.56	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8421	21114	34251	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8421	21114	34252	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8811	22482	36461	2.87	5.0E-71	X13487.1	NT	Human Prd4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10530	23227	36461	1.45	5.0E-71	5726600	NT	Homo sapiens (IG-1) mRNA-binding protein 3 (KOCT), mRNA
10901	23581	36831	2.93	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11147	23814	37097	2.57	5.0E-71	11438059	NT	Homo sapiens similar to hypothetical protein FL20163 (H. sapiens) (LOC63325), mRNA
340	13141	25778	102.7	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
340	13141	25778	102.7	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2889	19556	28299	1.97	4.0E-71	4509890	NT	Homo sapiens plasminogen (PLG) mRNA
4394	17131	29762	3.37	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SPT100) mRNA, complete cds
4626	17654	30296	5.57	4.0E-71	7657602	NT	Homo sapiens putative home-binding protein (SOUL), mRNA
5069	17788	30404	1.1	4.0E-71	7016352	NT	Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 3 (130KD) (CRSP3), mRNA
7833	20628		1.41	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.3 PTR5 repetitive element
10591	23285	36523	3.39	3.0E-71	AA657683.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210006
1208	19389	28628	2.02	2.0E-71	AL163200.2	NT	Human mRNA for KIAA0272 gene, partial cds
5237	18043	30672	8.24	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5237	18043	30673	8.24	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
8871	17948	30543	0.55	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721.1t.434 (synonym: Hs43) Homo sapiens cDNA clone DKFZp434D1721.5
8803	21594	34735	0.64	2.0E-71	BF195585.1	EST_HUMAN	7d55c11.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221.3 similar to TRQ92165 Q92165 PUTATIVE FOUR REPEAT ION CHANNEL.1

Page 355 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10485	23131	36357	3.88	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10486	23131	36358	3.88	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10593	23287	36524	3.21	2.0E-71	BE018477.1	EST_HUMAN	h387a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW-R23B_HUMAN P64727 UV EXCISION REPAIR PROTEIN RAD23B HOMOLOG B ;
11552	24151	37463	1.36	2.0E-71	BF149733.1	EST_HUMAN	Tnu0222 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11552	24151	37464	1.36	2.0E-71	BF149733.1	EST_HUMAN	Tnu0222 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11576	24178	37490	2.35	2.0E-71	R55628.1	EST_HUMAN	Y77C11.t1 Scores breast 2NDBH8st Homo sapiens cDNA clone IMAGE:184772 5'
12038	24691		8.43	2.0E-71	T95485.1	EST_HUMAN	Y43609.t1 Scores fetal liver spleen TnFLS Homo sapiens cDNA clone IMAGE:120320 5'
623	13402	26037	1.83	1.0E-71	A1077927.1	EST_HUMAN	OY1503.s1 Scores senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:655916 3' similar to contains LOR1 b2 LOR1 repetitive element;
920	13687	26351	2.37	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1078	13836	26494	6.16	1.0E-71	AF205690.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1317	14068	26740	11.71	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2074	14806	27536	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2.L16 mRNA, partial cds
2074	14806	27537	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2.L16 mRNA, partial cds
2698	15407	28142	3.91	1.0E-71	7657153	NT	Homo sapiens hairyenhancer-ds-split related with YRPW motif-like (HEYL), mRNA
3463	16249	28903	2.53	1.0E-71	AF118665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3593	16338	28982	5.88	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3593	16338	28983	5.89	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3639	16392	29031	0.98	1.0E-71	BE122850.1	EST_HUMAN	O2_15 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA clone O2_15 5' similar to Homo sapiens chromosome 19
3639	16392	29032	0.98	1.0E-71	BE122850.1	EST_HUMAN	O2_15 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA clone O2_15 5' similar to Homo sapiens chromosome 19
3724	18477	29114	2	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
4437	17173	29801	1.82	1.0E-71	D28476.1	NT	Human mRNA for KIA0045 gene, complete cds
4562	17287	29816	0.98	1.0E-71	H23178.1	EST_HUMAN	Ym150H10.1 Scores infant brain TM1B Homo sapiens cDNA clone IMAGE:52528 5'
6543	19405	32420	1.07	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
6986	19579	32726	1.39	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIA0559 protein, partial cds
7211	19898	32871	13.35	1.0E-71	U80753.1	NT	Homo sapiens CAGL 79 mRNA, partial cds

Page 356 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8048	20740	33872	0.69	1.0E-71	AF105287.1	NT	Homo sapiens glyican-6 (GPO6) mRNA, complete cds
8069	20763	33891	2.26	1.0E-71	11425430	NT	Homo sapiens myomelein (M-protein) 2 (165KD) (MYOM2), mRNA
8345	21038	34174	4.09	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
8345	21038	34174	4.08	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9123	21819	34382	0.78	1.0E-71	S72393.1	NT	CSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
9508	22857	35752	7.89	1.0E-71	AY007843.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
9968	22816		2.05	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10436	23082	36309	1.45	1.0E-71	11433142	NT	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA
10584	23375		2.68	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10766	23476	36720	2.18	1.0E-71	11418603	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11093	23763	37037	1.73	1.0E-71	11417197	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11093	23763	37038	1.73	1.0E-71	11417197	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12401	24786		4.66	1.0E-71	AB011398.1	NT	Homo sapiens gene for ALE-4, complete cds
398	13183	25830	1.72	9.0E-72	AB87695.1	EST_HUMAN	wk95g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705
398	13183	25831	1.72	9.0E-72	AB87695.1	EST_HUMAN	HYPOHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
6020	18801	31782	0.97	8.0E-72	BF035752.1	EST_HUMAN	wk95g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705
4092	16834	29458	2.63	7.0E-72	4501868	NT	HYPOHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
4092	16834	29459	2.63	7.0E-72	4501868	NT	601458747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662451 5'
4092	16834	29459	2.63	7.0E-72	4501868	NT	Homo sapiens acinlase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4092	16834	29460	2.63	7.0E-72	4501868	NT	Homo sapiens acinlase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7024	19716	32773	2.99	7.0E-72	S41664.1	NT	Homo sapiens acinlase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
12520	24868		1.9	7.0E-72	F28289.1	EST_HUMAN	(pseudogene) PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
8283	20677		4.14	6.0E-72	AL163248.2	NT	HSPD13670 HMB3 Homo sapiens cDNA clone s40000515002
60	12889	25521	1.05	5.0E-72	BF333707.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
61	12889	25522	1.05	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
61	12889	25522	1.05	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
61	12889	25522	1.05	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
61	12889	25522	1.05	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
61	12889	25522	1.05	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1117	13874		3.62	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6851	19551	32581	1.69	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2R22 Homo sapiens cDNA clone NT2R2203751 5'

Page 357 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7731	20394	33509	0.73	5.0E-72	AA316932.1	EST_HUMAN	EST188312 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to FAC1
8876	21387	34614	3.71	5.0E-72	AW161274.1	EST_HUMAN	au8003.yt Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR-Q98785 Q98785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
9861	22511	35708	0.89	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAK901 5'
11208	23871	37157	3.45	5.0E-72	BF331571.1	EST_HUMAN	MR4-B10598-010800-005-005 BT0598 Homo sapiens cDNA
11209	23871	37158	3.45	5.0E-72	BF331571.1	EST_HUMAN	MR4-B10598-010800-005-005 BT0598 Homo sapiens cDNA
11643	24240	37563	1.61	5.0E-72	BE208545.1	EST_HUMAN	ba08008.yt NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
11643	24240	37564	1.61	5.0E-72	BE208545.1	EST_HUMAN	ba08008.yt NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
12107	25368		2.82	5.0E-72	BE926846.1	EST_HUMAN	QV1-B10632-280800-342-at10 BT0632 Homo sapiens cDNA
5378	18178	30868	0.82	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
8482	19229	32230	0.68	4.0E-72	T87947.1	EST_HUMAN	yd33a01.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
7309	19992	33069	2.03	4.0E-72	5729987	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
9684	22336	35531	1.3	4.0E-72	89239693	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10282	22939	36152	0.48	4.0E-72	AW836230.1	EST_HUMAN	RC3-L10023-200100-012-d11 LT0023 Homo sapiens cDNA
10282	22939	36153	0.48	4.0E-72	AW836230.1	EST_HUMAN	RC3-L10023-200100-012-d11 LT0023 Homo sapiens cDNA
							qh67.c02.xt Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR-Q14498 Q14498 SPLICING FACTOR, [1] contains Alu repetitive element; contains element L1 repetitive element;
10320	22697	36186	0.92	4.0E-72	AI248796.1	EST_HUMAN	ae23709.s1 NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW-CPTR_FLAPR
11256	23917	37210	1.57	4.0E-72	AA465388.1	EST_HUMAN	P46181 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11256	23917	37211	1.57	4.0E-72	AA465388.1	EST_HUMAN	ae23709.s1 NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW-CPTR_FLAPR
11514	24114	37424	7.79	4.0E-72	HY8421.1	EST_HUMAN	P46181 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11537	24234	37555	1.75	4.0E-72	7657057	NT	yd28a03.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11537	24234	37556	1.75	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11537	24234	37556	1.75	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11680	24275	37597	2.18	4.0E-72	T81910.1	EST_HUMAN	yd28a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109849 3'
12453	24822	31025	8.92	4.0E-72	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
18	12846	26469	0.69	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA
893	13652		1.52	3.0E-72	AA72823.1	EST_HUMAN	af63a06.t1 Soares_testis_NHT Homo sapiens cDNA clone 1310280 3'

Page 358 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1132	13888	26546	6.64	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1132	13888	26547	6.64	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1171	13925	26587	0.72	3.0E-72	U60226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1171	13925	26588	0.72	3.0E-72	U60226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1510	14256	26942	1.24	3.0E-72	BE242161.1	EST_HUMAN	TCAP1E1262 Pediatric acute myelogenous leukemia cell (FAB M1) Bay/cr-HGSC project=TCOA Homo sapiens cDNA clone TCAP1262
3072	15938	28481	11.45	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3273	16034	28684	2.17	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20595 (FLJ20595), mRNA
3803	16555	29186	2.69	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha -T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4508	17243	29376	3.12	3.0E-72	11416156	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4716	17447	30078	1.07	3.0E-72	AF167672.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4716	17447	30080	1.07	3.0E-72	AF167672.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4802	17591	30215	0.95	3.0E-72	AI654337.1	EST_HUMAN	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5433	18232	31221	1.27	3.0E-72	4759033	NT	w531603.x1 NC1_GGAP_G08 Homo sapiens cDNA clone IMAGE:2307254.3
5591	18676	31621	2.1	3.0E-72	AF073367.1	NT	Homo sapiens synaptonemal W (SEMAW) mRNA
5591	18676	31622	2.1	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6074	18853	31819	4.82	3.0E-72	AB029004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6074	18853	31820	4.82	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6516	18281	32284	3.63	3.0E-72	4826987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7485	20157	33249	2.15	3.0E-72	U80017.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
8075	20769	33958	0.96	3.0E-72	5031892	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
10331	22978	36168	1.2	3.0E-72	X98289.1	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
5860	18656	31507	1.91	2.0E-72	11428671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
8593	21683	34832	0.71	2.0E-72	BF308560.1	EST_HUMAN	607890419F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4131461.5
8593	21683	34833	0.71	2.0E-72	BF308560.1	EST_HUMAN	607890419F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4131461.5
10640	23331	36569	2.47	2.0E-72	AA79277.1	EST_HUMAN	q128509.at Soares, Iselis, NHT Homo sapiens cDNA clone 1391609.3 similar to gb:X02067.H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12449	24819	31022	5.75	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylcholine transferase translocator mRNA, complete cds
2068	14800	27527	1.19	1.0E-72	AA846225.1	EST_HUMAN	at33002.at Soares, parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1387395.3

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5680	18473	31390	3.83	1.0E-72	7857676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6464	19231	32231	1.31	1.0E-72	11921578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6464	19231	32232	1.31	1.0E-72	11921578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6536	20063	32305	1.2	1.0E-72	AV51818.1	EST_HUMAN	AV51818 NP2 Homo sapiens cDNA clone NPDAIE11.5'
7537	20207	33304	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-H1 0578-170500-012-g02 HT0578 Homo sapiens cDNA
7537	20207	33305	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-H1 0578-170500-012-g02 HT0578 Homo sapiens cDNA
8491	22144	35324	10.25	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
8491	22144	35325	10.25	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1444	14191	26876	1.35	9.0E-73	AV374988.1	EST_HUMAN	MR0-GT0063-071069-002-H11 GT0063 Homo sapiens cDNA
10871	23551		15.11	9.0E-73	11424039	NT	Homo sapiens fibronectin protein L13a (RPL13A), mRNA
1015	13774	26434	2.29	8.0E-73	AW071755.1	EST_HUMAN	ws5506.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TR.Q59050
8463	19292	31180	1	8.0E-73	4505798	NT	Q68050 HYPOTHETICAL PROTEIN MJ1656.
8478	19245	32245	5.16	8.0E-73	11428469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7694	20686	33817	2.87	8.0E-73	AF113129.1	NT	Homo sapiens lysosome homolog (LOC57151), mRNA
						NT	Homo sapiens vacuolar ATPase isoform VA08 mRNA, complete cds
9253	21932	35105	6.25	8.0E-73	BE019900.1	EST_HUMAN	bb52a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:204093_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Musca domestica cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9640	22292	35484	1.92	8.0E-73	11526037	NT	Homo sapiens Interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9640	22292	35485	1.92	8.0E-73	11526037	NT	Homo sapiens Interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10507	22153	35376	0.45	8.0E-73	4507628	NT	Homo sapiens Interleukin 12 receptor, beta 1 (IL12RB1), mRNA
11673	24172	37488	1.29	8.0E-73	11418789	NT	Homo sapiens transition protein 1 (during histone to prolamine replacement) (TNP1) mRNA
12508	24859	31012	3.31	8.0E-73	11418789	NT	Homo sapiens DEAD-box protein (HAGE), mRNA
1112	13869	26528	0.89	7.0E-73	8923250	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (GZ2P1), mRNA
3285	16086	28705	1.18	7.0E-73	AL163206.2	NT	Homo sapiens hypochelical protein FLJ20309 (FLJ20309), mRNA
4891	17618		1.35	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C008
154	12969		3.07	6.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7072	19763	32827	3.48	6.0E-73	BE169674.1	EST_HUMAN	QV0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5173	17982	30497	2.2	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
3318	14067	26741	2.77	3.0E-73	AV1843789.1	EST_HUMAN	CH0-CH0044-260100-164-08 CN0044 Homo sapiens cDNA
6598	19361	32374	0.71	3.0E-73	AA138403.1	EST_HUMAN	z196004.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to
8656	21348	34462	0.65	3.0E-73	AV729428.1	EST_HUMAN	gb:223084_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8656	21348	34463	0.65	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071.5'
						EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071.5'

Page 360 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11611	24209		1.61	3.0E-73	AI004040.1	EST_HUMAN	cut1002.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1625965 3'
12734	25003		1.5	3.0E-73	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12738	25005		1.54	3.0E-73	AV898081.1	EST_HUMAN	RC3-NN00066-270400-011-c04 NN00066 Homo sapiens cDNA
831	13601	26271	1.43	2.0E-73	AF139897.1	NT	Homo sapiens BAS31 (BAS31) mRNA, partial cds
1539	14674		1.78	2.0E-73	AV898081.1	EST_HUMAN	RC3-NN00066-270400-011-c04 NN00066 Homo sapiens cDNA
2288	15021		1.3	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3177	15940	28150	3.99	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3538	16294	28943	0.91	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3539	16294	28944	0.91	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4401	17138		1.03	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6344	19114	32102	0.89	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6344	19114	32103	0.89	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6389	19158	32159	6.27	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
6600	19393	32376	1.27	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6600	19393	32377	1.27	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7698	20392	33478	0.69	2.0E-73	MF94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
7701	20394	33478	0.73	2.0E-73	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
9432	22110	35284	0.52	2.0E-73	AF198349.1	NT	Gallus gallus Dcch2 protein (Dcch2) mRNA, complete cds
9432	22110	35285	0.52	2.0E-73	AF198349.1	NT	Gallus gallus Dcch2 protein (Dcch2) mRNA, complete cds
10322	22968	36189	1.21	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10384	23040	36267	1.31	2.0E-73	11486980	NT	Homo sapiens supervillin (SVL), transcript variant 1, mRNA
10394	23040	36268	1.31	2.0E-73	11486980	NT	Homo sapiens supervillin (SVL), transcript variant 1, mRNA
10887	23662	36917	3.37	2.0E-73	4657612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10887	23662	36918	3.37	2.0E-73	4657612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11020	23662	36956	1.82	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12293	14674		1.83	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN00066-270400-011-c04 NN00066 Homo sapiens cDNA
1776	14518	27221	1.71	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000460 5'
2468	15205	27946	1.12	1.0E-73	AF198349.1	NT	Gallus gallus Dcch2 protein (Dcch2) mRNA, complete cds
6266	19399	32016	1.07	1.0E-73	BE151293.1	EST_HUMAN	GM-H1T0262-11159-042-H10 H10262 Homo sapiens cDNA
9369	22061	35230	1.37	1.0E-73	AI147427.1	EST_HUMAN	igb1007.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1899637 5' similar to contains element MER22 repetitive element
11428	23195	36426	2.65	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617106 5'

Page 361 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
723	13407	26150	1.06	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6824	18613	31644	2.2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
5924	18613	31645	2.2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
10781	23474	25236.1	1.36	8.0E-74	N52236.1	EST_HUMAN	Hyd5g10.1 st Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:245929 3'
1942	14677	27390	2.59	7.0E-74	AJ001689.1	NT	Homo sapiens NKGD gene, exon 10
3322	16082	28732	1.08	7.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
9142	21873	39338	2.83	7.0E-74	BE067432.1	EST_HUMAN	601649284F1 NIH_MGC.73 Homo sapiens cDNA clone IMAGE:3932997 5'
12505	24856	31011	5.51	7.0E-74	BE26305.1	EST_HUMAN	60119192F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:353565 5'
1100	13858	26518	2.4	6.0E-74	AF109607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2314	15039	27776	11.78	6.0E-74	BE388260.1	EST_HUMAN	60128352F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3605453 5'
2314	15039	27777	11.78	6.0E-74	BE388260.1	EST_HUMAN	60128352F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3605453 5'
2887	18634	28279	1.32	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-asst-h-03-QJ1.1st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706365 3'
2887	18634	28280	1.32	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-asst-h-03-QJ1.1st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706365 3'
3700	16453	29092	1.34	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3700	16453	29093	1.34	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
6281	19088	30744	3.02	6.0E-74	11058013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
885	13654	29322	7.33	6.0E-74	AW020968.1	EST_HUMAN	d1T708.Y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2706	15413	30784	2.62	5.0E-74	AW382758.1	EST_HUMAN	PMO-CT02985-271099-001-N07 CT02985 Homo sapiens cDNA
5322	18125	30784	1.86	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5703	18497	31419	12.98	5.0E-74	X89870.1	NT	H. sapiens mRNA for TPCR16 protein
5748	18540	31462	7.41	6.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5816	18608	31536	1.84	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
5816	18608	31537	1.84	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6795	19539	32567	5.98	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7689	19539	32567	0.9	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7936	20631	33758	2.78	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10536	23328	36565	2.56	5.0E-74	Y08420.1	NT	H. sapiens mRNA for HIP-1
10836	23328	36568	2.56	5.0E-74	Y08420.1	NT	H. sapiens mRNA for HIP-1
10757	23442	36687	2.68	5.0E-74	5729768	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
273	13080	28723	1.79	4.0E-74	D87675.1	NT	Homo sapiens cDNA for amyloid precursor protein, complete cds
832	13602	28272	5.15	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds

Page 362 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1955	14680	27403	2.02	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1955	14680	27404	2.02	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2055	14797	27523	2.75	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2055	14797	27524	2.75	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2128	14850	27589	1.89	4.0E-74	AB032984.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2427	15148	27682	27.23	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3088	18863	28495	5.2	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3518	16274	28928	0.82	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4041	16786	29414	1.03	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4520	17255	29889	2.23	4.0E-74	7862183	NT	Homo sapiens KIA00569 gene product (KIA00569), mRNA
4573	17308	29937	0.88	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5015	17736	30343	0.99	4.0E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase3-ketocyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5015	17736	30344	0.96	4.0E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase3-ketocyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
8448	21140		8.45	3.0E-74	AA300378.1	EST_HUMAN	EST113131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8473	21165	34306	0.79	3.0E-74	9968912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9272	22026	35198	2.88	3.0E-74	M78984.1	EST_HUMAN	EST101132 Subtracted hippocampus, Striatum (est. #936203) Homo sapiens cDNA clone HPCPF91
10237	22855	36099	2.68	3.0E-74	AA601483.1	EST_HUMAN	nt07608.s1 NC1_GCAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
938	13705	26370	176.01	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
938	13705	26371	176.01	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1152	13907	26570	1.11	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-147D
1222	13972	26844	1.36	2.0E-74	AI850528.1	EST_HUMAN	w61607.X1 NC1_GCAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG95_HUMAN
1580	14336	27024	3.79	2.0E-74	4885198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element ; homolog (EGFR) mRNA
1580	14336	27025	3.79	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2009	15321	28083	0.94	2.0E-74	AI857280.1	EST_HUMAN	homo201 EGFR mRNA
4945	17672	30281	2.44	2.0E-74	AL365082.1	NT	PT2_15_G111.tumor2 Homo sapiens cDNA 3'
4945	17672	30282	2.44	2.0E-74	AL365082.1	NT	Novel human gene mapping to chromosome 22
4945	17672	30282	2.44	2.0E-74	AL365082.1	NT	Novel human gene mapping to chromosome 22

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4849	17678	30286	1.11	2.0E-74	J02983.1	NT	Human platelet glycoprotein IIB mRNA, 3' end
5709	25074	31424	2.8	2.0E-74	BE711134.1	EST_HUMAN	RCB-HT0078-220600-011-C03 HT0078 Homo sapiens cDNA
5806	25077	31521	1.89	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5809	25077	31522	1.69	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5876	25077	31521	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5878	25077	31522	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
7003	19855	32748	0.82	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE3827549 5'
7841	20536	33663	1.29	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9282	22036	35208	3.05	2.0E-74	AL163204.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
12234	24687		3.95	2.0E-74	AA185181.1	EST_HUMAN	z09a0.6.x1 Syntrophin muscle 837209 Homo sapiens cDNA clone IMAGE328018 3'
52	12881	25509	1.89	1.0E-74	7657334	NT	Homo sapiens Mitochondrial-related kinase (MINK), mRNA
328	13129	25764	5.02	1.0E-74	AW816405.1	EST_HUMAN	QV4-S10234-181199-037-005 S10234 Homo sapiens cDNA
487	13272	25907	1.05	1.0E-74	8922828	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
489	13277	25912	13.6	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
587	13367	25995	1.47	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259), mRNA
768	13638	26187	1.81	1.0E-74	AB020840.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
879	13744	26406	2.27	1.0E-74	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C048
2223	14851	27690	4.39	1.0E-74	AB002050.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3136	15900	28545	3.55	1.0E-74	4758687	NT	Homo sapiens membrane, alpha, class 2A, member 1 (MAN2A1), mRNA
3369	18125	28782	0.9	1.0E-74	AA238549.1	EST_HUMAN	z00a01.11 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE387776 5'
3365	18125	28783	0.9	1.0E-74	AA238549.1	EST_HUMAN	z00a01.11 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE387776 5'
3301	16851	29292	0.88	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
3301	16851	29293	0.89	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
3350	16700	29338	4.81	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4042	16787	29415	1.15	1.0E-74	BE030360.1	EST_HUMAN	RC2-B10642-270300-018-008 B10642 Homo sapiens cDNA
6605	19368	32380	1.88	1.0E-74	M69814.1	NT	Human neurofilament (NF) gene, complete cds
7526	20187	33291	1.15	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
7956	20650	33773	1.13	1.0E-74	BE549105.1	EST_HUMAN	60107008F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE3456260 5'
7955	20650	33774	1.13	1.0E-74	BE549105.1	EST_HUMAN	60107008F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE3456260 5'
8704	21395	34543	4.82	1.0E-74	AF214582.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8733	21426	34571	0.66	1.0E-74	BF331951.1	EST_HUMAN	MKRD-HT0596-220500-021-a03 HT0596 Homo sapiens cDNA
10146	22788	36001	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10140	22788	36002	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10380	23026	36241	1.38	1.0E-74	11420546	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA

Page 364 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11885	24458	37800	2.92	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
11885	24813		5.01	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12103	14951	27690	1.58	1.0E-74	AB020259.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12587	24897		1.53	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2650	15360		3.68	8.0E-76	AF178228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 35 (DNMT3B), mRNA, complete cds
12254	24700		1.86	8.0E-75	AL193202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2319	15044	27781	1.47	6.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCL CGAP_P222 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb.M14123_cds4
7688	20382	33466	0.67	5.0E-75	AA573446.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
7688	20382	33467	0.81	5.0E-75	AA573446.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
8608	21498	34643	0.94	5.0E-75	BE272325.1	EST_HUMAN	h69603.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
9015	21705	34955	0.6	5.0E-75	AA132811.1	EST_HUMAN	801126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989665 5'
8063	21782	34946	0.78	5.0E-75	BE561655.1	EST_HUMAN	2017068.11 Stralagene colon (8637204) Homo sapiens cDNA clone IMAGE:587174 5'
9063	21782	34947	0.78	5.0E-75	BE561655.1	EST_HUMAN	801346908F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687488 5'
8273	22027	35197	1.53	5.0E-75	BF690254.1	EST_HUMAN	801346908F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:3687488 5'
10134	22782	35993	2.39	5.0E-75	AI839623.1	EST_HUMAN	h31c12.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
110	12931	25908	2.16	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN;
446	13232		1.02	4.0E-75	N38757.1	EST_HUMAN	QV1.BT0632.210200-076-602 BT0632 Homo sapiens cDNA
1769	14501	27202	1.3	4.0E-75	AW897200.1	EST_HUMAN	y8b108.17 Soares melanocyte ZNHHM Homo sapiens cDNA clone IMAGE:269055 5'
2833	19521	28266	4.89	4.0E-75	BE409484.1	EST_HUMAN	CNC-NN000571 150400-335-at11 NN0057 Homo sapiens cDNA
3492	16248	28902	0.94	4.0E-75	6922637.1	NT	801303068F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3639344 5'
8442	18241	31128	0.56	4.0E-75	11417946	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
8442	18241	31129	0.56	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6175	18933	31628	5.78	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6681	19421	32436	2.26	4.0E-75	11417946	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
6681	19421	32437	2.26	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10594	23279	35517	18.12	4.0E-75	7659505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
682	13747	25409	3.72	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
983	13747	25409	2.41	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1828	14567	27570	2.76	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2106	14936	27570	1.11	3.0E-75	4607334	NT	Homo sapiens mRNA for KIAA0361 protein, partial cds
2422	15143	27878	5.88	3.0E-75	4759153	NT	Homo sapiens synaptonemal-associated protein, 28kD (SNAP29), mRNA

Page 365 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15787	28434	0.97	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21, segment HS21C001
3164	15547	28597	1.32	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3345	15104	28757	0.75	3.0E-75	M72303.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3345	15104	28768	0.76	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4147	16989	28521	3.27	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4404	17141	29769	0.73	3.0E-75	763242.1	NT	Homo sapiens KIAA0371 protein (KIAA0371), mRNA
5171	17980	30493	0.83	3.0E-75	11420955	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5171	17980	30494	0.83	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6671	19588	32623	1.68	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6871	19588	32624	1.68	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7035	19727	32783	4.58	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7035	19727	32784	4.58	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7622	20193	33284	2.52	3.0E-75	4855632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7522	20193	33285	2.52	3.0E-75	4855632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8883	21574	34717	1.21	3.0E-75	11420804	NT	Homo sapiens small T (Drosophila homolog), zinc finger protein (SNAIL), mRNA
8577	22230	35414	0.77	3.0E-75	11420222	NT	Homo sapiens Drosophila Kich like protein (DKELCHL), mRNA
10440	23066	36314	2.28	3.0E-75	11436430	NT	Homo sapiens dynein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
5587	18394		1.41	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cDABED02.5
6848	21340	34454	2.45	2.0E-75	A311783.1	EST_HUMAN	q691 e02.11 NCL CGAP_Xi65 Homo sapiens cDNA clone IMAGE:1615699 3' similar to TR-Q68386 Q68386
2076	14808	27639	1.12	1.0E-75	4506328	NT	POU5F1 GENE
2076	14808	27640	1.12	1.0E-75	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2301	15026	27792	6.68	1.0E-75	AW168135.1	EST_HUMAN	XB60402.x1 NCL CGAP_UK Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.1
2347	15713	28366	3.27	1.0E-75	X52221.1	NT	PTPR7 repetitive element
8819	21008		4.27	1.0E-75	AA399270.1	EST_HUMAN	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
9028	21895	35167	3.75	1.0E-75	BF313645.1	EST_HUMAN	z157h03.s1 Soares_testes_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gpM13932 40S
9028	21895	35168	3.75	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
9028	21895	35168	3.75	1.0E-75	BF313645.1	EST_HUMAN	60180029AF1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10797	23480		10.83	1.0E-75	AA684377.1	EST_HUMAN	60180029AF1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11033	23704	38972	2.58	1.0E-75	AF223391.1	NT	ac77h06.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11860	24444	37785	1.38	1.0E-76	AA417112.1	EST_HUMAN	z404029.1 Scores_bas1c NIH Homo sapiens cDNA clone IMAGE:730829 5'
12152	17812	30598	1.64	1.0E-76	BE894192.1	EST_HUMAN	601437130FT NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922303 5'
43	12872	25403	1.24	9.0E-76	A1652848.1	EST_HUMAN	w303010.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
43	12872	25404	1.24	9.0E-76	A1652848.1	EST_HUMAN	w303010.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
9801	22452	35654	43.62	9.0E-76	M12837.1	NT	Human ferritin Heavy subunit mRNA, complete cds
917	13684	26347	1.06	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
917	13684	26348	1.06	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2910	15678	26325	1	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
6078	18658	31825	8.36	8.0E-76	11427442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7388	20087	33145	1.26	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7466	20139	33231	0.86	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8165	20889	34027	0.67	8.0E-76	11416981	NT	Homo sapiens AIMA-1 protein (LOC51151), mRNA
8995	21685	34835	0.55	8.0E-76	AB046764.1	NT	Homo sapiens mRNA for KIAA1544 protein, partial cds
10277	22925	36137	1.35	8.0E-76	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
10584	23260	36497	4.81	8.0E-76	10442821	NT	Homo sapiens calyculin IAP repeat-containing 8 (BIRC8), mRNA
12491	24849		2	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
759	13531	26181	1.41	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3288	16049	26597	2.97	7.0E-76	AF056590.1	NT	Homo sapiens cAMP-specific phosphodiesterase BA (PDE8A) mRNA, partial cds
3284	16055	26704	7.55	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3330	16080	26743	0.93	7.0E-76	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2, translocated to, 1, cyclin D-related (CBFA2T1) mRNA
4338	17077	26706	4.73	7.0E-76	4507184	NT	Homo sapiens saphirelin reductase (7.8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4338	17077	26708	4.73	7.0E-76	4507184	NT	Homo sapiens saphirelin reductase (7.8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1212	13982		31.63	6.0E-76	BE396293.1	EST_HUMAN	601312019FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3638757 5'
11442	23209	36440	3.76	6.0E-76	BE273201.1	EST_HUMAN	601142255FT NIH_MGC 14 Homo sapiens cDNA clone IMAGE:3560229 5'
1936	14671	27395	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1936	14671	27398	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1936	14671	27397	4.83	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5189	17666	30512	1.29	4.0E-76	BE783412.1	EST_HUMAN	601471725FT NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3874470 5'
8923	22571	35768	6.42	4.0E-76	D81625.1	EST_HUMAN	HUM178001B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178001 5'

Page 387 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9823	22571	35769	6.42	4.0E-76	D81625.1	EST_HUMAN	HUM176001B Human fetal brain (Tfujlwera) Homo sapiens cDNA clone GEN-178G01 5'
615	13393	26026	3.2	3.0E-76	BF516262.1	EST_HUMAN	UHH-BW1-amz-b-04-QJ1.1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
615	13393	26027	3.2	3.0E-76	BF516262.1	EST_HUMAN	UHH-BW1-amz-b-04-QJ1.1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1684	14340	27029	3.28	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1594	14340	27030	3.28	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3422	16179	26828	4.88	3.0E-76	BF375693.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3422	16179	26829	4.88	3.0E-76	BF375693.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4058	16803	28434	1.07	3.0E-76	BE346893.1	EST_HUMAN	H87T12.1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:Q64886 Q64886
5158	17691	37795	2.07	3.0E-76	Z41314.1	EST_HUMAN	KAA0782 PROTEIN ;
5846	18441	31354	1.09	3.0E-76	AA160911.1	EST_HUMAN	2073407.1 Stratiotes paniceus (8937209) Homo sapiens cDNA clone IMAGE:592524 5' similar to
8275	19046	32025	9.57	3.0E-76	AF285981.1	EST_HUMAN	gbL32276 MIXED LINEAGE KINASE 1 (HUMAN);
8050	20744	33877	0.88	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
8616	22269	35456	3.34	3.0E-76	AW299353.1	EST_HUMAN	y20g10.r1 Soares melanocyte ZNHRM Homo sapiens cDNA clone IMAGE:271842 5'
9641	22293	35488	0.86	3.0E-76	AA442309.1	EST_HUMAN	xs4901.r1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
9641	22293	35487	0.86	3.0E-76	AA442309.1	EST_HUMAN	xs4941.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:2757481 5'
11878	25191	30812	1.93	3.0E-76	AW807894.1	EST_HUMAN	xs4941.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:2757481 5'
11979	28398	30802	4.86	3.0E-76	AW856455.1	EST_HUMAN	EST1380059 MAG2 resequences, MAGJ Homo sapiens cDNA
275	13082	25725	1.59	2.0E-76	D84295.1	NT	EST1368525 MAG2 resequences, MAGJ Homo sapiens cDNA
333	13134	25768	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
333	13134	25769	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
448	15234	25768	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
448	15234	25769	4.39	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
576	13356	26984	1.09	2.0E-76	4503944	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP-1) mRNA
1008	13768	26430	1	2.0E-76	4759053	NT	Homo sapiens glucagon (GCG) mRNA
1526	14273	26980	1.91	2.0E-76	4504028	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1526	14273	26981	1.91	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1921	14658	27368	0.91	2.0E-76	AA253954.1	EST_HUMAN	zs50011.1 Stratiotes schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2846	15614	28261	3.34	2.0E-76	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3291	16052	28701	2.06	2.0E-76	AA445992.1	EST_HUMAN	xs49402.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
3291	16052	28702	2.06	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3291	16052	28702	2.06	2.0E-76	AA445992.1	EST_HUMAN	xs49402.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3469	16226	29879	0.97	2.0E-76	AI821149.1	EST_HUMAN	ec83b02.v5 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:869153 5' similar to TR.O14591
4114	13082	25726	1.23	2.0E-76	D84265.1	NT	O14591 SIMILARITY TO P22059 :
4895	17622	30240	6.21	2.0E-76	AW879618.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5065	17774	30390	1.49	2.0E-76	5031660	NT	QV3-O10028-220300-132-b11 OT0028 Homo sapiens cDNA
5229	18033						Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (ED1L3) mRNA
5531	18326	31233	6.47	2.0E-76	AF127845.1	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7334	20016	33004	0.78	2.0E-76	AB023004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7590	20230	33333	1.91	2.0E-76	11426908	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
10182	22830	36045	3.53	2.0E-76	11437410	NT	Homo sapiens TPCRB80 protein (HSTPCR88P), mRNA
10839	23621	36763	3.58	2.0E-76	7648607	NT	Homo sapiens HIRA interacting protein 4 (dms-like) (HIRIP4), mRNA
4265	17008	29638	2.38	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4265	17008	29639	2.38	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5362	18164	30848	8.12	1.0E-76	BE76637.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6150	18927		0.72	1.0E-76	AA333207.1	EST_HUMAN	EST17301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
6825	19486	32508	4.53	9.0E-77	BE889525.1	EST_HUMAN	601512439F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3913737 5'
12644	24941		1.4	8.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636755 5'
182	12894	28633	0.92	8.0E-77	R83144.1	EST_HUMAN	jp11102.1 Soares breast 3N6HBst Homo sapiens cDNA clone IMAGE:187155 5' similar to
4486	17221	29849	1.09	8.0E-77	BF205181.1	EST_HUMAN	SP-ANKK_HUMAN C01484 ANKYRIN, BRAIN VARIANT 1 ;
5366	18168	30854	1.74	8.0E-77	4506230	NT	601869826F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109303 5'
11360	24048	37351	1.91	8.0E-77	AA019770.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mbr34-homolog) (PSMD7)
11360	24048	37352	1.91	8.0E-77	AA019770.1	EST_HUMAN	mRNA
12620	24925	31008	4.02	8.0E-77	R02245.1	EST_HUMAN	262602.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
1922	14859	27370	2.4	7.0E-77	AA625755.1	EST_HUMAN	262602.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
2411	15132	27688	2.52	7.0E-77	4505844	NT	ye99104.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains
2411	15132	27689	2.32	7.0E-77	4509544	NT	MER10 repetitive element ;
256	13064	25703	8.53	6.0E-77	4504600	NT	209101.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:745392 3'
1534	14281	26669	3.22	6.0E-77	A1204068.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
1214	13964	26631	2.11	5.0E-77	AF041015.1	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
1339	14087	26763	1.77	5.0E-77	4551256	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
2887	15400	28139	0.99	5.0E-77	AF192866.1	NT	ye77112.s1 Soares fetal lung, N4HL19W Homo sapiens cDNA clone IMAGE:1745063 3'
							7 Homo sapiens glucocorticoid receptor (GCR) gene, exon 2
							Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
							Homo sapiens biased-like kinase 1 (TLK1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2187	15472	28214	0.99	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
2187	15472	28214	0.99	5.0E-77	8394578	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4852	17389	30022	2.47	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4855	17389	30023	2.47	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4884	17611	30231	2.96	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728.1 434 (synonym: hies) Homo sapiens cDNA clone DKFZp434G1728.5'
4886	16603	32642	0.57	5.0E-77	MT3975.1	NT	Homo sapiens protein kinase C beta-1 type (PRKCB1) mRNA, complete cds
7730	20393	33508	0.69	5.0E-77	8923318	NT	Homo sapiens hypothetical protein FLJ20343 (FLJ20343), mRNA
8266	20960	34069	1.28	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8266	20960	34100	1.28	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9450	22078	35246	2.48	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9450	22078	35250	2.48	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10388	23034	36249	1.22	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10388	23034	36250	1.22	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11794	24384	37116	3.12	5.0E-77	U37194.1	NT	Human UNC-104 and KIF1A-related protein mRNA, partial cds
11794	24384	37117	3.12	5.0E-77	U37194.1	NT	Human UNC-104 and KIF1A-related protein mRNA, partial cds
1855	14701	27417	1.09	3.0E-77	6730038	NT	Homo sapiens SET domain and maltrin transposase fusion gene (SETMAR) mRNA
1855	14701	27418	1.09	3.0E-77	6730038	NT	Homo sapiens SET domain and maltrin transposase fusion gene (SETMAR) mRNA
10188	22836	36050	0.79	3.0E-77	H65187.1	EST_HUMAN	SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10188	22836	36051	0.79	3.0E-77	H65187.1	EST_HUMAN	SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10785	23468	36709	3.98	2.0E-77	BF35971.1	EST_HUMAN	PIG-M10078-06080-005-g03 MT0078 Homo sapiens cDNA
1330	14078	28763	1.4	2.0E-77	AV764817.1	EST_HUMAN	AV764817 MDS Homo sapiens cDNA clone MDSBTF10.5'
1412	14160	26844	1.91	2.0E-77	AW987712.1	EST_HUMAN	RC3-EN0063-170200-011-001 BN0063 Homo sapiens cDNA
2084	14816	27548	1.13	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2086	14827	27660	5.23	2.0E-77	7708315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2602	15589	28033	1.92	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2602	15589	28054	1.92	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4012	16759	28396	1.98	2.0E-77	BE044316.1	EST_HUMAN	hca3305.x1 Soares, N.F., T. QBG, S.J. Homo sapiens cDNA clone IMAGE3040113 3' similar to SW/GA02 HUMAN P-10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4379	17116	28749	0.74	2.0E-77	AB13519.1	EST_HUMAN	hw2202.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE2260466 3' similar to TR-O65245
4379	17116	28750	0.74	2.0E-77	AB13519.1	EST_HUMAN	hw2202.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE2260466 3' similar to TR-O65245

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4557	17292		0.98	2.0E-77	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4717	17449	30082	1.69	2.0E-77	AA653025.1	EST_HUMAN	ns66g12.x1 NIH CGAP_P12 Homo sapiens cDNA clone IMAGE:1188938 similar to SW:RL28_HUMAN
5965	18652	31553	1.9	2.0E-77	BE289040.1	EST_HUMAN	P47914.605 RIBOSOMAL PROTEIN L29 [1] contains element MSR1 repetitive element;
6080	18859	31826	1.73	2.0E-77	BE787143.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
7074	19765	32829	15.45	2.0E-77	AB833003.1	EST_HUMAN	601476002F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876505 5'
8427	21120	34259	0.82	2.0E-77	AB92707.1	EST_HUMAN	at74809.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
8428	22108	35280	5.05	2.0E-77	U50321.1	NT	Q13311 TAX1-BINDING PROTEIN TXBP151 [1];
8428	22108	35281	5.05	2.0E-77	U50321.1	NT	q170c09.x1 NGL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1
8695	22545	35738	0.47	2.0E-77	BF310349.1	EST_HUMAN	CE057966 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN;
8695	22545	35739	0.47	2.0E-77	BF310349.1	EST_HUMAN	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 7
42	12870	25489	1.03	1.0E-77	AB033102.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 7
42	12870	25490	1.03	1.0E-77	AB033102.1	NT	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
266	13074	25714	7.19	1.0E-77	4502166	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
266	13074	25715	7.19	1.0E-77	4502166	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
855	15584	26288	17.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
855	15584	26287	17.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1912	14849	27390	0.9	1.0E-77	AW058119.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2445	15164	27602	1.32	1.0E-77	AB029024.1	NT	w83a05.x1 Soares thymus NHFT8 Homo sapiens cDNA clone IMAGE:2536160 3'
3040	15803	28491	1.72	1.0E-77	4603300	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
4320	17059	28684	3.37	1.0E-77	7706298	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4488	17223	29861	16.41	1.0E-77	AJ229041.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4603	17338	29967	2.29	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5010	17732	30337	1	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5010	17732	30338	1	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5839	18627	31691	2.45	1.0E-77	AF089944.1	NT	Homo sapiens dyactin 1 (DCTN1) gene, exons 27 and 28

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7390	20089	33148	0.58	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6K1) mRNA
8752	21444	34591	2.86	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
8752	21444	34592	2.86	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9268	22022	35192	0.6	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10342	22889	36208	1.86	4.0E-78	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10342	22889	36207	1.86	4.0E-78	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11396	24002	37305	5.18	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CaBP1) mRNA, complete cds
11547	24146	37456	2.15	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12517	24866	31016	3.67	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
157	12972	25610	1.39	3.0E-78	AF065901.1	NT	Homo sapiens eRF1 gene, complete cds
157	12972	25611	1.39	3.0E-78	AF065901.1	NT	Homo sapiens eRF1 gene, complete cds
3746	16499		0.69	3.0E-78	AF065901.1	EST_HUMAN	Homo sapiens eRF1 gene, complete cds
3768	16548	29181	0.72	3.0E-78	AF065901.1	EST_HUMAN	Homo sapiens eRF1 gene, complete cds
4084	16548	29181	0.66	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
5094	17813	30430	0.93	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
10166	22834		5.14	3.0E-78	BE144758.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
10802	23582	36932	1.97	3.0E-78	BE159318.1	EST_HUMAN	QMG-HT0180-041059-006-c07 HT0180 Homo sapiens cDNA
3119	15894		2.17	2.0E-78	U04490.1	NT	QMG-HT03957-150200-114-g09 HT0397 Homo sapiens cDNA
3995	18743		1.87	2.0E-78	AA311872.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
7387	20047	33126	1.54	2.0E-78	AW402306.1	EST_HUMAN	EST182363 Jurkat T-cells VI Homo sapiens cDNA 5' end
7387	20047	33127	1.54	2.0E-78	AW402306.1	EST_HUMAN	UHF-BKO-eaf-g-10-Q-Jr.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7631	20297	33405	3.99	2.0E-78	BF689800.1	EST_HUMAN	UHF-BKO-eaf-g-10-Q-Jr.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7940	20635	33762	2.33	2.0E-78	AV171477.1	EST_HUMAN	6021865267 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4295959 5'
8351	21044	34180	1.4	2.0E-78	AI557509.1	EST_HUMAN	AV171477 DCB8 Homo sapiens cDNA clone DCBAWF09 5'
8351	21044	34180	1.4	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16 B07.7 tumor2 Homo sapiens cDNA 3'
11017	23689	36952	3.27	2.0E-78	AI197837.1	EST_HUMAN	P2.1_16 B07.7 tumor2 Homo sapiens cDNA 3'
11068	23738	37012	3.89	2.0E-78	N66951.1	EST_HUMAN	gib00065.x1 NCI_CGAP_Br25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WIP-R90.1
4123	16865	29491	3.07	1.0E-78	4507098	NT	CE08325 PROTEIN KINASE
4123	16865	29492	3.07	1.0E-78	4507098	NT	2448712.1 Scars: fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:295623 3'
5222	18029	30655	2.63	1.0E-78	11417304	EST	Homo sapiens synaptosomal-associated protein 25kD (SNAP25) mRNA
6857	17634	30670	0.76	1.0E-78	AV648698.1	EST_HUMAN	Homo sapiens synaptosomal-associated protein 25kD (SNAP25) mRNA
7736	20401	33517	0.65	1.0E-78	AI122163.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51308), mRNA
							AV648698 GLC Homo sapiens cDNA clone GLC8M01 3'
							AV122163 MAMMA1 Homo sapiens cDNA clone MAMMA1001765 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8050	20753		3.28	1.0E-78	U52733.1	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12045	24655	31117	1.39	1.0E-78	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12477	25244	30718	1.55	1.0E-78	AF050918.1	EST_HUMAN	wab20b08.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2298915.3'
4950	17384	30078	4.05	9.0E-79	11626891	NT	Homo sapiens peptide YY (PYY), mRNA
4811	17542	30186	8.05	9.0E-79	BE000637.1	EST_HUMAN	RC2-8J0074-000305-014-c12 BN0074 Homo sapiens cDNA
5546	18149	30829	10.87	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6248	19022	31594	2.38	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E5) mRNA
7251	25108		0.99	8.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7473	20146	33239	0.70	8.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L16.1), mRNA
7473	20146	33240	0.79	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8244	20938	34074	0.49	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8244	20938	34075	0.49	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8981	21682	34802	5.1	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8981	21682	34803	5.1	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9280	22034	35206	0.58	9.0E-79	D07075.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10263	22911	36121	0.82	9.0E-79		NT	Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA
10318	22965	36192	1.73	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10318	22965	36193	1.73	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11001	23674	36930	3.13	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11497	24098	37410	3.35	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
11497	24098	37411	3.55	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
12725	16478	29115	0.91	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21D010
11890	17910	30596	1.82	8.0E-79	8567387	NT	Homo sapiens perlecan (Drosophila) homolog 3 (PER3), mRNA
3247	16009	28560	28.39	7.0E-79	BE610848.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875857.3'
11689	24460		4.32	6.0E-79	AA469828.1	EST_HUMAN	284004.s1 Soares_fetal_liver_spleen_1NFLS_51 Homo sapiens cDNA clone IMAGE:482558.3' similar to TR.Q15409 Q15400 NEUTRAL PROTEASE LARGE SUBUNIT
11478	24079	37390	2.52	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21D082
3173	15836		1.49	4.0E-79	8922326	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
305	13109	25749	1.28	3.0E-79	AF114488.1	NT	Homo sapiens intracellular short isoform (ITSN) mRNA, complete cds
957	13722	28388	3.85	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I (Ch) gene, complete cds
3095	15860	28501	1.61	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
6277	18082	30738	5.24	3.0E-79	AF110322.1	NT	Homo sapiens MST1016 (MST016) mRNA, complete cds
5637	18432	31345	1.24	3.0E-79	AB020989.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds

Page 374 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5682	18457	31371	0.93	3.0E-78	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC 38 Homo sapiens cDNA clone IMAGE:3884554 5'
5682	18457	31372	0.93	3.0E-78	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC 38 Homo sapiens cDNA clone IMAGE:3884554 5'
5682	18476	31392	3.56	3.0E-79	11428770	NT	Homo sapiens actin 1 (NTN1), mRNA
5682	18476	31393	3.56	3.0E-79	11428770	NT	Homo sapiens actin 1 (NTN1), mRNA
5646	19408	32422	0.87	3.0E-79	BE268693.1	EST_HUMAN	60112058F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3352985 5'
5680	19442	32457	3.35	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
6860	19442	32458	3.35	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7726	20389	33503	0.79	3.0E-79	6912466	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8084	20768	33887	1.61	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8303	21970	35144	1.33	3.0E-79	10835036	NT	Homo sapiens beta-tropoelastin repeat domain 3 (TTG3), mRNA
10245	22893		1.24	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GKCC Homo sapiens cDNA clone GKCAHE11 5'
10768	23452	36694	1.52	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10768	23452	36695	1.52	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
281	13098		0.99	2.0E-79	HE3129.1	EST_HUMAN	y4803.x1 Soares fetal liver spleen 1NF13 Homo sapiens cDNA clone IMAGE:209541 3'
619	13398	26033	1.6	2.0E-79	BE379926.1	EST_HUMAN	601159416F2 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:351107 5'
607	13874	26339	2.28	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2), mRNA
1012	13772		2.09	2.0E-79	AI523747.1	EST_HUMAN	BT1807.XT NQ1 CGAP_P28 Homo sapiens cDNA clone IMAGE:2118683 3'
1781	14522	27226	1.12	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1781	14522	27227	1.12	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
2144	14874	27607	5.93	2.0E-79	4585983	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2144	14874	27608	5.93	2.0E-79	4585983	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2189	14916	27652	1.07	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2721	15428	28166	1.09	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
3893	18643	29283	0.83	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLIC4 (CLIC4) mRNA, complete cds
4144	18886	29517	1.08	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
5685	18382		1.22	2.0E-79	AA312223.1	EST_HUMAN	EST182926 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, coxs1d B0303.15
5640	18435	31348	0.8	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6149	18926	31689	1.14	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
6884	17941	30577	0.89	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7087	19758	32822	1.7	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7087	19758	32823	1.7	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7599	20594	33821	1.08	2.0E-79	4508442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL-1) mRNA

Page 375 of 536

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8416	21108	34247	2.25	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8694	21356	34503	0.58	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8864	21356	34504	0.58	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8902	21593	34734	1.65	2.0E-79	11432184	NT	Homo sapiens similar to A1Pase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M9.9 (H. sapiens) (LOC38381), mRNA
9892	22840	38580	1.44	2.0E-79	S72869.1	NT	H4Q105170-pulitive cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
9992	22840	38581	1.44	2.0E-79	S72869.1	NT	H4Q105170-pulitive cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10958	23389	39527	12.34	2.0E-78	U71819.1	NT	Human contactin 1 precursor (CNTN1) mRNA, complete cds
10959	23632	39880	4.05	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
10959	23632	39881	4.05	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
10959	23632	39881	4.05	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
11936	17908	30594	2.16	2.0E-78	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12018	24548	31108	5.19	2.0E-78	AB020840.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12238	24690	31075	2.89	2.0E-78	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6462	25091	33945	3.76	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-280600-017-510 NN0087 Homo sapiens cDNA
8143	20837	33946	0.78	1.0E-79	BE394211.1	EST_HUMAN	61311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
11623	24220	37543	2.05	1.0E-79	BF087408.1	EST_HUMAN	QV2-HT0640-120600-355-a05 HT0640 Homo sapiens cDNA
12047	25333	28551	1.8	1.0E-79	A1460115.1	EST_HUMAN	ar78a04.x1 Barcode colon HPLR87 Homo sapiens cDNA clone IMAGE:2151438 3'
3143	15607	28551	2.35	9.0E-80	AA725948.1	EST_HUMAN	al23a05.a1 Soares, Italia, NHT Homo sapiens cDNA clone 1343648 3'
3143	15607	28552	2.35	9.0E-80	AA725948.1	EST_HUMAN	al23a05.a1 Soares, Italia, NHT Homo sapiens cDNA clone 1343648 3'
6912	22581	35757	1.14	8.0E-80	BE798603.1	EST_HUMAN	61581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636081 5'
11245	23907	37199	8.66	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
11245	23907	37200	8.66	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3588	16342		1.31	8.0E-80	U94887.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7504	20776	33268	3.07	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7504	20776	33269	3.07	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8002	21599	35142	1.13	8.0E-80	8005621	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8002	21599	35143	1.13	8.0E-80	8005621	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
880	13649	26318	1.12	6.0E-80	AM42187.1	EST_HUMAN	H59402.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEN_HUMAN
1039	14384	27071	2.22	6.0E-80	U64898.1	NT	Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ; Homo sapiens NRD convertase mRNA, complete cds

Page 376 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4252	16993	29620	1.08	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4252	16993	29621	1.08	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5712	18505	31427	1.78	6.0E-80	11421482	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
5984	18766	31729	3.37	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dylin heavy chain (DNAH9 gene)
6155	18913	31882	4.69	6.0E-80	11436738	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6179	18956		1.17	6.0E-80	7682303	NT	Homo sapiens KIA0841 protein (KIA0841), mRNA
6230	19004	31980	0.96	6.0E-80	M18553.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
8723	21415	34558	3.22	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8723	21415	34559	3.22	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8977	21608	34761	1.61	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9259	21838	35118	0.83	6.0E-80	AF101495.1	NT	Homo sapiens HSPC145 mRNA, complete cds
9791	22412	35619	1.48	6.0E-80	U20211.1	NT	Human cdc photoreceptor GMP-photodiesterase alpha' subunit gene, exon 21
10851	23541	36788	2.83	6.0E-80	11427365	NT	Homo sapiens Cyf19 mRNA, complete cds
11187	23852	37136	26.56	6.0E-80	AF228730.1	NT	Human peroxisome targeting signal 2 receptor (Pex7) mRNA, complete cds
11702	24297	37623	1.59	6.0E-80	U76580.1	NT	Homo sapiens N-acetylglucosaminase-phosphate nuclease mRNA, complete cds
11758	24347	37677	1.5	6.0E-80	AF102265.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11802	24392	37725	2.26	6.0E-80	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11802	24392	37726	2.26	6.0E-80	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11906	13649	26318	1.88	6.0E-80	AI422197.1	EST_HUMAN	tf59d02.x1 NCL CGAP Bm23 Homo sapiens cDNA clone IMAGE-2103459.3' similar to SW:NUEM_HUMAN Q16795 NADH-LIBUQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR;
12028	26217		2.42	6.0E-80	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12216	24678		5.78	6.0E-80	AB028900.1	NT	Homo sapiens GST gene for carboside sulfotransferase, exon 1, 2, 3, 4, 5
12707	25341		1.94	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
12804	25051	30556	1.35	6.0E-80	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
574	13354	29083	0.74	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
815	13566	29293	1.97	6.0E-80	AF108930.1	NT	Homo sapiens serine-threonine protein kinase (MN8H) mRNA, complete cds
816	13566	29294	1.97	6.0E-80	AF108930.1	NT	Homo sapiens serine-threonine protein kinase (MN8H) mRNA, complete cds
1166	13320		2.39	5.0E-80	X91647.1	NT	H sapiens next gene (exon 12)
1439	14186		2.26	5.0E-80	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
2361	15083	27821	1.99	6.0E-80	U89338.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2431	15152	27895	1.95	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2797	15502	28242	1.87	5.0E-80	4504282	NT	Homo sapiens R3 histone family, member J (H3FJ) mRNA
4018	19764	29393	1.37	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4018	19764	29394	1.37	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4900	17627	30244	1.28	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C069
8255	20349	34086	1.04	5.0E-80	8910283	NT	Homo sapiens keratin complex 2, gene 6g (Krt2-6g), mRNA
9157	21868	35056	8.77	4.0E-80	F25816.1	EST_HUMAN	HSPD13155 HMG Homo sapiens cDNA clone s400045F03
211	13023		8.98	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4661	17395	30030	1.7	3.0E-80	BF086009.1	EST_HUMAN	PMA-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4850	17580		3.77	3.0E-80	BE817485.1	EST_HUMAN	QYA-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5730	18522	31443	2.89	3.0E-80	AI091875.1	EST_HUMAN	cc28a12.x1 Soares NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:036760 C05790 PIG-L.1
1790	14530	27238	5.08	2.0E-80	R33321.1	EST_HUMAN	Yp65a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
1853	14591	27307	1.19	2.0E-80	AI444821.1	EST_HUMAN	RET487 subcloned retina cDNA library Homo sapiens cDNA clone RET487
2049	14782	27600	5.82	2.0E-80	AL043118.2	EST_HUMAN	DKFZp434D1323.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6708	19623	32687	0.93	2.0E-80	AA582952.1	EST_HUMAN	nc80d01.s1 NCJ CGAP_C08 Homo sapiens cDNA clone IMAGE:1090177 3'
6813	19474	32465	1.71	2.0E-80	11421630	NT	Homo sapiens Gggl transport complex protein (90 kDa) (GTC90), mRNA
7151	19838	32908		2.0E-80	TT6216.1	EST_HUMAN	Yc68112.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to SP-K1CR_XENLA P08902 KERATIN, TYPE I CYTOSKELETAL ENDO B:
9057	21749	34005	1.41	2.0E-80	AW084270.1	EST_HUMAN	EST1376343 MAGC resequences. MAGH Homo sapiens cDNA
9658	22320	35516	1	2.0E-80	AJ007278.1	NT	Homo sapiens GGT gene, exon 6
10790	23463	39705	4.49	2.0E-80	AA393362.1	EST_HUMAN	Z7012.17 Soares testis 1N1T Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
331	13132		2.25	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.1
782	13554	28216	1.37	1.0E-80	AF231820.1	NT	Homo sapiens chromosome 21 segment HS21C103
1947	14682		2.44	1.0E-80	AJ732856.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
5060	17779	30397	0.99	1.0E-80	4557610	NT	repetitive element 1
5244	18050		6.43	1.0E-80	BE386915.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
5881	18687	31608	6.58	1.0E-80	L10247.1	NT	561274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815433 5'
6408	19176	32174	1.38	1.0E-80		NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7106	19794	32850	0.96	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7472	20145	33237	2.53	1.0E-80	AB48731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
7472	20145	33238	2.53	1.0E-80	AB48731.1	EST_HUMAN	wq25605.x1 NCJ CGAP_K011 Homo sapiens cDNA clone IMAGE:2472286 3'
7472	20145	33238	2.53	1.0E-80	AB48731.1	EST_HUMAN	wq25605.x1 NCJ CGAP_K011 Homo sapiens cDNA clone IMAGE:2472286 3'

Page 378 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8130	20824	33690	2.84	1.0E-30	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
8601	21288	34435	1.72	1.0E-30	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
8601	21283	34436	1.72	1.0E-30	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
9185	21855	35018	1.21	1.0E-30	AF245219.1	NT	Homo sapiens probable mannosyl binding C-type lectin DC-SIGNR mRNA, complete cds
9185	21855	35020	1.21	1.0E-30	AF245219.1	NT	Homo sapiens probable mannosyl binding C-type lectin DC-SIGNR mRNA, complete cds
10325	22972	36182	0.95	1.0E-30	D63478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10548	23244	36476	5.25	1.0E-30	11841276	NT	Homo sapiens similar to rat myomesin (LOC64182), mRNA
10548	23244	36480	5.25	1.0E-30	11841276	NT	Homo sapiens similar to rat myomesin (LOC64182), mRNA
12289	24719	31051	1.57	1.0E-30	11471901	NT	Homo sapiens meningo (disrupted in balanced translocation) 1 (MNT), mRNA
12498	24853	31034	3.08	1.0E-30	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
10583	23278	35515	1.46	8.0E-31	AI251732.1	EST_HUMAN	ch80g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
10583	23278	35516	1.46	8.0E-31	AI251732.1	EST_HUMAN	ch80g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
11102	23772	37048	8.48	8.0E-31	BE394925.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3652070 5'
7162	19839	32806	3.58	7.0E-31	AI822115.1	EST_HUMAN	ze91c03.x8 Scores_Fetal_Lung_NHL_19W Homo sapiens cDNA clone IMAGE:289918 3'
4354	17092	29126	5.29	6.0E-31	BE256329.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352940 5'
4354	17092	29127	5.26	6.0E-31	BE256329.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352940 5'
5201	18009	30630	2.1	8.0E-31	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5201	18009	30631	2.1	8.0E-31	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7489	20161	33253	0.97	6.0E-31	AF038650.1	NT	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
9136	21824	34699	1.39	6.0E-31	AA360017.1	EST_HUMAN	EST19129 Fetal lung il Homo sapiens cDNA 5' end
11803	24390	37723	1.61	6.0E-31	BE356092.1	EST_HUMAN	601312822F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3659284 5'
12430	24803	31041	2.29	6.0E-31	BE356092.1	EST_HUMAN	602163665F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4234601 5'
12430	24803	31042	2.29	6.0E-31	BF676022.1	EST_HUMAN	602163665F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4234601 5'
2214	14942	27682	2.8	5.0E-31	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3346480 5'
8311	21005	34143	1.83	5.0E-31	AB007623.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8311	21005	34144	1.83	5.0E-31	AB007623.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9548	22201	35383	0.77	5.0E-31	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9548	22201	35384	0.77	5.0E-31	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11577	24176	37491	2.23	5.0E-31	9506634	NT	Homo sapiens hypothetical protein (FJ111045), mRNA
11577	24176	37491	2.23	5.0E-31	9506634	NT	Homo sapiens hypothetical protein (FJ111045), mRNA
11839	24423	37764	1.3	5.0E-31	11526341	NT	Homo sapiens armadillo repeat gene deletions in velocardiofacial syndrome (ARVCF), mRNA
686	13461	28109	2.03	4.0E-31	AI521435.1	EST_HUMAN	h80012.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:212702 3' similar to TR-Q5560 Q85560
1815	14555	27270	1.31	4.0E-31	AW178612.1	EST_HUMAN	h98d02.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COPO_BOVIN P53c20 COATOMER GAMMA SUBUNIT ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3168	15031	28580	3.58	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3919	18372	29013	0.88	4.0E-81	AF004608.1	EST_HUMAN	vs60103.11 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2605269 3' similar to TR:O43815 O43815
4139	16881	29509	2.28	4.0E-81	AF263306.1	NT	STRATIN ;
4139	16881	29510	2.28	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4360	17088	29733	1.33	4.0E-81	8923208	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
							Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
7177	19863	32934	1.11	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent L type, alpha 2/delta subunit (CACNA2), mRNA
7299	19882	33058	0.57	4.0E-81	11420544	NT	Homo sapiens delta variant gene 1 (ETV1), mRNA
8185	20879	34016	3.59	4.0E-81	X06896.1	NT	Human mRNA for amyloid A(781) protein
8443	21135	34271	3.43	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
8443	21135	34272	3.43	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9126	21814	34680	6.1	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10001	22849	35861	1.53	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10070	22718	39336	0.71	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11140	23807	37086	3.2	4.0E-81	4756085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11140	23807	37087	3.2	4.0E-81	4756085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11928	25280	30731	3.63	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11928	25280	30732	3.63	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12463	24831	31030	1.53	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12463	24831	31031	1.53	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12597	24911	31004	4.82	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1244	13993	28658	12.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1244	13993	28659	12.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2371	15093	27832	1.23	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A), mRNA, complete cds
2989	15755	28420	5.83	3.0E-81	4506280	NT	Homo sapiens plectrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2989	15755	28421	5.83	3.0E-81	4506280	NT	Homo sapiens plectrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2837	19605	28254	2.97	2.0E-81	BE784636.1	EST_HUMAN	801474072F NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
2837	19605	28255	2.97	2.0E-81	BE784636.1	EST_HUMAN	801474072F NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
3765	18507	29144	0.71	2.0E-81	AV161542.1	EST_HUMAN	hg8501.1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
7857	20552	33678	0.6	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55688), mRNA

Page 380 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1402	14149	26826	1.13	1.0E-81	W26539.1	EST_HUMAN	3333 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3944	16397	29037	1.07	1.0E-81	AW960688.1	EST_HUMAN	EST372728 IMAGE:3838280 5'
4479	17214	29839	3.56	1.0E-81	AA040370.1	EST_HUMAN	Z44809.1 Soares_pregnan_luteus_NHMPU Homo sapiens cDNA clone IMAGE:486825 5' similar to PIR-S92437 S92437 Cmp-92-diacylglycerol synthase - fruit fly;
4600	17335	29694	6.99	1.0E-81	BE047996.1	EST_HUMAN	Z44504.Y1 NCI_OCAP_Bms92 Homo sapiens cDNA clone IMAGE:2291526 5'
5167	17890	37768	4.99	1.0E-81	U87928.1	NT	Human acetylcholinesterase (AChE) gene, exon 3
5269	18075	30704	4.1	1.0E-81	U87928.1	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5289	18075	30706	4.1	1.0E-81	U87928.1	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5415	18214	30922	0.85	1.0E-81	AA255569.1	EST_HUMAN	Z44504.Y1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:082475 5' similar to SW-PRIZ_HUMAN P49843 DNA PRIMASE 58 KD SUBUNIT ;
5568	18365	31273	3.47	1.0E-81	U62351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (GTNN2) mRNA, partial cds
5668	18595	31274	3.47	1.0E-81	U62351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (GTNN2) mRNA, partial cds
6054	18834	31786	1.81	1.0E-81	BF67464.1	EST_HUMAN	602137847.1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4274335 5'
6453	19221	32218	0.59	1.0E-81	U87928.1	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6453	19221	32219	0.59	1.0E-81	U87928.1	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6639	19401	32416	0.87	1.0E-81	AJ133289.1	NT	Homo sapiens catenin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7659	20333	33444	8.45	1.0E-81	U87928.1	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
9876	22328	35523	5.09	1.0E-81	BE658278.1	EST_HUMAN	601845051.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9878	22328	35524	5.06	1.0E-81	BE658278.1	EST_HUMAN	601845051.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9889	22519	35715	5.06	1.0E-81	BE594367.1	EST_HUMAN	601343180.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
10003	22951	35863	1.59	1.0E-81	AA630784.1	EST_HUMAN	ac14d06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW-YP39_YEAST P38126 HYPOTHETICAL 60.6 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION ;
10005	22953	35865	3.27	1.0E-81	BE744545.1	EST_HUMAN	601577339.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10005	22953	35866	3.27	1.0E-81	BE744545.1	EST_HUMAN	601577339.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10405	23051	36269	1.99	1.0E-81	AW697550.1	EST_HUMAN	CMAS-NN0059-140400-147412 NN0059 Homo sapiens cDNA
10850	23540	36787	2.9	1.0E-81	AW697550.1	EST_HUMAN	CMAS-NN0059-140400-147412 NN0059 Homo sapiens cDNA
11029	23700	36966	1.97	1.0E-81	AW844968.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11029	23700	36967	1.97	1.0E-81	AW844968.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11240	16397	29037	1.72	1.0E-81	AW690658.1	EST_HUMAN	EST372728 IMAGE:3838280 5'
11507	24708	37421	1.99	1.0E-81	BF204233.1	EST_HUMAN	601657714.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110489 5'
12132	24622	31093	4.13	1.0E-81	U87928.1	NT	Homo sapiens photoboln (similar to epoliprotein B mRNA coding protein) (DJ742C19.2), mRNA
12	12939	25452	3.6	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds

Page 381 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
104	12930	25452	2.45	8.0E-82	AF161406.1	NT	Homo sapiens HSPC238 mRNA, partial cds
257	13065	25704	1.1	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
785	13567	28227	2.83	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
867	13836	28306	0.84	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1474	14221	28907	1.42	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1654	14400	27089	1.43	8.0E-82	871580.1	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4219	15960	29585	0.9	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1433	14180		1.7	7.0E-82	BF095327.1	EST_HUMAN	60145853.1 F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3852089 6'
2769	15474	28216	1.2	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000762 3'
11759	24350	37682	1.71	7.0E-82	AA663747.1	EST_HUMAN	ae89404.61 Sivalagene schizo brain S11 Homo sapiens cDNA clone IMAGE:369342 3'
4104	16847	29473	0.71	5.0E-82	AA515612.1	EST_HUMAN	m69491.1 s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:325198 3'
1688	14412	27103	49.82	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5409	18208	30915	0.8	4.0E-82	BF351891.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5409	18208	30916	0.8	4.0E-82	BF351891.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5871	18468	31381	0.65	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
11716	24310	37633	11.61	4.0E-82	AB97300.1	EST_HUMAN	wp75609.x1 NCL CGAP_Bin28 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR.O75276
12374	24773		5.05	4.0E-82	AF029701.2	NT	O76276 K01 ; Homo sapiens presenilin-1 gene, exons 1 and 2
271	13079	25721	21.65	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (prolesse nexin-1, Alzheimer disease) (APP), mRNA
687	13462	26110	3.11	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-015-02 BN0120 Homo sapiens cDNA
770	13542	26203	5.7	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
850	13620	26290	10.65	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (prolesse nexin-1, Alzheimer disease) (APP), mRNA
1039	13769		18.58	3.0E-82	AA725948.1	EST_HUMAN	al23405.61 Soares, Isatis, NHT Homo sapiens cDNA clone 1343548 3'
1333	14082	26758	1.25	3.0E-82	AA75073.1	EST_HUMAN	RCGP10001-190100-021-B02 P10001 Homo sapiens cDNA
1450	14197	26881	3.44	3.0E-82	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C065
1894	14631	27341	1.91	3.0E-82	BE613322.1	EST_HUMAN	RC1-BN0005-260700-015-g04 BN0005 Homo sapiens cDNA
2000	14735	27459	1.63	3.0E-82	4501922	NT	Homo sapiens adenylyl cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCVAP1R1) mRNA
3268	16028		2.52	3.0E-82	545381.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA

Page 382 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4854	17593	30216	0.98	3.0E-82	AA135979.1	EST_HUMAN	zr35b04.r1 Striatogene lung calcitonin 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN D07537 POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE ;
8052	20746	33878	3.14	3.0E-82	11432508	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8454	21146	34287	0.88	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8454	21146	34288	0.88	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9724	22376	35576	3.23	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
9724	22376	35576	3.23	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
983	13393	25990	2.95	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
983	13393	25990	2.95	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1681	14426	27121	1.21	2.0E-82	AL046390.1	EST_HUMAN	DKFZ434M117.1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZ434M117 5'
3827	16578	29210	1.25	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4208	16949	29575	1.17	2.0E-82	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4521	17256	29890	1.01	2.0E-82	AB023019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4521	17256	29890	1.01	2.0E-82	AB023019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4818	17547	30172	2.85	2.0E-82	AF045555.1	NT	Homo sapiens wiser1 (WBSCR1) and wiser5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5021	17742	30352	1.46	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5021	17742	30353	1.46	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5394	18184	30874	5.65	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6082	19851	31827	4.73	2.0E-82	AF294982.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7551	25426		0.91	2.0E-82	AI476428.1	EST_HUMAN	tr21g05.41 Soares_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7705	20369	33482	0.85	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20728 (FLJ20728), mRNA
8204	20898	34035	2.16	2.0E-82	11321570	NT	Homo sapiens aili (Drosophila) homolog 3 (SLIT3), mRNA
8598	21260	34397	0.45	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
8598	21260	34398	0.45	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
10009	22857	35870	1.84	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10009	22857	35871	1.84	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11237	23900	37187	1.27	2.0E-82	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11237	23900	37188	1.27	2.0E-82	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11279	23940	37253	4.45	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11279	23940	37254	4.45	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11780	24341	37670	1.91	2.0E-82	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDL3), mRNA
11957	24508		1.58	2.0E-82	N94950.1	EST_HUMAN	z531d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12485	24844		3.47	2.0E-82	AA011276.1	EST_HUMAN	201g09.11 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:295568 5'
12775	25029		1.95	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y-box 10 (SOX10)) mRNA
578	13359	25935	1.14	1.0E-82	11845921	NT	Homo sapiens SRY (sex determining region Y-box 10 (SOX10)) mRNA
1186	13938		0.77	1.0E-82	BE685106.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1283	14072	26879	3.71	1.0E-82	BE604368.1	EST_HUMAN	RC4-B10310-11030-015-10 B10310 Homo sapiens cDNA
1284	14073	26880	1.26	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8941	21533	34878	1.13	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9553	22206	35350	0.59	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10145	22783		1.17	1.0E-82	BF515938.1	EST_HUMAN	U1-H1BW1-404-03-0-U1 s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10946	23337	30578	2.34	1.0E-82	AL103209.2	NT	Homo sapiens chromosome 21 segment HS21C089
8915	21307	34449	4.51	9.0E-83	BF672220.1	EST_HUMAN	602180403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291961 6'
10174	22822	35039	0.53	9.0E-83	BE263347.1	EST_HUMAN	601173346F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1392	14139	26816	3.33	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3914362 5'
1676	15523	27115	5.53	8.0E-83	N66351.1	EST_HUMAN	za48f12.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:295523 3'
1335	14084	26769	0.97	7.0E-83	AW386529.1	EST_HUMAN	QV4-L10016-271268-068-111 L10016 Homo sapiens cDNA
2868	15935		1.88	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCL CGAP_Pha1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repulsive element;
4765	17497		6.68	7.0E-83	BF221613.1	EST_HUMAN	7c37a07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3847893 3' similar to TR:Q9Y316 Q9Y316 DJ207H1.1;
5900	18742	31702	0.58	7.0E-83	11428657	NT	Homo sapiens KIAA1000 gene product (KIAA1000), mRNA
11717	24311	37634	1.4	7.0E-83	5728753	NT	Homo sapiens transcription factor CA150 (CA150) mRNA
11717	24311	37635	1.4	7.0E-83	5729753	NT	Homo sapiens transcription factor CA150 (CA150) mRNA
394	13179	29826	1.88	9.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1779	14520	27224	1.5	6.0E-83	AW573088.1	EST_HUMAN	M3103.X1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3017	15783	28432	0.71	6.0E-83	AW816405.1	EST_HUMAN	SW4-ST0234-181189-037-405 ST0234 Homo sapiens cDNA
3046	19812		1.08	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5211	18018	30641	2.02	6.0E-83	4507666	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5933	18716	31674	1.52	6.0E-83	AJ010770.1	NT	Homo sapiens hyaluronan gene, exons 1-50
7401	20079	33190	2.27	8.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9675	22228	35413	2.85	6.0E-83	4505514	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9699	22321	35517	2.34	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
9699	22321	35518	2.34	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11517	24117		2.53	6.0E-93	AA486105.1	EST_HUMAN	ab146101 Strigene lung (H937210) Homo sapiens cDNA clone IMAGE:540810 3' similar to contains THR12 THR repetitive element.
11908	24472		4.27	6.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
925	13592		2.03	6.0E-93	AF70883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 3
2043	15526		1.55	5.0E-93	AF003051.1	NT	Homo sapiens 2S5 proteasome regulatory subunit (SU02) mRNA, complete cds
3629	19392	29022	1.18	6.0E-93	AF133207.2	NT	Novel human gene mapping to chromosome X
3888	16536	29275	0.77	6.0E-93	4885180	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5020	17741	30350	11.53	6.0E-93	4557013	NT	Homo sapiens cathepsin (CAT) mRNA
6020	17741	30351	11.53	6.0E-93	4557013	NT	Homo sapiens cathepsin (CAT) mRNA
5093	17812	30428	1.07	6.0E-93	5031660	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
5093	17812	30429	1.07	6.0E-93	5031660	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
625	13404	29039	1.72	4.0E-93	AF224559.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
977	13742		4.9	3.0E-93	AA358311.1	EST_HUMAN	EST179542 Placenta 1 Homo sapiens cDNA similar to endogenous retrovirus ERV9
2780	15495		1.33	3.0E-93	AA632654.1	EST_HUMAN	np8707.at NIC_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element.
6483	19250		0.62	3.0E-93	AI217223.1	EST_HUMAN	qf73a06.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1621692 3' similar to TR:Q92814
1792	14532	27240	1.86	2.0E-93	AA593492.1	EST_HUMAN	cd4g05.at Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1755082 3'
1792	14532	27241	1.86	2.0E-93	AA593492.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216.
1918	14655	27365	4.07	2.0E-93	NG6951.1	EST_HUMAN	cd4g05.at Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1621692 3' similar to TR:Q92814
2856	19524	28268	1.1	2.0E-93	BE823694.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216.
3293	18026		1.89	2.0E-93	11430634	NT	Q92814 MYELOBLAST KIAA0216.
3756	19508		0.7	2.0E-93	AL163202.2	NT	Q92814 MYELOBLAST KIAA0216.
4302	17041	29608	4.11	2.0E-93	AF202879.1	NT	Q92814 MYELOBLAST KIAA0216.
4604	17339	29668	6.14	2.0E-93	7706398	NT	Q92814 MYELOBLAST KIAA0216.
4604	17339	29669	6.14	2.0E-93	7706398	NT	Q92814 MYELOBLAST KIAA0216.
5189	17997	30620	0.9	2.0E-93	U06679.1	NT	Q92814 MYELOBLAST KIAA0216.
5755	19547	31468	0.85	2.0E-93	11428081	NT	Q92814 MYELOBLAST KIAA0216.
6676	18692	31603	1.31	2.0E-93	BE885401.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216.
6647	19409	32423	1.12	2.0E-93	AF129533.1	NT	Q92814 MYELOBLAST KIAA0216.
7336	20017	33095	6.36	2.0E-93	AF129533.1	NT	Q92814 MYELOBLAST KIAA0216.

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7704	20387	33480	0.64	2.0E-83	BF105097.1	EST_HUMAN	60182200F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042318 5'
7742	20438	33580	0.78	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7742	20438	33581	0.78	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7886	20581	33710	1.79	2.0E-83	U66707.1	NT	Rattus norvegicus desmin-180 mRNA, complete cds
8213	20907	34042	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8213	20907	34043	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8494	22147	35328	0.48	2.0E-83	5453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
9194	22147	35329	0.48	2.0E-83	5453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
8934	22582	35760	4.01	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
9934	22582	35781	4.01	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10016	22694	35881	1.39	2.0E-83	AU117659.1	EST_HUMAN	U-HF-BNO-smad-R-07-0-LJ1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081852 5'
10089	22737	35952	0.77	2.0E-83	AW505600.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone IMAGE:3081852 5'
10753	23438	36882	6.64	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
10845	23527	36770	2.19	2.0E-83	AL134452.1	EST_HUMAN	DKFZp447J135_r1 347 (synonym: hibr1) Homo sapiens cDNA clone DKFZp447J135 5'
10845	23527	36771	2.19	2.0E-83	AL134452.1	EST_HUMAN	DKFZp447J135_r1 347 (synonym: hibr1) Homo sapiens cDNA clone DKFZp447J135 5'
12522	24869		3.85	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1390	14137	25813	2.18	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-oxoacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1390	14137	25814	2.18	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-oxoacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1442	14189	25873	0.98	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1442	14189	25874	0.98	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
3176	15942	26593	1.18	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0859), mRNA
3650	16000	26237	3.93	1.0E-83	AF063768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4220	16891	26566	1.99	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4831	17562	30164	3.36	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6598	18359	32373	1.65	1.0E-83	AI027614.1	EST_HUMAN	ov6908.8.1 Scores, lexis_NHT Homo sapiens cDNA clone IMAGE:1646431 3' similar to gb:M64241.QM PROTEIN (HUMAN);
3776	16528	29167	3.5	7.0E-84	BE901209.1	EST_HUMAN	RC2-FN0119-200600-011-p05 FN0119 Homo sapiens cDNA clone IMAGE:3958853 5'
1272	14021	26688	3.5	6.0E-84	BE838964.1	EST_HUMAN	RC2-FN0119-200600-011-p05 FN0119 Homo sapiens cDNA
2398	15117	27654	8.26	6.0E-84	AA176574.1	EST_HUMAN	ae6860.3.1 Stratiotes schizoid brain S11 Homo sapiens cDNA clone IMAGE:371020 3'
5160	17892		3.33	6.0E-84	ALD28653.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434H0322 5'

Page 386 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5431	18230	30943	1.87	6.0E-84	A4897339.1	EST_HUMAN	cl47 g03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gp.M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); Homo sapiens acyl-LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
5574	18371	31282	1.04	6.0E-84	11428718	NT	Homo sapiens acyl-LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
5574	18371	31283	1.04	6.0E-84	11428718	NT	Homo sapiens acyl-LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
7373	20053	33134	2.84	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0016-160600-004-F02 L'T0016 Homo sapiens cDNA Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
7591	20259	33367	0.87	6.0E-84	AF038391.1	NT	PMO-LT0016-160600-004-F02 L'T0016 Homo sapiens cDNA Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
7972	20897	33789	2.37	6.0E-84	BE770189.1	EST_HUMAN	PMO-LT0016-160600-004-F02 L'T0016 Homo sapiens cDNA Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
697	13472	26121	0.71	6.0E-84	AA382911.1	EST_HUMAN	EST16094 Testis 1 Homo sapiens cDNA 5' end
3013	15779		1.82	5.0E-84	AF109716.1	NT	Homo sapiens chromosome 3 subtelomeric region
6015	19796	31759	0.59	5.0E-84	AA167678.1	EST_HUMAN	z639e07.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:532100 5' similar to TR:G463915 G463915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.; Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11533	24133	37436	3.17	5.0E-84	11428740	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11652	24249	37570	1.77	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11852	24249	37571	1.77	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11813	24401	37738	1.44	5.0E-84	11433950	NT	Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA
1369	14136	28812	2.19	4.0E-84	AI665321.1	EST_HUMAN	wa/604.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O49847 NARDILYSIN PRECURSOR;
4897	17624	30242	1.79	4.0E-84	AF099507.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5476	18274	31168	1.36	4.0E-84	11386768	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5476	18274	31169	1.36	4.0E-84	11386768	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6175	18652	31925	1.88	4.0E-84	AF099505.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7547	20217	33319	14.38	4.0E-84	11421325	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8809	21601	34847	1.21	4.0E-84	4557528	NT	Homo sapiens disc, large (Disophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8809	21601	34848	1.21	4.0E-84	4557528	NT	Homo sapiens disc, large (Disophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10535	23517	36759	4.51	4.0E-84	AB032966.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
308	13112	25732	1.24	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1953	14883	27401	1.15	3.0E-84	AF026200.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2001	14736	27460	2.41	3.0E-84	AL096880.1	NT	Novel human mRNA containing zinc finger C2H2 type domains Homo sapiens DNA, DLEC1 to ORGTL4 gene region, section 1/2 (DLEC1, ORGTL3, ORGTL4 genes, complete cds)
3578	16333	28977	1.07	3.0E-84	AB028898.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRIS1) mRNA, complete cds
3731	16483	29121	5.2	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRIS1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10790	28473		3.55	3.0E-84	AI993901.1	EST_HUMAN	wu20d05.x1 Soares_Diedigraefc_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gbL05093.60S RIBOSOMAL PROTEIN L18A (HUMAN);
2098	14829	27663	6.94	2.0E-84	BE669397.1	EST_HUMAN	CM1-BT0765-190600-272-508 BT0765 Homo sapiens cDNA
2098	14829	27664	6.94	2.0E-84	BE669397.1	EST_HUMAN	CM1-BT0765-190600-272-508 BT0765 Homo sapiens cDNA
2944	15710	28362	9.31	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MTF1L) mRNA, complete cds
2962	15728	28378	0.77	2.0E-84	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
6439	18238	30953	0.92	2.0E-84	BF611576.1	EST_HUMAN	UHH-B14-act-a-02-01a1 NCI CGAP SubB Homo sapiens cDNA clone IMAGE:3084663 3'
6439	18238	30953	0.92	2.0E-84	BF611576.1	EST_HUMAN	UHH-B14-act-a-02-01a1 NCI CGAP SubB Homo sapiens cDNA clone IMAGE:3084663 3'
6540	18305	32310	0.75	2.0E-84	H63370.1	EST_HUMAN	yt56a11.s1 Soares fetal liver spleen NFILS Homo sapiens cDNA clone IMAGE:203324 3'
7655	20651		1.35	2.0E-84	AI298874.1	EST_HUMAN	qms7c09.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1886728 3'
8284	20978	34118	0.49	2.0E-84	AL103204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8284	20978	34119	0.49	2.0E-84	AL103204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9245	21824	35094	0.81	2.0E-84	AI120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
9631	22283	35476	0.61	2.0E-84	H22841.1	EST_HUMAN	yt46a11.t1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT
12159	24643	31100	3	2.0E-84	BF446000.1	EST_HUMAN	P26044 BETA-2-GLYCOPROTEIN1;
12159	24643	31101	3	2.0E-84	BF446000.1	EST_HUMAN	ne330a02.x1 Lupsaki_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR-08UGS3 Q8UGS3 DJ756023.1;
304	13108	25748	1.89	1.0E-84	AF114488.1	NT	ne330a02.x1 Lupsaki_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR-08UGS3 Q8UGS3 DJ756023.1;
536	13319	25953	20.64	1.0E-84	4507852	NT	Homo sapiens tyrosine 3-monooxygenase/tyrosine 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
703	13478		1	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5) mRNA
1270	14019	26865	3.17	1.0E-84	AA084379.1	EST_HUMAN	am85b1.s1 Strassmann schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
2048	14781	27508	1.82	1.0E-84	BE392137.1	EST_HUMAN	601308006P1 NIF_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2220	14948	27688	1.13	1.0E-84	11427167	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
3733	16499	29123	2.49	1.0E-84	AJ220951.1	EST_HUMAN	nw12606.s1 NCI CGAP SS1 Homo sapiens cDNA clone IMAGE:1239108 3'
4393	17120	29752	5.01	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AM1.1 and CBRT1 on chromosome 21q22; segment 1/3
4651	17385	30017	3.53	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323.T1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4651	17385	30018	3.53	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323.T1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4855	17720	29752	2.67	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AM1.1 and CBRT1 on chromosome 21q22; segment 1/3
5153	17870	30483	1.15	1.0E-84	7656008	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2) mRNA
5630	18619	31651	0.98	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6087	18875	31844	1.41	1.0E-84	U73482.1	NT	uterine water channel=28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6781	19525	32952	1.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6781	19525	32953	1.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7007	19699	32753	2.32	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7359	20049	33130	1.28	1.0E-84	8393894	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7501	20137	33229	2.42	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8495	22113	35519	3.05	1.0E-84	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PPT15), mRNA
9670	22322	35519	0.53	1.0E-84	AF224511.1	NT	Homo sapiens Cx2-binding protein CABP3 (CABP3) gene, exon 8 and partial cde
9690	17600	30588	3.05	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9690	17600	30589	3.05	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10496	23142	36368	1.08	1.0E-84	11437366	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4), mRNA
12046	24563		2.34	1.0E-84	11417612	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RX1), mRNA
12151	24563	31098	3.2	1.0E-84	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
948	13712		1.08	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C009
1051	13810	26469	2.39	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cde
1051	13810	26470	2.39	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cde
1360	14108	26763	0.95	9.0E-85	4758669	NT	Homo sapiens leucidin (LDPL), mRNA
1572	14319	27004	1.23	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1572	14319	27005	1.23	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1670	14415	27108	3.6	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4225	19856	29591	0.96	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C080
4824	17555	30177	0.98	9.0E-85	5801979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4856	17555	30208	1.12	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1114	18701	26530	1.45	7.0E-85	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cde
11642	24239		4.32	7.0E-85	AF113210.1	NT	Homo sapiens NS1P030 mRNA, complete cde
11392	23968	37300	3.35	6.0E-85	11438573	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp-His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11392	23968	37301	3.35	6.0E-85	11438573	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp-His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11766	24357	37690	1.29	6.0E-85	AA403053.1	EST_HUMAN	z62801.1 Scores: NHT Homo sapiens cDNA clone IMAGE726889 5' similar to TR-G1335769 G1335769 GAG-POL POLYPROTEIN ;
2392	15055	27792	1.49	5.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C084

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4398	17138		0.8	5.0E-35	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1a) mRNA, complete cds
5394	18188	30851	1.4	5.0E-35	BF035674.1	EST_HUMAN	601458946F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882402 5'
5394	18188	30852	1.4	5.0E-35	BF035674.1	EST_HUMAN	601458946F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882402 5'
11063	22733	37005	2	5.0E-35	AF224695.1	NT	Homo sapiens meniscoidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12743	17136		5.28	5.0E-35	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1a) mRNA, complete cds
6056	18836	31707	1.51	4.0E-35	BF607910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4240087 5'
6056	18836	31708	1.51	4.0E-35	BF607910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4240087 5'
10472	23118		1.3	4.0E-35	BE078933.1	EST_HUMAN	RC1-BT0623-120200-011-007 BT0623 Homo sapiens cDNA
1276	14026	26594	2.88	3.0E-35	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6 yes5309.1 Scores: fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121504 5'
1773	14515	27215	3.51	3.0E-35	187465.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4280	17019	28646	6.53	3.0E-35	BE237189.1	EST_HUMAN	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4841	17571	30194	1.45	3.0E-35	11024695	NT	Homo sapiens leucine-rich protein (LPRP), mRNA
5316	18120	30777	1.07	3.0E-35	11436001	NT	Homo sapiens met proto-oncogene (hepatocellular growth factor receptor) (MET), mRNA
5894	18775	31737	0.63	3.0E-35	11422024	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6043	18823	31783	5.71	3.0E-35	7682309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6043	18823	31784	5.71	3.0E-35	7682309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6853	19533		7.79	3.0E-35	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7295	19978	33055	0.91	3.0E-35	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK), KIAA0821 protein (KIAA0821), mRNA
7771	20467	33591	1.89	3.0E-35	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8406	21099	34235	0.74	3.0E-35	11525829	NT	Homo sapiens CGI-81 protein (LOC51109), mRNA
8877	21593	34712	3.8	3.0E-35	11430868	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
8206	22085	35287	0.90	3.0E-35	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB), mRNA
8206	22085	35258	0.98	3.0E-35	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB), mRNA
10381	23027	36242	0.58	3.0E-35	AF088442.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
10730	23418	36959	1.88	3.0E-35	BE150392.1	EST_HUMAN	RC1-HT0268-031289-012-109 HT0268 Homo sapiens cDNA
11490	24091	37403	2.25	3.0E-35	5031860	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11824	24408	37402	1.70	3.0E-35	AB029030.1	NT	Homo sapiens mRNA for KIAA1107 protein, partial cds
11824	24408	37443	1.78	3.0E-35	AB029030.1	NT	Homo sapiens mRNA for KIAA1107 protein, partial cds
12840	24937		1.98	3.0E-35	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1017	13777	28438	2.34	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1383	14130	28903	0.97	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51940) mRNA
1398	14146	28924	8.28	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1399	14146	28925	8.28	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2228	14694	27682	1.33	2.0E-85	U10523.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2828	14063	28435	5.28	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (POMT21L1), mRNA
3022	16788	28435	1.18	2.0E-85	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4300	17039	29069	4.51	2.0E-85	4503880	NT	Homo sapiens plasminogen (PLG) mRNA
4527	17262	28866	1.22	2.0E-85	4828977	NT	Homo sapiens reelin (RELN) mRNA
4854	17584	30207	0.97	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9173	21843	35009	3.18	2.0E-85	A1760820.1	EST_HUMAN	wb7f08.x1 NCL CGAP_KH72 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSY1 repetitive element
9549	22202	35385	1.08	2.0E-85	A191459.1	EST_HUMAN	wb49d03.x1 Scores_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2331481 3'
10182	22810	36028	1.32	2.0E-85	A1863394.1	EST_HUMAN	wb64d12.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2285	15010	27850	2.86	1.0E-85	BE794306.1	EST_HUMAN	001591118FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2392	18113	27851	8.42	1.0E-85	BE618392.1	EST_HUMAN	001462817FT NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866021 5'
9881	22333	35528	4.39	1.0E-85	BE257817.1	EST_HUMAN	001109738FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
10842	23524	36768	2.77	1.0E-85	AA778785.1	EST_HUMAN	245f03.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10842	23524	36767	2.77	1.0E-85	AA778785.1	EST_HUMAN	245f03.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10919	23599	36847	1.73	1.0E-85	BF311662.1	EST_HUMAN	0011897003FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
10919	23599	36848	1.73	1.0E-85	BF311662.1	EST_HUMAN	0011897003FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
10997	23870	36927	1.28	1.0E-85	Y00032.1	NT	Human mRNA for T-cell cyclophilin
11773	24394	37698	2.41	1.0E-85	A1198420.1	EST_HUMAN	q15fa07.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1860488 3'
12550	24722	37053	4.4	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12595	24722	37053	4.74	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1409	14160	27682	11.19	9.0E-96	BE274217.1	EST_HUMAN	001120778FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
11688	24293	37618	1.57	8.0E-86	4503224	NT	Homo sapiens cyclochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
916	13683	28345	2.34	7.0E-86	AA660801.1	EST_HUMAN	988f08.x1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
916	13683	28348	2.34	7.0E-86	AA660801.1	EST_HUMAN	988f08.x1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6103	18881	31848	1.02	7.0E-86	9858888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6103	18881	31849	1.02	7.0E-86	9858888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6880	17559	30553	6.65	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type 1) binding protein 1 (TAX1BP1), mRNA
8843	21335	34478	3.06	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15

Table 4

Single Exon Probes Expressed in Brain

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9599	22252		1.39	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9598	22310	35508	2.27	7.0E-86	1152307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
10882	22362	35509	1.72	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA160 (H. sapiens) (LOC63170), mRNA
10882	22362	35510	1.72	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA160 (H. sapiens) (LOC63170), mRNA
1271	14020	29986	2.88	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (liponamide) (OGDH), mRNA
5105	17823	30440	2.64	6.0E-86	Y19139.1	NT	Homo sapiens enteropeptidase gene, exons 20 and 21
5107	17825	30442	1.07	6.0E-86	6005883	NT	Homo sapiens 24 kDa intrinsic membrane protein (PMP24), mRNA
206	13018	25660	4.98	4.0E-86	BE547173.1	EST	Homo sapiens cDNA clone IMAGE3458830 5'
5944	18728	31684	12.1	4.0E-86	BE26843.1	EST	Homo sapiens cDNA clone IMAGE3531853 5'
11205	13018	25660	2.18	4.0E-86	BE547173.1	EST	Homo sapiens cDNA clone IMAGE3458830 5'
5509	18307	31208	6.97	3.0E-86	AW340946.1	EST	Homo sapiens cDNA clone IMAGE287118 3'
8160	20854	33985	1.05	3.0E-86	AW723239.1	EST	Homo sapiens cDNA clone HTB85004 5'
10120	22768	35980	3.37	3.0E-86	BE886479.1	EST	Homo sapiens cDNA clone IMAGE3911303 5'
11413	23180	39408	5.14	3.0E-86	AI659240.1	EST	Homo sapiens cDNA clone IMAGE2251371 3'
11708	24303	37628	1.6	3.0E-86	11037056	NT	Homo sapiens myosin X (MYO10), mRNA
280	13068	25706	2.02	2.0E-86	AA308284.1	EST	EST177232 Jurkat T-cells v1 Homo sapiens cDNA 5' end
405	13190		2.69	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1168	13922	26584	3.21	2.0E-86	N58977.1	EST	Y129408.1 Scores, multiple sclerosis_2NNHNSP Homo sapiens cDNA clone IMAGE283478 5'
1478	14225	26910	1.93	2.0E-86	4758827	NT	Homo sapiens neuraxin III (NRXN3), mRNA
1478	14225	26911	1.93	2.0E-86	4758827	NT	Homo sapiens neuraxin III (NRXN3), mRNA
2188	14617	27651	6.09	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2286	14692	27732	1.65	2.0E-86	ABG3103.1	NT	Human sapiens mRNA for KIAA1277 protein, partial cds
3410	16168	28817	1.3	2.0E-86	AW98142.1	EST	EST378215 MAGe resequences, MAGI Homo sapiens cDNA
3729	16481	29118	3.64	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3729	16481	29119	3.64	2.0E-86	AF156778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4019	16765		2.84	2.0E-86	AW915742.1	EST	Human sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4737	17489	30106	3.26	2.0E-86	AF055490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5782	18573	31501	1.52	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5782	18573	31502	1.52	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6874	25098	32476	0.69	2.0E-86	11419429	NT	Homo sapiens similar to ecdystrolide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7008	20603	33733	0.69	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8414	21107		0.47	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C0027

Single Exon Probes Expressed in Brain

[illegible]

Page 393 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9971	22819	35822	3.95	7.0E-87	AL043314.2	EST_HUMAN	DKFZP434N0323.1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZP434N0323.5'
9971	22819	35823	3.95	7.0E-87	AL043314.2	EST_HUMAN	DKFZP434N0323.1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZP434N0323.5'
10369	29129		0.61	7.0E-87	AC01665.1	EST_HUMAN	cd59h01.s1 Soare, NIHMPU, S1 Homo sapiens cDNA clone IMAGE:160667.3'
10806	23489	36724	6.85	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
10806	23489	36725	6.85	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
35171	19273	28927	0.99	6.0E-87	7657213	NT	Homo sapiens hominally upregulated neu tumor-associated kinase (HUNK), mRNA
51728	17946	30463	0.69	8.0E-87	7657213	NT	Homo sapiens hominally upregulated neu tumor-associated kinase (HUNK), mRNA
6327	19097	32065	2.02	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10625	23378		4.13	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC83102), mRNA
11351	13891	26551	1.42	5.0E-87	AA382811.1	EST_HUMAN	EST198094 Testis 1 Homo sapiens cDNA 5' end
12297	13891	26551	1.56	5.0E-87	AA382811.1	EST_HUMAN	EST198094 Testis 1 Homo sapiens cDNA 5' end
945	13711	26376	1.51	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
1149	13904	26598	13.59	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2024	14759	27488	1.53	4.0E-87	AB007925.1	NT	Homo sapiens CGI-60 protein (LOC31626), mRNA
2421	15142	27874	1.03	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC31626), mRNA
2421	15142	27875	1.03	4.0E-87	7706299	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11thorax) (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
3457	19213	28866	1.8	4.0E-87	5174574	NT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5360	18182	30846	2.77	4.0E-87	C00321	SWISSPROT	TCBAP1E4051 Podiatric pre-B cell acute lymphoblastic leukemia Beyer-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
5954	18798	31695	4.53	4.0E-87	BE247284.1	EST_HUMAN	Homo sapiens tuberin (TSC2) gene, exon 10
7970	20334	33445	0.72	4.0E-87	L48524.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11118	23789	37055	3.44	4.0E-87	M60076.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12396	25268	30721	1.5	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12396	25268	30722	1.5	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12541	24881		2.25	4.0E-87	11417812	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4), mRNA
2779	15484	28223	2.77	2.0E-87	4895420	NT	Homo sapiens HEVBA1 Homo sapiens cDNA clone HEMBA100307.5'
3764	16516	29164	0.83	2.0E-87	AL116635.1	EST_HUMAN	CUK1-TN0038-156600-556-108 TN0038 Homo sapiens cDNA
4857	17586	30209	1.28	2.0E-87	BF376911.1	EST_HUMAN	RC5-HT0960-200300-031-004 HT0960 Homo sapiens cDNA
4907	17634	30249	1.47	2.0E-87	BE176478.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843790.5'
5575	18372	31284	10.34	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730.5'
5575	18372	31285	10.34	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730.5'
6234	16008		9.91	2.0E-87	BE597163.1	EST_HUMAN	601341363F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3683348.5'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6509	16362	32376	0.69	2.0E-87	N48128.1	EST_HUMAN	y21607.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243398 5'
6893	18600	32938	0.81	2.0E-87	AV554143.1	EST_HUMAN	AV554143 GLC Homo sapiens cDNA clone GLDSDG04 3'
7073	19764	32828	1.58	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:3331511 5'
7126	19814	32892	0.84	2.0E-87	11433048	NT	Homo sapiens hest domain and RLD 2 (HERC2), mRNA
7353	20034	33112	39.61	2.0E-87	N48128.1	EST_HUMAN	y21607.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243398 5'
7567	20255	33362	35.45	2.0E-87	N48128.1	EST_HUMAN	y21607.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243398 5'
8204	20398	34127	17.42	2.0E-87	X62951.1	NT	Human cytochrome P-450 2C8 mRNA
9885	22337		5.72	2.0E-87	BE831136.1	EST_HUMAN	601278315F1 NH_MGC_39 Homo sapiens cDNA clone IMAGE:3810639 5'
1159	15321		2.09	1.0E-87	7705983	NT	Homo sapiens putative glycoprotein transfer protein (LOC51054), mRNA
1411	14159	26840	1.1	1.0E-87	AW351977.1	EST_HUMAN	PM2-CT0285-141089-001-g04 CT0285 Homo sapiens cDNA
1411	14159	26841	1.1	1.0E-87	AW351977.1	EST_HUMAN	PM2-CT0285-141089-001-g04 CT0285 Homo sapiens cDNA
3597	16451	26090	0.23	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cytochrome
3717	16470	26108	2.43	1.0E-87	4759827	NT	Homo sapiens neuraxin III (NRXN3), mRNA
5095	17814	30431	0.69	1.0E-87	AF114487.1	NT	Homo sapiens Interactin long isoform (ITSN), complete cds
5095	17814	30432	0.69	1.0E-87	AF114487.1	NT	Homo sapiens Interactin long isoform (ITSN), complete cds
5149	12933	26570	1.04	1.0E-87	AJ004091.1	EST_HUMAN	cd50d4.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1620199 3'
6132	18910	31878	1.91	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10), gene, exon 8
6132	18910	31879	1.91	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10), gene, exon 8
7077	19768	32832	0.62	1.0E-87	AF039517.1	NT	Homo sapiens corticotroph-releasing factor type 1 receptor, gene, exon 8
7077	19768	32833	0.62	1.0E-87	AF039517.1	NT	Homo sapiens corticotroph-releasing factor type 1 receptor, gene, exon 8
7083	19773	32838	1.18	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7288	19881	33057	1.23	1.0E-87	11431600	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8015	20710	33840	12.93	1.0E-87	AF214552.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC), gene, complete cds
8807	21498	34644	0.97	1.0E-87	A3022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8807	21498	34645	0.97	1.0E-87	A3022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9533	22168	33371	2.85	1.0E-87	BE616183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9533	22168	33372	2.85	1.0E-87	BE616183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10272	22920	36131	0.67	1.0E-87	M34428.1	NT	Human L-plastin mRNA, 5' end
10333	23326	35552	1.55	1.0E-87	6728867	NT	Homo sapiens hest domain and RLD 2 (HERC2), mRNA
10321	23601		1.82	1.0E-87	D100383.1	NT	Homo sapiens RGH1, gene, retrovirus-like element
10965	23641	36893	1.68	1.0E-87	5031680	NT	Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (EDL3), mRNA
10965	23641	36894	1.68	1.0E-87	5031680	NT	Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (EDL3), mRNA
12583	25404		3.54	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
12509	25240		3.94	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Page 395 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1084	13842	26500	10.24	9.0E-88	AF167485.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	14076	28750	2.76	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
1327	14078	28751	2.76	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
2115	14848	27975	1.57	9.0E-88	7681701	NT	Homo sapiens DKFZP568P1522 protein (DKFZP568P1522), mRNA
3617	16370	29012	1.35	9.0E-88	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4236	16977	29602	2.73	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4236	16977	29603	2.73	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4943	17670	30279	1.05	9.0E-88	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8919	21610	34754	3.82	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1820	14559		1.02	5.0E-88	7661837	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2845	15355	28100	3.76	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3030	15768	28414	0.9	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN), complete cds
3384	16143		2.28	5.0E-88	AI693217.1	EST_HUMAN	w688h08.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338796 3' similar to contains Alu repetitive element contains element MER22 MER22 repetitive element ;
4687	17421	30059	0.83	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN), complete cds
6872	19569	32625	3.19	5.0E-88	HT0932.1	EST_HUMAN	Yno06b70.1 Scars Infant brain, 1k18B Homo sapiens cDNA clone IMAGE:47129 5'
7830	20525	33650	1.8	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9211	21880	35057	0.45	5.0E-88	BF69206.1	EST_HUMAN	60215498F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
1306	14055	26729	1.42	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
1306	14055	26730	1.42	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
7143	19830	32899	1.43	4.0E-88	11416889	NT	Homo sapiens transforming growth factor, beta-induced, 08KD (TGFB1), mRNA
10827	23509	36749	1.8	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11471	24072	37390	1.89	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11471	24072	37391	1.89	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
715	13469	26140	1.85	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ121634 (FLJ121634), mRNA
1805	14545		1.98	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2948	15714	29397	4.11	3.0E-88	N60951.1	EST_HUMAN	z448f12.x1 Scars fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:296823 3'
4216	18657	29578	1.24	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4216	18657	29580	1.24	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4444	17180		4.06	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5216	18024	30646	2.85	3.0E-88	11429667	NT	Homo sapiens veldin-containing protein (VCP), mRNA

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5498	18295	31184	4.13	3.0E-88	9585888	NT	Homo sapiens poly(phenyl rubra vera 1; cell surface receptor (PRV1), mRNA
5818	18414	31327	3.65	3.0E-88	11420697	NT	Homo sapiens vral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6069	18848	31812	0.61	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6319	25083	32076	1.18	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6319	25088	32077	1.18	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6965	19447	32465	14.69	3.0E-88	AF279285.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7440	20117	33206	0.15	3.0E-88	11438400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7821	20516	33842	0.68	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8096	20790	33921	1.35	3.0E-88	AF034374.1	NT	Homo sapiens myoblast fusion cofactor b230 protein A and myoblast fusion cofactor b230 protein C mRNA, complete cds
9834	20405	33521	1.99	3.0E-88	11528282	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9828	22479	35680	0.59	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9828	22479	35681	0.58	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9857	22507	35705	1.28	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12138	24628	36432	6.97	3.0E-88	11417874	NT	Homo sapiens transcobalamin II; macrocytic anemia (TND2), mRNA
1013	13773	28432	3.32	2.0E-88	7305198	NT	Homo sapiens Celsr1, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1620	14367	27056	1.38	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAP mRNA, complete cds
1744	14486	27165	3.13	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAP mRNA, complete cds
3458	16214	28867	1.52	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAP mRNA, complete cds
4391	17128	29760	2.13	2.0E-88	5031666	NT	Homo sapiens dyx11c1, axonemal, light polypeptide 4 (DNAL4), mRNA
5821	18610	31639	5.63	1.0E-88	AW139565.1	EST_HUMAN	U1H-B1-aaa-d-04-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
5821	18610	31540	5.63	1.0E-88	AW139565.1	EST_HUMAN	U1H-B1-aaa-d-04-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6548	19313	32317	23.81	1.0E-88	AB007877.1	NT	Homo sapiens KIA00417 mRNA, complete cds
6548	19313	32318	23.81	1.0E-88	AB007877.1	NT	Homo sapiens KIA00417 mRNA, complete cds
7022	19714	32771	1.4	1.0E-88	AI096034.1	EST_HUMAN	wq70412.ct NCI CGAP GC08 Homo sapiens cDNA clone IMAGE:2478606 3'
7064	19774	32839	4.42	1.0E-88	AA488981.1	EST_HUMAN	sea4411.s1 NCI CGAP GC081 Homo sapiens cDNA clone IMAGE:324732 3' similar to WIP-B0272.2 CE00951
9141	21672	35037	0.6	1.0E-88	AA190368.1	EST_HUMAN	z8x7202.11 Stralagene HeLa cell s3 637216 Homo sapiens cDNA clone IMAGE:627170 5' similar to SWP-POL.1 HUMAN P10268 RETROVIRUS-RELATED POLYPROTEIN
9478	22313	35311	2.97	1.0E-88	AL043314.2	EST_HUMAN	DKFZP454N0323.1 434 (synonym: htes) Homo sapiens cDNA clone DKFZP454N0323 5'
11422	23189	36420	2.99	1.0E-88	AA991478.1	EST_HUMAN	ceb1903.s1 NCI CGAP GC03 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN)
12356	24760		3	1.0E-88	AL163240.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2739	15445	28164	1.33	8.0E-49	BE311557.1	EST_HUMAN	601142409F1 NH_MGC_14 Homo sapiens cDNA clone IMAGE:3505186 5'
8633	19495	32519	1.2	8.0E-49	11421514	NT	Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (serpin) 3A (H. sapiens) (LOC63232), mRNA
424	13210	25856	1.72	7.0E-49	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
424	13210	25857	1.72	7.0E-49	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
4828	17659	30181	2.86	7.0E-49	4557300	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
4878	17605	30228	3.35	7.0E-49	AL045748.1	EST_HUMAN	DKFZp434E246_r1.434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E246 5'
5345	18148	30527	1.34	7.0E-49	X99832.1	NT	H. sapiens GLN3 gene, complete CDS
5345	18148	30528	1.34	7.0E-49	X99832.1	NT	H. sapiens GLN3 gene, complete CDS
6250	18024	31697	0.57	7.0E-49	7548808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6250	18024	31698	0.57	7.0E-49	7548808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
7398	20076	33136	2.06	7.0E-49	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
7779	20474	33508	0.57	7.0E-49	11477118	NT	Homo sapiens KIAA0463 protein (KIAA0433), mRNA
7779	20474	33589	0.57	7.0E-49	11477118	NT	Homo sapiens KIAA0463 protein (KIAA0433), mRNA
8584	22237	35421	0.6	7.0E-49	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
10429	23075	36296	1.11	7.0E-49	X62048.1	NT	H. sapiens Wee1 hu gene
10429	23075	36297	1.11	7.0E-49	X62048.1	NT	H. sapiens Wee1 hu gene
10445	23091	36320	2.33	7.0E-49	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10445	23091	36321	2.33	7.0E-49	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
11203	23897	37154	1.45	7.0E-49	M59783.1	NT	Human aldose reductase (AR) gene, segment 2
12774	25028		1.7	7.0E-49	U87927.1	NT	Human acylate hydratase (ACO2) gene, exon 2
1002	13762	26423	0.73	6.0E-49	5903114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2210	14939	27076	1.27	6.0E-49	4508124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
2434	19155	27898	1.06	6.0E-49	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
2434	19155	27899	1.06	6.0E-49	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
3515	19271	28925	0.88	6.0E-49	7591817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4593	17328	29944	3.02	6.0E-49	AB07865.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4593	17328	29955	3.02	6.0E-49	AB07865.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5100	17819	30436	0.81	6.0E-49	6806916	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5100	17819	30437	0.81	6.0E-49	6806916	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5016	17737	30345	2.74	5.0E-49	BE244323.1	EST_HUMAN	TGBAP2/TCB933 Pediatric pre-B cell acute lymphoblastic leukemia BAYlor-HGSC project-TGBA Homo sapiens cDNA clone TGBAP0383
5016	17737	30346	2.74	5.0E-49	BE244323.1	EST_HUMAN	TGBAP2/TCB933 Pediatric pre-B cell acute lymphoblastic leukemia BAYlor-HGSC project-TGBA Homo sapiens cDNA clone TGBAP0383

Page 398 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7487	20169	33251	1.95	4.0E-89	BE762749.1	EST_HUMAN	QY5-NT0022-080600-219-q03 NT0022 Homo sapiens cDNA
11088	23768	37034	1.66	4.0E-89	AJ798672.1	EST_HUMAN	wd1603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:2348452 3'
2879	15046	28289	1.51	3.0E-89	AW676181.1	EST_HUMAN	EST398290 MAGE rescuesccc, MAGN Homo sapiens cDNA
7040	19731	32790	1.26	3.0E-89	AJ217358.1	EST_HUMAN	q117505.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:1844915 3'
10302	23148	36374	0.48	3.0E-89	AB002287.1	NT	Human mRNA for KIAA0299 gene, partial cds
10702	23393	36630	2.34	3.0E-89	N57357.1	EST_HUMAN	yw66a11.1 Soares_placenta_860weeks_2NH9P860W Homo sapiens cDNA clone IMAGE:249148 5' similar to SW-PI4K_HUMAN P42356 PHOSPHA IDYLINOSITOL 4-KINASE ALPHA;
123	13184	25832	0.87	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	13184	25833	0.87	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
359	13184	25832	1.65	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
359	13184	25833	1.55	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
517	13301	25933	3.17	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2883	15650	28293	1.53	2.0E-89	AJ222095.1	EST_HUMAN	q96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb-J04131
3540	19258	28946	1.01	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN) contains Alu repetitive element;
3540	19258	28947	1.01	2.0E-89	AA759149.1	EST_HUMAN	at70903.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320688 3'
4126	18857	29494	1.26	2.0E-89	AF098997.1	NT	Homo sapiens testis_NHT Homo sapiens cDNA clone 1320688 3'
4133	18875	29504	5.16	2.0E-89	X58742.1	NT	Homo sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4133	18875	29505	5.16	2.0E-89	X58742.1	NT	Homo sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4133	18875	29505	5.16	2.0E-89	X58742.1	NT	Homo sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4315	17054	29679	0.76	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4493	17199	29826	1.1	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5259	19065	30868	0.66	2.0E-89	BE541744.1	EST_HUMAN	60106506F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5393	18193	31418	1.61	2.0E-89	AB007546.1	NT	Homo sapiens gene for LEO12, complete cds
5702	18496	31418	0.63	2.0E-89	U03985.1	NT	Homo sapiens gene for LEO12, complete cds
6116	18894	31801	0.63	2.0E-89	AL163265.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7587	20237	33341	5.33	2.0E-89	U61004.1	NT	Homo sapiens chromosome 21 segment HS21C085
7835	20530	33657	3.07	2.0E-89	1142880.1	NT	Human GT24 (GT24) mRNA, partial cds
8316	21009	34146	1.02	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8152	21883	35052	0.6	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX6 related protein
9710	22381	35557	0.68	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1833 protein, partial cds
9710	22381	35557	0.68	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
9710	22381	35557	0.68	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5

Page 399 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11546	24036	37339	2.83	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11448	23216	38447	2.3	2.0E-48	5728867	NT	Homo sapiens hist domain and RLD 2 (HERC2), mRNA
11562	24181	37472	5.03	2.0E-86	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11718	24512	37636	2.11	2.0E-89	U10892.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11570	24169	37483	5.97	1.0E-98	BF168052.1	EST_HUMAN	h8r1d09.x1 NCI_CGAP_Ki671 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:064778 064778
11570	24169	37484	5.97	1.0E-89	BF168052.1	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
8126	20820	33956	1.57	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8126	20820	33957	1.57	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1041	13801	28459	2.23	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1042	13801	28459	2.19	8.0E-90	BE670561.1	NT	Homo sapiens chromosome 21 segment HS21C046
1307	15505	26731	3.78	8.0E-90	BE670561.1	EST_HUMAN	7a36003.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1307	15505	26732	3.78	8.0E-90	BE670561.1	EST_HUMAN	7a36003.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8498	21190	34293	0.55	8.0E-90	BE177830.1	EST_HUMAN	RC1-RT0598-120400-022-508 HT0598 Homo sapiens cDNA
10599	23293	36531	1.52	8.0E-90	A1222095.1	EST_HUMAN	qp96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN) contains Alu repetitive element;
10599	23293	36532	1.52	8.0E-90	A1222095.1	EST_HUMAN	qp96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN) contains Alu repetitive element;
10593	23639	36889	1.32	8.0E-90	AA705222.1	EST_HUMAN	28210.s1 Scores_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:481442 3'
10593	23639	36890	1.32	8.0E-90	AA705222.1	EST_HUMAN	28210.s1 Scores_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:481442 3'
816	13587		4.12	7.0E-90	AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAGNA1E) gene, exons 7-49, and partial cde, alternatively spliced
8323	21016		2.08	7.0E-90	AA78297.1	EST_HUMAN	al63208.s1 Scores_testis_NHT Homo sapiens cDNA clone 1375503 3'
8965	21656	34701	1.62	7.0E-90	BE982626.2	EST_HUMAN	601553537.1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3895824 3'
8965	21656	34702	1.62	7.0E-90	BE982626.2	EST_HUMAN	601553537.1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3895824 3'
10038	22984	35501	1.9	7.0E-90	H68846.1	EST_HUMAN	Y889604.s1 Scores_fetal_liver_spleen_NFLS_Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-CITC_HUMAN P11896 C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC ;
10038	22984	35502	1.9	7.0E-90	H68846.1	EST_HUMAN	Y889604.s1 Scores_fetal_liver_spleen_NFLS_Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-CITC_HUMAN P11896 C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC ;

Page 400 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10352	22899	36216	1.17	7.0E-60	BF525089.1	EST_HUMAN	6022071208F1 NC1 CGAP Brn54 Homo sapiens cDNA clone IMAGE:4214257 5'
4201	16942	29568	9.12	6.0E-60	8922398	NT	Homo sapiens hypothetical protein FLJ10338 (FLJ10338), mRNA
4201	16942	29569	9.12	6.0E-60	8922398	NT	Homo sapiens hypothetical protein FLJ10338 (FLJ10338), mRNA
5994	18979	31625	3.27	6.0E-60	U77700.1	NT	Homo sapiens HSCCN1 mRNA, partial cds
5994	18979	31626	3.27	6.0E-60	U77700.1	NT	Homo sapiens HSCCN1 mRNA, partial cds
8225	20919	34056	2.75	6.0E-60	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8225	20919	34057	2.75	6.0E-60	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
151	12963		19.84	5.0E-60	AB033344.1	NT	Homo sapiens TCEB gene, exon 1-10b
1170	13024	28588	3.08	5.0E-60	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1813	14553	27287	1.47	5.0E-60	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 (GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN)); contains Alu repetitive element
1813	14553	27288	1.47	5.0E-60	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 (GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN)); contains Alu repetitive element
2560	16274	28011	2.79	5.0E-60	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4503	17238	29871	2.05	5.0E-60	4508354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4822	17557	29892	0.98	5.0E-60	AL135549.1	EST_HUMAN	DKFZp762P1616 J1 762 (synonym: hmal2) Homo sapiens cDNA clone DKFZp762P1616 5'
5504	18302	31203	2.84	5.0E-60	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5606	18402	31318	1.31	5.0E-60	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5679	18302	31203	2.36	5.0E-60	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5679	18303	32407	0.74	5.0E-60	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934) mRNA
6631	19393	32408	0.74	5.0E-60	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934) mRNA
7114	19802	32867	2.04	5.0E-60	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
7114	19802	32867	2.04	5.0E-60	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
7463	20136	33228	9.01	5.0E-60	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
7780	20485	33609	0.44	5.0E-60	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
8192	20886	34025	5.08	5.0E-60	11346483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9096	21784	34950	0.58	5.0E-60	4826670	NT	Homo sapiens cadherin 18 (CDH18) mRNA
9576	22322	35416	1.06	5.0E-60	11419429	NT	Homo sapiens similar to actinucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
10161	22829	36044	0.58	5.0E-60	AF123503.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10312	22959	36178	0.5	5.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10312	22959	36178	0.5	5.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA

Page 401 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10344	22891	36209	9.16	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10402	23048	36284	0.84	6.0E-90	76820551	NT	Homo sapiens KIA03317 gene product (KIA03317), mRNA
10402	23048	36285	0.54	5.0E-90	7652051	NT	Homo sapiens KIA03317 gene product (KIA03317), mRNA
11731	24824	37648	2.41	5.0E-90	7682047	NT	Homo sapiens KIA03305 gene product (KIA03305), mRNA
12591	24048		2.08	5.0E-90	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
12841	24938		4.43	5.0E-90	AI523586.1	EST_HUMAN	af78105.x1 Barlebad, rat HPLRB8 Homo sapiens cDNA clone IMAGE:2128761 3'
295	13101	25742	1.93	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
295	13101	25743	1.93	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1004	13822	26482	3.28	4.0E-90	4503316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1684	14428	27125	8.08	4.0E-90	X68033.1	NT	H1 sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2892	16758	28405	0.98	4.0E-90	AF007544.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
3023	15789	28436	1.07	4.0E-90	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3023	15789	28437	1.07	4.0E-90	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4658	17343	30675	7.65	4.0E-90	D67675.1	NT	Homo sapiens DNA for arylidol precursor protein, complete cds
4743	17476	30109	2.17	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4768	17500	30123	2.33	4.0E-90	AB09887.1	NT	Homo probomom converting enzyme (NEC2) gene, exon 8
7751	20447	33570	1.08	3.0E-90	BF516168.1	EST_HUMAN	U1-HBW1-amyb-04-DJ1.s1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083939 3'
7751	20447	33571	1.08	3.0E-90	BF516168.1	EST_HUMAN	U1-HBW1-amyb-04-DJ1.s1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083939 3'
11630	24227	37651	17.81	3.0E-90	BE363833.1	EST_HUMAN	801395244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
11630	24227	37651	17.81	3.0E-90	BE363833.1	EST_HUMAN	801067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463834 5'
2100	13020	28662	4.71	2.0E-90	BE357913.1	EST_HUMAN	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1150	13005	28667	2.87	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1150	13005	28668	2.87	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3826	19577	29209	1.7	2.0E-90	A1138213.1	EST_HUMAN	qc5402.x1 Soares, placenta, 86weeks 2NBHPB29W/Homo sapiens cDNA clone IMAGE:1713410 3'
4840	17374	30008	1.05	2.0E-90	AB006827.1	NT	similar to SW-OLF3_MOUSE P23278 OLFATORY RECEPTOR OR3. ;
4853	17593	30208	7.31	2.0E-90	5728855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5595	18489	31410	4.86	2.0E-90	AW672688.1	EST_HUMAN	Homo sapiens GR92-related adaptor protein (GRAP) mRNA
9889	22341	35534	4.78	2.0E-90	11427320	NT	bc020153 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:075208 075208
9889	22341	35535	4.78	2.0E-90	11427320	NT	bc020153 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:075208 075208
9860	22510	35706	1.37	2.0E-90	AU118985.1	EST_HUMAN	HYPOTHETICAL 35.5 KD PROTEIN. ;
9889	22341	35534	4.78	2.0E-90	11427320	NT	Homo sapiens similar to lemlin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) [LOC83484], mRNA
9860	22510	35706	1.37	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to lemlin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) [LOC83484], mRNA
9860	22510	35706	1.37	2.0E-90	AU118985.1	EST_HUMAN	AJ0118855 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9860	22610	35707	1.37	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11477	23214	36446	2.8	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
270	13078	28720	4.55	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
365	15516	25805	1.38	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	15516	25805	1.43	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
369	13454	29098	2.32	1.0E-90	AJ237588.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
678	13454	29098	2.32	1.0E-90	AJ237588.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
679	13454	29098	2.32	1.0E-90	AJ237588.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	13487	28137	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	13487	28138	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1088	13946	28138	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1088	13946	28138	13.22	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1253	14033	28703	5.56	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1253	14033	28704	5.56	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1662	14408	27342	1.23	1.0E-90	BE379884.1	EST_HUMAN	801159503F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE351118 5'
1895	14632	27342	3.33	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC67187), mRNA
2858	15026	28271	8.46	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
4389	17126	29758	1.29	1.0E-90	AF187340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5589	18335	31295	2.59	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5746	18338	31490	0.96	1.0E-90	11428910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6473	19240	32240	0.57	1.0E-90	11418405	NT	Homo sapiens cytochrome P450, 51 (lanosterol 14-alpha-demethylase) (CYP51), mRNA
6973	19455	32475	0.65	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7204	19889	32968	0.84	1.0E-90	6006902	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7571	20240	33345	2.77	1.0E-90	11425768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 8 (SLC1A8), mRNA
8720	21412	34555	3.73	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9183	21863	35455	0.96	1.0E-90	AF163884.1	NT	Homo sapiens SVCA isoform (SNCA) gene, complete cds, alternatively spliced
9215	21894	35682	1.53	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9215	21894	35682	1.53	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
10557	22253	35063	1.9	1.0E-90	R25888.1	EST_HUMAN	Y94411.2 Soares infant brain T1B Homo sapiens cDNA clone IMAGE36477 5'
10897	23643	38989	1.76	1.0E-90	J04474.1	NT	Human branched chain alpha-keto acid dehydrogenase mRNA, 3' end
12680	24904	31001	1.49	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12680	24904	31002	1.49	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4172	19812	28542	6	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone a381 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1427	14174	28950	1.08	7.0E-91	AF033768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP50 mRNA, partial cds
8205	22039	34036	1.88	7.0E-91	11419234	NT	Homo sapiens melanin ring finger protein, 1 (UKRFL1), mRNA
10198	22846	35082	0.88	7.0E-91	AB04151.1	EST_HUMAN	CNMB1043-060289-076 BT043 Homo sapiens cDNA
3487	16223	28877	1.83	5.0E-91	AA702794.1	EST_HUMAN	Z88004.s1 Soares_fetal_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE-448015 3'
4480	17215	29840	11.73	5.0E-91	AU143539.1	EST_HUMAN	AU143539 789A1 Homo sapiens cDNA clone Y6AA1002087 5'
4480	17215	29841	11.73	5.0E-91	AU143539.1	EST_HUMAN	AU143539 789A1 Homo sapiens cDNA clone Y6AA1002087 5'
4757	17489	30116	0.97	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4757	17489	30117	0.97	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6519	19285	32289	1.25	5.0E-91	AB78995.1	EST_HUMAN	au4909.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE2518121 3' similar to SW-ASPG, FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYD)-L-ASPARAGINASE PRECURSOR, 1
8105	20789	33931	1.2	5.0E-91	BF314882.1	EST_HUMAN	601801624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8558	21350	34495	1.52	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLOBYF08 3'
8558	21350	34498	1.52	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLOBYF08 3'
12512	24919		1.74	5.0E-91	AI183566.1	EST_HUMAN	g97011.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MIR MIR repetitive element
3197	15660	28811	1.69	4.0E-91	AF155778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3197	15660	28812	1.69	4.0E-91	AF155778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
10848	23530	35775	4.49	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12094	24596	31082	1.98	4.0E-91	MT7994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838205) Homo sapiens cDNA clone HHCMC80 similar to Retrovirus-related gag polyprotein
12094	24596	31127	1.96	4.0E-91	MT7994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838205) Homo sapiens cDNA clone HHCMC80 similar to Retrovirus-related gag polyprotein
1613	14390	27049	3.07	3.0E-91	11430183	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1613	14390	27050	3.07	3.0E-91	11430183	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3334	16094	28748	1.62	3.0E-91	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3455	16211	28863	3.39	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3455	16211	28904	3.39	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3768	16520	29159	1.45	3.0E-91	AF04530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4551	17286	29915	3.79	3.0E-91	M30338.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5600	18395	31305	1.27	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5KD) (HE1), mRNA
6212	18937		2.48	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6488	19255	32256	5.82	3.0E-91	11497811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6468	19255	32257	6.82	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7538	20208	33306	4.97	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNL1B1) gene, exons 10 and 11
7538	20208	33307	4.97	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNL1B1) gene, exons 10 and 11
8669	21361	34509	2.58	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9185	21958	35023	2.83	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10803	22486	36723	1.41	3.0E-91	AB022179.2	NT	Homo sapiens ERM2 mRNA, complete cds
11160	23827	37105	1.98	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11160	23827	37106	1.86	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
12335	24749	31057	2	3.0E-91	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12667	17998	30488	4.35	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12667	17998	30490	4.35	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
47	12876	25601	5.08	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1223	13973	26945	6.31	1.0E-91	AW449746.1	EST_HUMAN	UHF-B13-alc-dT1-c-U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2735280 3'
5328	18131	30790	0.97	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6743	19577	32610	2.26	1.0E-91	BF348182.1	EST_HUMAN	60222038F1 NCI_CGAP_Brd67 Homo sapiens cDNA clone IMAGE:4157804 5'
6743	19577	32611	2.26	1.0E-91	BF348182.1	EST_HUMAN	60222038F1 NCI_CGAP_Brd67 Homo sapiens cDNA clone IMAGE:4157804 5'
12245	25540	32611	1.35	1.0E-91	H15212.1	EST_HUMAN	Ym3Y9603.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:46587 5'
1219	13970	26639	9.06	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1219	13970	26640	9.06	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5120	17833	30454	0.8	9.0E-92	AB020540.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5376	18178	30897	4.86	9.0E-92	J03007.1	NT	Human Na ⁺ /K ⁺ ATPase alpha-subunit mRNA, partial cds
5518	18316	31217	2.83	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6362	19132	32127	4.03	9.0E-92	AF310103.1	NT	Homo sapiens NALP1 mRNA, complete cds
7756	20452	33576	7.17	9.0E-92	AJ250568.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
7756	20452	33577	7.17	9.0E-92	AJ250568.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8272	20966	34107	0.82	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
8272	20966	34108	0.82	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
9174	21844	35010	1.95	9.0E-92	11422086	NT	Homo sapiens bromodomain A-initiated guanine nucleotide-exchange protein 2 (BIG2), mRNA
11161	23828	37106	1.85	9.0E-92	7706866	NT	Homo sapiens RNBB (RNBB), mRNA
91	12317	25554	2.25	8.0E-92	W2367.1	EST_HUMAN	203 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
279	13086	25728	3.29	8.0E-92	BE396963.1	EST_HUMAN	BC127351F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614887 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5041	17760	30374	0.95	8.0E-92	AW157571.1	EST_HUMAN	eu83h08.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:000302 060032 KIA0555 PROTEIN, contains element MER22 repetitive element ;
5308	18113	30771	0.65	8.0E-92	AB048820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
5411	18210	30918	0.97	8.0E-92	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
8451	19219	32217	1.31	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
8455	19223	32222	0.92	8.0E-92	AF175428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant: 1 (REV3L) mRNA, complete cds
7960	20085	34152	0.55	8.0E-92	11416981	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8324	21017	34153	3.91	8.0E-92	U04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8324	21017	34153	3.91	8.0E-92	U04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8422	21115	34263	0.58	8.0E-92	11428508	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
8950	21651	34801	2.82	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0651 protein, partial cds
9925	22573	35771	1.18	8.0E-92	Y13828.1	NT	Homo sapiens mRNA for MBNL protein
10707	23397	36036	3.2	8.0E-92	AF074383.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11333	24024	37229	1.81	8.0E-92	4503340	NT	Homo sapiens dihydropyrimidinase 5-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
23	12851	25466	1.82	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
64	12892	25525	1.01	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
230	15538	25680	0.87	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0753 protein, partial cds
230	15538	25681	0.87	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0755 protein, partial cds
577	13357		1.34	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1257	14006	26675	1.89	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2184	14913	27645	2.27	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2184	14913	27646	2.27	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2868	15282	28020	1.46	7.0E-92	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2728	15435	28171	2.2	7.0E-92	9005738	NT	Homo sapiens NRAS-related gene (DYS155E), mRNA
2757	15492	28205	1.23	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3340	17877	28750	1.06	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3340	17877	28751	1.06	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4647	17292	28912	2.59	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2890 nt]
4547	17292	28913	2.59	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2890 nt]

Page 406 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	17671	30280	0.98	7.0E-92	AL183281.2	NT	Homo sapiens chromosome 21 segment H521C08f1
5180	17989	30304	0.05	7.0E-92	AA446209.1	EST_HUMAN	zovBcd12c1 J Soares, testis_NHT Homo sapiens cDNA clone IMAGE:78176 5'
1882	15478	14523	1.28	3.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3905018 5'
2768	15473	29215	1.6	3.0E-92	BE509714.1	EST_HUMAN	601601242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5785	18577	31506	2.6	3.0E-92	AA376538.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
10984	23555	35594	2.72	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
10984	23555	35595	2.72	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
10984	23555	35596	2.72	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
174	12869	25627	1.68	2.0E-92	4803188.NT	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
174	12869	25628	3.67	2.0E-92	11423946.NT	EST_HUMAN	Homo sapiens hypodermal protein DJ462023.2 (DJ462023.2), mRNA
174	12869	25629	3.57	2.0E-92	11423946.NT	EST_HUMAN	Homo sapiens hypodermal protein DJ462023.2 (DJ462023.2), mRNA
732	13508	28162	1.33	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	13508	28163	1.33	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	13508	28163	1.33	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1709	14452		2.22	2.0E-92	S78653.1	NT	mip-mas-related Human, Genomic, 2416 nt [3]
1929	14665	27378	2.36	2.0E-92	AB181119.1	EST_HUMAN	wk27007.xt NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR-Q12844
1929	14665	27378	2.36	2.0E-92	AB181119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1929	14665	27379	2.38	2.0E-92	AB181119.1	EST_HUMAN	wk27007.xt NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR-Q12844
2041	14175	27504	5.58	2.0E-92	4500880.NT	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2694	15374	28113	19.2	2.0E-92	6912457.NT	NT	Homo sapiens syndecan 4 (amphiphysin, nudosin) (SDCA4) mRNA
3600	16333	28992	2.81	2.0E-92	AF231916.1	NT	Homo sapiens calnexin binding protein 1 (KIAA0330), mRNA
3600	16333	28993	2.81	2.0E-92	AF231916.1	NT	Homo sapiens chromosome 21 unknown mRNA
3600	16333	28993	2.81	2.0E-92	AF231916.1	NT	Homo sapiens chromosome 21 unknown mRNA
3674	16427	29068	5.57	2.0E-92	5803180.NT	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4256	19997	29926	1.23	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (ε-1), complete retrieval segment
4506	17654		2.51	2.0E-92	AL040437.1	EST_HUMAN	DKFPZ-43C0414_T1 434 (synonym: hies3) Homo sapiens cDNA clone DKFPZ-43C0414 5'
5673	18408		0.64	2.0E-92	AF016535.1	NT	Homo sapiens F-glycoprotein (mdr1) mRNA, complete cds
6209	19994		0.6	2.0E-92	4504756.NT	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA
6209	19994		0.6	2.0E-92	4504756.NT	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA
6517	19292	32285	3.03	2.0E-92	AB029891.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7384	20045		0.61	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7387	20045		0.78	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
8754	21446	34594	1.69	2.0E-92	AJ394074.1	EST_HUMAN	hd02n02.k1 Soares, NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR-O2271
10556	23350	36557	4.93	2.0E-92	11434800.NT	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
10556	23350	36557	4.93	2.0E-92	11434800.NT	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA

Page 407 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10930	23610	36859	1.46	2.0E-92	11434759	NT	Homo sapiens zinc finger protein 198 (ZNF198), mRNA
10978	23683	36905	2.54	2.0E-92	5903103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
12439	24809	31046	2.69	2.0E-92	AB023016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12697	16374	28113	2.61	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
1842	14590	27294	1.13	1.0E-92	R78078.1	EST_HUMAN	Y80608.1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:145574 5'
1842	14590	27295	1.13	1.0E-92	R78078.1	EST_HUMAN	Y80608.1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:145574 5'
2066	14798	27525	8.83	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA
8145	20839	33971	1.29	1.0E-92	BE439625.1	EST_HUMAN	HTM1-28BF HTMT Homo sapiens cDNA
							Q15022.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
							Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 contains Alu repetitive element; contains element
9062	21751	34910	3.82	1.0E-92	A1380356.1	EST_HUMAN	MER17 repetitive element;
9062	21751	34911	3.82	1.0E-92	A1380356.1	EST_HUMAN	Ig015022.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
2023	14758	27497	3	9.0E-93	AU121861.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 contains Alu repetitive element; contains element
							MER17 repetitive element;
2035	14770		5.48	9.0E-93	AA316723.1	EST_HUMAN	EST198414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2653	15993		1.45	9.0E-93	AF223391.1	NT	601281667.1 NIH MGSC 44 Homo sapiens cDNA clone IMAGE:3603832 5'
3602	16356	26995	1.11	9.0E-93	BE388571.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
11645	24242		9.71	9.0E-93	11418826	NT	U1-H-B10-aah-H-06-Q-U1.x1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6351	19121	32112	0.58	8.0E-93	AW014042.1	EST_HUMAN	U1-H-B10-aah-H-06-Q-U1.x1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6351	19121	32113	0.58	8.0E-93	AW014042.1	EST_HUMAN	60140521.F1 NIH MGSC 68 Homo sapiens cDNA clone IMAGE:3603908 5'
6496	19292	32263	2.81	8.0E-93	BF036364.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
239	13048	25687	9.92	7.0E-93	AF231919.1	NT	Homo sapiens T-cell lymphoma virus and metastasis 1 (TIAM1), mRNA
3073	15639	28492	0.84	9.0E-93	11626178	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
6581	19344	32358	1.02	9.0E-93	AB033093.1	NT	Homo sapiens PTH-responsive osteocalcin BT protein (B1) mRNA, complete cds
6817	19478	32501	1.12	9.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA0911 protein, partial cds
1359	14107	26922	3.51	5.0E-93	AB014511.1	NT	w60908.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2314670 3'
1366	14133	28807	7.28	6.0E-93	A1674184.1	EST_HUMAN	w60908.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2314670 3'
1368	14133	28808	7.28	6.0E-93	A1674184.1	EST_HUMAN	Human skeletal muscle 1.3 kb mRNA for tropomyosin
3227	15990	29643	2.98	5.0E-93	X04201.1	NT	Human somatic cytochrome c (HCT1) processed pseudogene, complete cds
5710	18503	31426	1.01	5.0E-93	M22878.1	NT	

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6018	18789		1.02	5.0E-93	AF045555.1	NT	Homo sapiens wiser1 (WBSQR1) and wiser6 (WBSQR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7514	20280	33388	3.6	5.0E-93	AF087136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8503	21195	34338	1	5.0E-93	4557528	NT	Homo sapiens discs, large (Discocephala) homolog 2 (chapsyn-110) (DLG2) mRNA
8503	21195	34359	1	5.0E-93	4557528	NT	Homo sapiens discs, large (Discocephala) homolog 2 (chapsyn-110) (DLG2) mRNA
9523	22176	35360	2.16	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec37B-1 mRNA, alternatively spliced, complete cds
9707	22358	35554	1.25	5.0E-93	60327166	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
9870	22618	35821	1.9	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10727	23416	36666	2.25	5.0E-93	11436599	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
12343	25052	30959	2.15	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
12805	25052	30959	1.44	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
88	12912		6.52	4.0E-93	AA456933.1	EST_HUMAN	2550409.11 Scarsa, testis, NIH: Homo sapiens cDNA clone IMAGE:786668 3' similar to SW:CLPA_FAT
432	13218	25863	1.39	4.0E-93	4557879	NT	P37387 CALPONIN, ACIDIC ISOFORM 1
432	13218	25864	1.39	4.0E-93	4557879	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
755	13527	26185	1.67	4.0E-93	7657454	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
755	13527	26187	1.67	4.0E-93	7657454	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
1160	13914	26577	1.53	4.0E-93	8623658	NT	Homo sapiens pascadillo (zefralfish) homolog 1, containing BRCT domain (PES1) mRNA
1870	14708	27424	4.3	4.0E-93	AF047677.1	NT	Homo sapiens pascadillo (zefralfish) homolog 1, containing BRCT domain (PES1) mRNA
2241	14969	27707	0.88	4.0E-93	AF157476.1	NT	Homo sapiens hypophyseal protein PLJ20731 (PLJ20731) mRNA
2397	15116	27855	1.65	4.0E-93	AL163301.2	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 In Inton 5
3553	16309	28958	0.73	4.0E-93	7705398	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4026	16771	29403	1.67	4.0E-93	4504654	NT	Homo sapiens chromosome 21 segment HS21C101
							Homo sapiens tumor antigen SLP-8p (HSC8) mRNA
							Homo sapiens Interleukin 18 receptor 1 (IL18R1) mRNA
5557	18354	31284	4.9	4.0E-93	T46964.1	EST_HUMAN	Y694c12.11 Stetigene liver (#637224) Homo sapiens cDNA clone IMAGE:76838 5' similar to similar to SP:AA4391 AA4391: SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11078	23748	37023	6.17	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKX Homo sapiens cDNA clone GKXDR07 5'
3543	16396	29036	7.35	3.0E-93	BF690030.1	EST_HUMAN	602246554F1 NIH MGCC 62 Homo sapiens cDNA clone IMAGE:4332096 5'
3543	16396	29036	7.35	3.0E-93	BF690030.1	EST_HUMAN	602246554F1 NIH MGCC 62 Homo sapiens cDNA clone IMAGE:4332096 5'
4210	16951		1.31	3.0E-93	AF225865.1	NT	Homo sapiens tanalin mRNA, complete cds
5697	18491	31412	0.79	3.0E-93	AI553853.1	EST_HUMAN	It22903.x1 NC1 CGAP Brn28 Homo sapiens cDNA clone IMAGE:2169076 3'
5697	18491	31413	0.79	3.0E-93	AI553853.1	EST_HUMAN	It22903.x1 NC1 CGAP Brn28 Homo sapiens cDNA clone IMAGE:2169076 3'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6488	19235	32236	1.21	3.0E-93	11426182	NT	Homo sapiens GGN6 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCHL2), mRNA
10708	23394	36631	4.27	3.0E-93	AB24829.1	EST_HUMAN	W62805.x1 NCL CGAP, GC8 Homo sapiens cDNA clone IMAGE:230489 3'
185	12988	25937	7.61	2.0E-93	AB016610.1	NT	Chlorococcus seethiens mRNA for ribosomal protein S4X, complete cds
185	12988	25938	7.61	2.0E-93	AB016610.1	NT	Chlorococcus seethiens mRNA for ribosomal protein S4X, complete cds
315	13119	25758	9.36	2.0E-93	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085
316	13119	25758	9.36	2.0E-93	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085
1810	14357	27046	1.33	2.0E-93	AF226896.1	NT	Homo sapiens tetrin mRNA, complete cds
2128	14857	27937	1.33	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2490	16207	27949	1.66	2.0E-93	BE26382.1	EST_HUMAN	60117695F1 NIH, MGC, 18 Homo sapiens cDNA clone IMAGE:3358220 5'
5332	18135	30764	5.42	2.0E-93	AW984385.1	EST_HUMAN	EST376458 IMAGE resequences, MAGH Homo sapiens cDNA
5342	18145	30824	0.86	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5455	18254		1.04	2.0E-93	BF361489.1	EST_HUMAN	QV8-HT0513-280300-126-h04 HT0513 Homo sapiens cDNA
5550	18347	31256	1.13	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC31318), mRNA
5555	18362	31270	0.65	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14, Homo sapiens cDNA clone 146
6594	19347		1.1	2.0E-93	AW60202.1	EST_HUMAN	U1HF-BND-ales-g-09-D-J1.1 NIH, MGC, 60 Homo sapiens cDNA clone IMAGE:3076329 5'
11014	23686	35946	1.27	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11014	23686	35947	1.27	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12233	24666		2.84	2.0E-93	AA126735.1	EST_HUMAN	Z12670.61 Soares, pregnant uterus, NBHPU Homo sapiens cDNA clone IMAGE:303348 3'
12314	24736		2.17	2.0E-93	L41825.1	NT	Homo sapiens GYP17 gene, 5' end
12571	24899		10.79	2.0E-93	BF03527.1	EST_HUMAN	60145853F1 NIH, MGC, 56 Homo sapiens cDNA clone IMAGE:3862086 5'
101	12827	25664	2.28	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
101	12827	25665	2.28	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
505	13269	25923	4.25	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (Q132819 C1.1), mRNA
588	13368	25994	4.57	1.0E-93	AI146755.1	EST_HUMAN	oy64b08.x1 NCL CGAP, CIL1 Homo sapiens cDNA clone IMAGE:1672603 3' similar to TR.Q62384.Q62384
852	13822	26292	9.91	1.0E-93	D87075.1	NT	ZINC FINGER PROTEIN, .
1144	13899	26560	2.6	1.0E-93	4903872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1215	13955	26632	7.65	1.0E-93	8623270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67KD) (GAD1), transcript variant GAD87, mRNA
1215	13955	26633	7.65	1.0E-93	8623270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1322	14071	26744	1.5	1.0E-93	AB04783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1324	14073	26746	0.89	1.0E-93	AF167706.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2337	15061	27798	1.33	1.0E-93	AF231981.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
							Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds

Page 410 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2460	15164	27024	1.7	1.0E-93	AF055046.1	NT	Homo sapiens MHC class 1 region
2511	15228		0.96	1.0E-93	AL131200.1	NT	Novel human gene mapping to chromosome 1
2825	14022	26889	1.47	1.0E-93	BE297389.1	EST_HUMAN	601177688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965.5
2825	14022	26860	1.47	1.0E-93	BE297389.1	EST_HUMAN	601177688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965.5
2834	15700	28349	7.48	1.0E-93	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3210	15973		1.27	1.0E-93	AF231981.1	NT	Homo sapiens long chain polynaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4395	17132	29763	2.6	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5479	18278	31173	2.38	1.0E-93	U76509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5479	18278	31174	2.38	1.0E-93	U76509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5678	18472	31389	0.96	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
5825	18614	31548	10.32	1.0E-93	4557702	NT	Homo sapiens neurofibronin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6104	18882	31680	1.4	1.0E-93	7662241	NT	Homo sapiens KIAA0572 gene product (KIAA0572), mRNA
6694	19611	32650	2.01	1.0E-93	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7150	19837	32607	3.49	1.0E-93	D42072.1	NT	Human mRNA for NF1 N1sform-exon11, complete cds
8159	20852	33984	2.54	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8441	21133	34269	1.2	1.0E-93	Y10163.1	NT	H. sapiens mRNA for MEK1D protein
8547	21293	34382	1.38	1.0E-93	AF192032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKG) mRNA, complete cds
9352	20423	33542	1.79	1.0E-93	AB040918.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
9356	20427	33546	1.28	1.0E-93	AF081585.1	NT	Human Prk44 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9488	22141	33319	8.29	1.0E-93	X13474.1	NT	Human Prk44 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9488	22141	35320	8.29	1.0E-93	X13474.1	NT	Human Prk44 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9625	22276	35467	0.79	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10045	22993	33910	0.92	1.0E-93	11433546	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12487	24848		1.84	1.0E-93	AJ29325.1	NT	Homo sapiens GGT1 gene, exon 1
12568	24895		2.64	1.0E-93	11417865	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12739	25391		1.49	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10492	23138		1.03	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3944	16954	28933	1.63	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5293	18088	30747	4.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5293	18088	30748	4.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5957	18739	31693	4.22	5.0E-94	AA72434.1	EST_HUMAN	zg87g05.s1 Soares_fetalHeart_NHH19W Homo sapiens cDNA clone IMAGE:409594.3

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6910	19848	32693	1.29	5.0E-94	AI15903.1	EST_HUMAN	Q183405.s1 Soares, total_fetus Nb2H-F9_9w Homo sapiens cDNA clone IMAGE:1623565 3'
8537	21229	34371	1.11	5.0E-94	BF529115.1	EST_HUMAN	502042163F1 NCI CGAP_Brm97 Homo sapiens cDNA clone IMAGE:4180023 5'
12209	25394	30619	0.95	5.0E-94	T80398.1	EST_HUMAN	y499004.s1 Soares fetal liver spleen NFILS Homo sapiens cDNA clone IMAGE:116239 3'
12758	28017		1.5	5.0E-94	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12761	25021		1.86	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160KD subunit (CPSF1), mRNA
1834	14573		2.64	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein, L27 mRNA, complete cds
2682	16372	28111	0.92	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3661	18414	29053	1.38	4.0E-94	AW197851.1	EST_HUMAN	x189112.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3661	18414	29054	1.38	4.0E-94	AW197851.1	EST_HUMAN	x189112.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4659	17403	30038	2.87	4.0E-94	AI591312.1	EST_HUMAN	tw11110.x1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2289403 3' similar to TR.Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE 1
6376	19145	32143	1.82	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6376	19145	32144	1.82	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6812	19473		1.18	4.0E-94	L27988.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11431	23108	39420	1.5	4.0E-94	11548782	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
597	13375	26005	1.44	3.0E-94	AB022785.1	NT	Homo sapiens A3H2L gene, complete cds, similar to Drosophila eat2 gene
704	13479	26127	0.88	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1733	14475	27173	1.19	3.0E-94	AF167708.1	NT	Homo sapiens cyclase-rich repeat-containing protein S52 precursor, mRNA, complete cds
1733	14475	27174	1.19	3.0E-94	AF167706.1	NT	Homo sapiens cyclase-rich repeat-containing protein S52 precursor, mRNA, complete cds
1765	14507	27208	2.91	3.0E-94	4857568	NT	Homo sapiens EYA binding protein t300 (EP300) mRNA
2073	14805	27534	1.27	3.0E-94	11427779	NT	Homo sapiens hepatic leukemia factor (HLF), mRNA
2073	14805	27536	1.27	3.0E-94	11427779	NT	Homo sapiens hepatic leukemia factor (HLF), mRNA
4168	16806	29534	0.83	3.0E-94	AA484805.1	EST_HUMAN	zw6308.r1 Soares, total_fetus Nb2H-F9_9w Homo sapiens cDNA clone IMAGE:774762 5'
5595	18390	31301	3.41	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6059	18639	31800	1.33	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6360	19130	32125	4	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7698	20369	33473	1.7	3.0E-94	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8098	20762	33923	1.18	3.0E-94	AF152009.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8486	21178	34322	4.35	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
8482	22145	35326	5.23	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-L mRNA, complete cds
11043	22713	35983	3.26	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11679	24274	37956	1.84	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9853	22305	35501	0.7	2.0E-94	AI910393.1	EST_HUMAN	w30H11.x1 NCI CGAP Cg18 Homo sapiens cDNA clone IMAGE:2391813 3'
9853	22305	35502	0.7	2.0E-94	AI910393.1	EST_HUMAN	w30H11.x1 NCI CGAP Cg18 Homo sapiens cDNA clone IMAGE:2391813 3'
144	12859	28601	1.94	1.0E-94	BE265714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3088	15951	28492	2.07	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3088	15951	28493	2.07	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4328	17055	28604	1.7	1.0E-94	9506892	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20745), mRNA
5982	18765	31727	0.64	1.0E-94	AE000289.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6173	18950	31822	0.73	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314.1 434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:45053 5'
6182	18959	31933	0.72	1.0E-94	AB0270.1	EST_HUMAN	J87602.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
6426	19194	32190	0.88	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCC9F05 5'
8012	20707	33535	0.63	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8012	20707	33537	0.63	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9155	21888	35054	2.76	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9887	22339	35533	2.04	1.0E-94	BE780478.1	EST_HUMAN	601488748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872069 5'
11000	23673	35929	3.08	1.0E-94	U65690.1	NT	Homo sapiens IL-1 receptor antagonist IL-1RA (IL-1RN) gene, alternatively spliced forms, complete cds
11288	23948	37245	2.82	1.0E-94	AI272244.1	EST_HUMAN	ap22a02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1859122 3' similar to TR_Q62845
11754	24345	37675	1.72	1.0E-94	11418871	NT	Q92845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, mRNA
12330	12959	25601	1.45	1.0E-94	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12608	12959	25601	1.51	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1459	14206	26892	1.93	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3153	15916	28561	1.45	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3153	15916	28562	1.45	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5320	18123	30781	1.33	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5320	18123	30782	1.33	9.0E-95	X82569.1	NT	Musculus glyT1 gene (exons 1c and 2)
8320	18123	30782	1.33	9.0E-95	X82569.1	NT	Musculus glyT1 gene (exons 1c and 2)
8150	20844	33974	1.77	8.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4409	17235	29866	3.18	8.0E-95	AI700988.1	EST_HUMAN	w60e04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
4489	17235	29897	3.18	8.0E-95	AI700988.1	EST_HUMAN	w60e04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
6849	19548	32578	0.76	8.0E-95	11419376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7141	19828	32897	1.76	8.0E-95	11425529	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7141	19828	32898	1.76	8.0E-95	11425529	NT	Homo sapiens proteasome (prosome, macropain) 28S subunit, non-ATPase, 11 (PSMD11), mRNA
7141	19828	32899	1.76	8.0E-95	11425529	NT	Homo sapiens proteasome (prosome, macropain) 28S subunit, non-ATPase, 11 (PSMD11), mRNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8097	20791	33922	1.97	8.0E-05	AF032897.1	NT	Homo sapiens pobastium charnel subunit (HERG-3) mRNA, complete cds
8285	22019	35187	2	8.0E-05	11420944	NT	Homo sapiens KIA00255 gene product (KIA00255), mRNA
9265	22019	35188	2	8.0E-05	11420944	NT	Homo sapiens KIA00255 gene product (KIA00255), mRNA
9748	22309	35604	3.1	8.0E-05	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH1) mRNA
9778	22330		2.94	8.0E-05	AB037818.1	NT	Homo sapiens mRNA for KIA1395 protein, partial cds
10135	22763	35994	0.8	8.0E-05	9849523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila homolog) (EGR2), mRNA
10813	23077	35546	1.3	8.0E-05	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11468	24069	37377	1.86	8.0E-05	10984024	NT	Homo sapiens HGF-binding transcription factor Zhangfei (ZF), mRNA
12535	24870		12.4	8.0E-05	AA02058.1	EST_HUMAN	zab401 at Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.11 L1 repetitive element;
289	13077	25718	32.81	7.0E-05	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
289	13077	25719	32.81	7.0E-05	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4333	17072	29701	5.18	7.0E-05	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4380	17117		1.3	7.0E-05	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C04.6
91177	21805	34971	1.31	4.0E-05	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
9356	18159	30842	1.88	3.0E-05	BFG26041.1	EST_HUMAN	602071146F1 NCI CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4214147 5'
5888	25071	31284	0.83	3.0E-05	45033564	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7268	19952	33027	1.51	3.0E-05	AW658121.1	EST_HUMAN	EST370191 MAGE resequenced, MAGE Homo sapiens cDNA
7268	19952	33028	1.51	3.0E-05	AW658121.1	EST_HUMAN	EST370191 MAGE resequenced, MAGE Homo sapiens cDNA
8278	20972	34113	0.55	3.0E-05	AW157233.1	EST_HUMAN	ag93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783789 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1];
8278	20972	34114	0.55	3.0E-05	AW157233.1	EST_HUMAN	ag93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783789 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1];
9255	21834	35107	1.89	3.0E-05	7692289	NT	TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1];
9255	21834	35108	1.89	3.0E-05	7692289	NT	Homo sapiens KIA00763 gene product (KIA00763), mRNA
9847	22209	35495	0.73	3.0E-05	BIF213446.1	EST_HUMAN	Homo sapiens KIA00763 gene product (KIA00763), mRNA
10782	23475	39716	1.49	3.0E-05	R83150.1	EST_HUMAN	60184521F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4070451 5'
1339	14385	27072	2.31	2.0E-05	7682027	NT	Yp87a11.1 Soares fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:194468 5'
1639	14385	27073	2.31	2.0E-05	7682027	NT	Homo sapiens KIA00255 gene product (KIA00255), mRNA
							Homo sapiens KIA00255 gene product (KIA00255), mRNA
							Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1834	14659	27384	2.51	2.0E-05	4507512	NT	
1937	14872	27388	1.92	2.0E-05	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3958852 5'
2428	15147	27880	2.22	2.0E-05	5453865	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2428	15147	27881	2.22	2.0E-05	5453865	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2468	15188	27625	3.25	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2517	15233	27973	1.95	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3155	15233	28564	1.96	2.0E-95	AF015452.1	NT	Homo sapiens Ursulin-gamma mRNA, complete cds
3552	15307	28566	3.07	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51165), mRNA
3552	15307	28957	3.07	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51165), mRNA
3605	16338	28998	1.29	2.0E-95	AB037607.1	NT	Homo sapiens mRNA for KIAA1366 protein, partial cds
3732	16485	29122	0.69	2.0E-95	AI090284.1	EST_HUMAN	qim01.c02.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1680646 3' similar to WP.T23G7.4
4328	17087	29695	1.32	2.0E-95	7657185	NT	CE03705
4478	17701	30303	2.72	2.0E-95	7661979	NT	Homo sapiens hypothelical protein (HS22B1A), mRNA
5392	18192	30884	4.21	2.0E-95	7705764	NT	Homo sapiens KIAA0197 gene product (KIAA0187), mRNA
5392	18192	30885	4.21	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51056), mRNA
5611	18407	31319	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5611	18407	31320	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5651	18446	31360	0.7	2.0E-95	11522583	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6051	18831	31794	5.04	2.0E-95	M59724.1	NT	Human muscle-type phosphotransferase (PFK-M) gene, exon 7
6358	19126	32122	1.16	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6358	19126	32123	1.16	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6478	19243	32243	2.45	2.0E-95	AF23737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6698	19593	32617	1.82	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9041	21731	34866	1.08	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10260	22926	36142	0.94	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10624	23317	36557	2.48	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
11700	24295	37620	3.02	2.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11700	24295	37621	3.02	2.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12289	24724	31055	2.3	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12688	24980	30994	4.66	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5527	18325	31226	8.41	1.0E-95	AA284651.1	EST_HUMAN	z23h04.1 Soares ovary tumor NHHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
5527	18325	31227	8.41	1.0E-95	AA284651.1	EST_HUMAN	z23h04.1 Soares ovary tumor NHHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7414	20091	33176	4.3	1.0E-98	BF370000.1	EST_HUMAN	RC8-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
7414	20091	33176	4.3	1.0E-98	BF370000.1	EST_HUMAN	RC8-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8094	20788	33520	1.49	9.0E-98	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
8424	18223		2.71	8.0E-98	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-068 LT0019 Homo sapiens cDNA
3889	18639	29278	0.74	7.0E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3478	16232	28896	20.13	8.0E-98	M28873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3' end
5552	18349	31259	0.74	8.0E-98	11422642	NT	Homo sapiens eukaryotic transferase 6 (N-acetylglucosaminidase alpha 2,3-aldyltransferase) (SIAT6), mRNA
11534	24134	37439	3.36	6.0E-98	7862289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11534	24134	37440	3.36	6.0E-98	7862289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11584	24183	37498	2.05	6.0E-98	8223839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11769	24390	37692	1.83	6.0E-98	7862289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11769	24390	37693	1.83	6.0E-98	7862289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
312	13116	26764	2.74	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
822	13592	26260	4.08	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
822	13592	26261	4.08	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2824	15336		1.43	5.0E-96	11416787	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
4848	17576		1.39	5.0E-96	X60812.1	NT	H. sapiens DNA for monomine oxidase type A (7) (partial)
6853	18318	32324	1.15	6.0E-96	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6884	19601	32539	5.18	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6884	19601	32840	5.18	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6923	19639	32706	0.71	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0660 protein, partial cds
7415	20092	33177	1.88	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8005	20700	33828	1.35	5.0E-96	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8005	20700	33829	1.35	5.0E-96	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
11793	24393	37716	12.32	3.0E-96	H68658.1	EST_HUMAN	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4169	16598		4.24	2.0E-96	4503088	NT	Y87M12.1 Soares fetal liver spliced INFLS Homo sapiens cDNA clone IMAGE:212327 5'
406	13181		0.91	2.0E-96	AL163248.2	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
730	13504	28195	4.24	2.0E-96	BE149074.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4708	17440	30072	1.89	2.0E-96	BE149074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7361	20042	33120	0.62	2.0E-96	BF369731.1	EST_HUMAN	QVA-GN0120-250900-427-512 GN0120 Homo sapiens cDNA
7361	20042	33121	0.62	2.0E-96	BF369731.1	EST_HUMAN	QVA-GN0120-250900-427-512 GN0120 Homo sapiens cDNA
8878	21570		5.63	2.0E-96	AV689461.1	EST_HUMAN	AV088451 OKC Homo sapiens cDNA clone GKCFMD07 5'
12009	24643		2.81	2.0E-96	AV249440.1	EST_HUMAN	12819351 SpRime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:281935 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
608	13386	26016	2.6	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
608	13386	26017	2.6	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
655	13433	26074	3.38	1.0E-06	Y18890.1	NT	Human endogenous retrovirus Type K (HERV-K), gag, pol and env genes
1774	14616	27216	2.56	1.0E-06	AW850504.1	EST_HUMAN	EST1387124-MAGE sequences, MAGE Homo sapiens cDNA
1774	14616	27217	2.59	1.0E-06	AW850504.1	EST_HUMAN	EST1387124-MAGE sequences, MAGE Homo sapiens cDNA
2262	15527	27729	1.08	1.0E-06	U51472.2	NT	Felis catus superfast myosin heavy chain (abMyHC) mRNA, complete cds
6569	17946	30541	1.3	1.0E-06	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6849	19431	32447	0.67	1.0E-06	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8111	20805	33938	1.24	1.0E-06	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8111	20805	33939	1.24	1.0E-06	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8516	21308	34450	20.66	1.0E-06	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8749	21441	34588	2.09	1.0E-06	AF274953.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10059	22707	35924	1.24	1.0E-06	AB033118.1	NT	Homo sapiens mRNA for KIAA1260 protein, partial cds
10059	22707	35925	1.24	1.0E-06	AB033118.1	NT	Homo sapiens mRNA for KIAA1260 protein, partial cds
11999	13388	26016	1.97	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
11999	13388	26017	1.97	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
7457	20131		2.6	6.0E-07	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
8332	21524	34670	0.69	6.0E-07	BE868012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE3625133 5'
8332	21524	34671	0.69	6.0E-07	BE868012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE3625133 5'
10467	23143	35369	0.57	6.0E-07	AA320332.1	EST_HUMAN	EST122672 Adipose tissue, while II Homo sapiens cDNA 5' end
10467	23143	35370	0.57	6.0E-07	AA320332.1	EST_HUMAN	EST122672 Adipose tissue, while II Homo sapiens cDNA 5' end
11382	23989	37290	1.46	6.0E-07	X15804.1	NT	Human mRNA for alpha-actinin
7913	20608	33739	1.91	5.0E-07	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
8042	20736	35869	11.79	5.0E-07	AA418028.1	EST_HUMAN	z67a12.31 Scores_NHMPU_S1 Homo sapiens cDNA clone IMAGE767756 3' similar to TR-G1304125
9574	22227	35412	2.66	5.0E-07	BF154812.1	EST_HUMAN	G1304125 PMS4-MRNA
11535	24135	37441	1.98	5.0E-07	BE1148597.1	EST_HUMAN	RCO-BT0812-250600-032-a09 BT0812 Homo sapiens cDNA
11535	24135	37442	1.98	5.0E-07	BE1148597.1	EST_HUMAN	MRO-HT0241-150500-010-B02 HT0241 Homo sapiens cDNA
918	13985	26349	1.59	4.0E-07	BE000436.1	EST_HUMAN	GNO-H1008-170300-238-a09 BN0108 Homo sapiens cDNA
928	13985	26369	1.04	4.0E-07	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
928	13985	26369	1.04	4.0E-07	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1803	14640	27349	1.07	4.0E-07	5433372	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA

Page 417 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5478	18277	31172	0.61	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
5765	18596	31482	0.95	4.0E-97	U08002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (NMR2A) mRNA; complete cds
5795	18566	31483	0.95	4.0E-97	U08002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (NMR2A) mRNA; complete cds
6725	18559	32590	8.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6725	18559	32591	8.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6921	19657	32703	1	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
6988	19450	32498	1.05	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
9039	20731	33663	0.57	4.0E-97	4657708	NT	Homo sapiens laminin, alpha 2 (matrosin, congenital muscular dystrophy) (LAMA2) mRNA
9259	20930	34087	2.83	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
9518	21210	34353	0.76	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9147	21878	35043	1.23	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0364 protein, partial cds
9147	21878	35044	1.23	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0364 protein, partial cds
11116	23768	37063	1.88	4.0E-97	11893122	NT	Homo sapiens mRNA for KIAA1250 protein, partial cds
11116	23768	37063	1.88	4.0E-97	11893122	NT	Homo sapiens mRNA for KIAA1250 protein, partial cds
11412	23179	36407	3.61	4.0E-97	AB02557.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11415	23182	36411	1.62	4.0E-97	AB033116.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11415	23182	36412	1.62	4.0E-97	AB033116.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
12180	24852		7.76	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
236	13046	25695	1.14	3.0E-97	AB022968.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
854	13624	26294	29.53	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
854	13624	26295	29.53	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1422	15590	26855	1.29	3.0E-97	4768613	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2440	16529	27695	1.68	3.0E-97	U98255.1	NT	Human beta-pituitary-adenin (BAM22) gene, exon 7
3254	16016	28687	1.3	3.0E-97	5174478	NT	Homo sapiens pericentriolar factor 1 (PCF11) mRNA
4729	17461	30098	12.89	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6333	19103	32091	2.46	1.0E-97	BE566486.1	EST_HUMAN	60133952071 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821.5
9344	20415	33534	1.16	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-q05 HT0258 Homo sapiens cDNA
9344	20415	33535	1.16	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-q05 HT0258 Homo sapiens cDNA
9864	22316	35513	1.6	1.0E-97	RT0887.1	EST_HUMAN	y8c08.s1 Soxas fetal liver spleen TFLS Homo sapiens cDNA clone IMAGE:128134.3
10604	22293	36538	3.44	1.0E-97	11427157	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
10604	22298	36539	3.44	1.0E-97	11427157	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA

Page 418 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	23941	37235	2.03	1.0E-07	AA553761.1	EST_HUMAN	nk29p02.s1 NCI_GGAP Co11 Homo sapiens cDNA clone IMAGE:1014662 3'
11445	23212	36443	14.01	1.0E-07	11428272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
11445	23212	36444	14.01	1.0E-07	11428272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
881	13650	28319	3.82	9.0E-08	BE090873.1	EST_HUMAN	PMA-BT0724-010400-008-at12 BT0724 Homo sapiens cDNA
1253	14002	28670	1.12	9.0E-08	83933092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6210	18985		0.71	9.0E-08	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
7160	18976	32949	0.87	9.0E-08	768187.1	NT	Homo sapiens leucyl-tRNA synthetase, mitochondrial (KIAA0028), mRNA
7286	19699	33046	0.6	9.0E-08	11418408	NT	Homo sapiens A kinase (PRKA) anchor protein (jolla) 9 (AKAP9), mRNA
7825	20520	33646	4.79	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7825	20520	33647	4.79	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8014	21704	34854	8.28	9.0E-08	X06989.1	NT	Human mRNA for amyloid A(751) protein
9124	21812	34977	1.5	9.0E-08	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9192	21862	35027	1.59	9.0E-08	AB037786.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
9238	21817		0.96	9.0E-08	AF057728.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9267	22021	35190	1.14	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), mRNA
9267	22021	35191	1.14	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), mRNA
10160	22808	36026	0.45	9.0E-08	AF141325.2	NT	Homo sapiens histone polyphosphatase 1-phosphatase (NPP1) gene, complete cds
10926	23008	36856	2.63	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10926	23008	36857	2.63	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11004	23076	36932	1.39	9.0E-08	11418682	NT	Homo sapiens mitogen-activated protein kinase kinase 7 (MAPKK7), mRNA
11850	24434	37776	1.39	9.0E-08	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11850	24434	37777	1.39	9.0E-08	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
1351	14059	28774	0.92	9.0E-08	AB033768.1	NT	Homo sapiens HPAD-cowpox10 mRNA for preprolysin deaminase type 1, complete cds
1719	14462	27161	2.7	9.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1719	14462	27162	2.7	9.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3776	16527	29168	8.69	9.0E-08	AB017007.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5991	18772	27638	0.59	9.0E-08	BE885873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2176	14005	27393	1.14	9.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2613	15524	28087	0.99	9.0E-08	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2753	15453		2.9	9.0E-08	AB014807.1	EST_HUMAN	7818101 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7818101
6847	19547	32578	1.9	9.0E-08	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6847	19547	32577	1.9	9.0E-08	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA

Page 419 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8849	21341	34485	2.73	3.0E-08	146698.1	EST_HUMAN	X017609.1 Scores adult brain N265H565Y Homo sapiens cDNA clone IMAGE:178240 5'
9197	21688	35033	0.48	3.0E-08	8822088	EST	Homo sapiens uncharacterized bone marrow protein BN039 (BN039), mRNA
9783	22434	35939	1.42	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.1 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
9783	22434	36940	1.42	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.1 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
10371	23017	36233	0.86	3.0E-08	BE900454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
10872	23552	36769	4.11	3.0E-08	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11863	24447	37789	1.96	3.0E-08	L28405.1	NT	Homo sapiens (flu) mRNA, complete cds
12068	25262		1.47	3.0E-08	BE382519.1	EST_HUMAN	601297695F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3629213 5'
12751	25013		3.95	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
2071	14803	27531	2.66	2.0E-08	BE294281.1	EST_HUMAN	601172558F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2231	14659	27699	1.53	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4284	17005	29637	0.8	2.0E-08	AF032697.1	NT	Homo sapiens placental channel subunit (HERG-3) mRNA, complete cds
4306	17045	29870	3.21	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FAGL4) mRNA
4776	17508	30129	1.34	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRNL) gene, exon 16
4776	17508	30130	1.34	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRNL) gene, exon 16
5131	17849	30466	1.39	2.0E-08	4758975	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
5292	18097	30767	4.03	2.0E-08	7706512	NT	Homo sapiens P12 domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6557	19322	33239	1.15	2.0E-08	4503768	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7523	20194	33289	1.07	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7523	20194	33287	1.07	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8506	21198	34342	4.94	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8591	21283	34421	0.56	2.0E-08	L76969.1	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8591	21283	34422	0.56	2.0E-08	L76969.1	NT	Homo sapiens NKAT1 db mRNA, complete cds
9437	22115	35290	1.48	2.0E-08	X12684.1	NT	Homo sapiens arginase gene exon 3 (EG 3.6.3.1)
10373	22660		1.37	2.0E-08	7705988	NT	Homo sapiens arginase gene exon 3 (EG 3.6.3.1)
11155	23822	37103	1.42	2.0E-08	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
368	13181	25629	16.4	1.0E-08	AJ862007.1	EST_HUMAN	M69604.x1 NCI CGAP U1 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RL2B_HUMAN
442	13228	25571	2.12	1.0E-08	AY098611.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A ;
1789	14529	27237	11.24	1.0E-08	N46818.1	EST_HUMAN	PMO-BN0085-10300-001-008 BN0085 Homo sapiens cDNA Y23105.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L28 - human ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5234	18040	30568	3.4	1.0E-98	AA159854.1	EST_HUMAN	z88500.r1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:528240 5' similar to TR:G80592
5482	18281	31178	1.1	1.0E-98	BE390627.1	EST_HUMAN	G80592 NEBULIN, 1
5482	18281	31178	1.1	1.0E-98	BE390627.1	EST_HUMAN	607284936F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:380592 5'
5482	18281	31178	1.1	1.0E-98	BE390627.1	EST_HUMAN	607284936F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:380592 5'
8859	21957	34726	2.7	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
8859	21957	34726	2.7	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
8859	21957	34726	2.7	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5728	18520	31442	0.88	9.0E-99	AB05004.1	EST_HUMAN	QV-BT073-191298-012 B1073 Homo sapiens cDNA
5728	18520	31442	0.88	9.0E-99	AB05004.1	EST_HUMAN	QV-BT073-191298-012 B1073 Homo sapiens cDNA
5949	18731	31091	4.21	9.0E-99	AY98635.1	EST_HUMAN	EST130711 IMAGE:2163421 3' similar to SW:BD_HUMAN
11058	23736	37009	2.75	9.0E-99	AA79929.1	EST_HUMAN	Int6807 x1 NGL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11058	23736	37010	2.75	9.0E-99	AA79929.1	EST_HUMAN	P69557 BH3 INTERACTING DOMAIN DEATH AGONIST
11390	23956	37288	2.13	9.0E-99	AA134604.1	EST_HUMAN	P69557 BH3 INTERACTING DOMAIN DEATH AGONIST
8627	21319	34491	1.96	7.0E-99	AF035808.1	NT	z80402.r1 Striatum lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
5743	18535	31458	10.03	7.0E-99	AF001888.1	NT	TR:G66294 G66294 GPH-ANCHORED PROTEIN P137.1
11610	24208	37532	2.96	7.0E-99	AF001888.1	NT	Human endogenous retrovirus, complete genome
459	13244	25886	1.89	6.0E-99	U00917.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
3668	18618	29258	1.15	6.0E-99	AW976364.1	EST_HUMAN	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
4689	17433	30064	1.21	6.0E-99	4502680	NT	Human G2 protein mRNA, partial cds
6503	19268	32270	0.72	6.0E-99	L43610.1	NT	EST138873 IMAGE:2163421 3' similar to SW:BD_HUMAN
6578	19341	32354	1.01	6.0E-99	L43610.1	NT	Homo sapiens CD34 antigen (CD34) mRNA
8003	20598	33828	1.18	6.0E-99	X99701.1	NT	Homo sapiens GAP-like protein (LOC81306), mRNA
8022	20717	33949	0.53	6.0E-99	6601580	NT	Homo sapiens polyomavirus kidney disease (PKD1) gene, exons 27-30
8693	21355	34502	2.28	6.0E-99	AB036429.1	NT	Homo sapiens polyomavirus kidney disease (PKD1) gene, exons 27-30
8762	21454	34602	3.33	6.0E-99	AF060255.1	NT	H sapiens mRNA for estrogen receptor
8821	21513	34657	0.6	6.0E-99	11431894	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8821	21513	34658	0.6	6.0E-99	11431894	NT	Homo sapiens NOST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10520	23313	36563	3.89	6.0E-99	AF060255.1	NT	Homo sapiens NOST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11433	23200	36431	2.01	6.0E-99	6910279	NT	Homo sapiens NOST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11433	23200	36432	2.01	6.0E-99	6910279	NT	Homo sapiens NOST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1957	14893	27406	1.38	5.0E-99	Y11365.1	NT	H.sapiens IMPA gene, exon 8
4526	17261	28995	1.56	5.0E-99	AF008660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S2A2 to TORBV12S2 region
11208	24674	31000	2.81	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH MGCC 71 Homo sapiens cDNA clone IMAGE:3914391 5'
8220	20914		4.88	3.0E-99	M95586.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
1217	13968		6.88	2.0E-99	AW274792.1	EST_HUMAN	X039608.x1 NCI CGAP_HNS Homo sapiens cDNA clone IMAGE:279874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKAL, NON-MUSCLE ISOFORM (HUMAN);
3253	18015	28658	1.29	2.0E-99	M30338.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4506	17241	29874	1.04	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSO) gene, nuclear gene encoding mitochondrial protein, complete cds
7574	20243	33346	0.58	2.0E-99	AF287737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8608	21300	34444	9.55	2.0E-99	W23507.1	EST_HUMAN	Z946008.r1 Soares_Jeal_Jung_NHL19W Homo sapiens cDNA clone IMAGE:306835 5' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
6050	21739	34897	0.76	2.0E-99	R78254.1	EST_HUMAN	y81b09.r1 Soares_placenta_N2zHP Homo sapiens cDNA clone IMAGE:145625 5'
11048	23719	36960	3.39	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
11788	24378	37708	1.48	2.0E-99	10863969	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
307	13111	28761	1.63	1.0E-99	AF114487.1	NT	Homo sapiens interocin long isoform (ITSN) mRNA, complete cds
370	13189	28908	1.02	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (80KD) (GABPA), mRNA
1400	14147	28828	2.09	1.0E-99	M30338.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1549	14295	28881	2.64	1.0E-99	AF102523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1949	14295	28962	2.64	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1920	14657	27397	1.41	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38KD) (FKBP6) mRNA, and translated products
1920	14657	27398	1.41	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38KD) (FKBP6) mRNA, and translated products
3923	15649	28499	1.36	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alphaR) mRNA, complete cds
4347	17086	29715	2.82	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4347	17086	29716	2.82	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5658	18453	31397	0.68	1.0E-99	7692349	NT	Homo sapiens cell recognition molecule Caspr2 (KIA00868), mRNA
8707	18622	32656	1.28	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
8707	18622	32656	1.28	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7039	25104	32788	0.78	1.0E-99	X68022.1	NT	H.sapiens E6-AP gene exon 2
9099	21787		1.49	1.0E-99	11418721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9420	22036	35270	1.71	1.0E-99	AW940174.1	EST_HUMAN	h02702.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11084	23754	37026	2.01	1.0E-99	7427514	NT	O02711 PRO-POLYUTASE POLYPROTEIN
11084	23754	37030	2.01	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11084	23754	37030	2.01	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11141	23808	37088	1.8	1.0E-99	5901879	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11350	24040	37343	2.77	1.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11884	24525		6.88	1.0E-98	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	12830	28443	0.95	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	12830	25443	1.53	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
66	12894	25528	1.54	1.0E-100	11418230	NT	Homo sapiens testis-specific XK-related protein on Y (XKRY), mRNA
66	12894	25527	1.54	1.0E-100	11418230	NT	Homo sapiens testis-specific XK-related protein on Y (XKRY), mRNA
85	12911	25550	0.99	1.0E-100	AW275237.1	EST_HUMAN	XV/811.x1 NCI CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2824605 3'
155	12979	25618	1.24	1.0E-100	AL163205.2	NT	Homo sapiens chromosome 21 segment HS21C006
309	13113	25753	0.83	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
334	13135	25770	3.08	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Striatum (cat633826) Homo sapiens cDNA clone HFBGR32
427	13213		1.28	1.0E-100	AF003528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
477	13263		7.19	1.0E-100	X89531.1	NT	G gene DNA for ZNF80 gene homolog
498	13280	25915	1.33	1.0E-100	BE180609.1	EST_HUMAN	RC3-H1028-04050-022-539 HT0926 Homo sapiens cDNA
988	13758	28418	3.22	1.0E-100	7681685	NT	Homo sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
988	13758	28418	3.22	1.0E-100	7681685	NT	Homo sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
1415	14163	26846	3.14	1.0E-100	BF530735.1	EST_HUMAN	60207206AF1 NCI CGAP_Brn57 Homo sapiens cDNA clone IMAGE:2722184 3'
1558	14255		1.14	1.0E-100	AW207555.1	EST_HUMAN	UHL-B1-afic-07-0-U1s1 NCI CGAP_Sub33 Homo sapiens cDNA clone IMAGE:2722184 3'
1543	14289	28978	1.81	1.0E-100	AI200657.1	EST_HUMAN	p8209.x1 Soares, testes, NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
1855	14584	27309	1.41	1.0E-100	AB032894.1	NT	P81061 CYSTATIN1
2238	14966		1.39	1.0E-100	D83349.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2439	15169	27804	1.33	1.0E-100	XG2468.1	NT	Hai mRNA for short type PB-catharin, complete cds
2710	15417	28165	2.38	1.0E-100	11418976	NT	Hi sapiens mRNA for IFN-gamma (pK-G)
3018	15784		5.5	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4186	16927	29558	1.52	1.0E-100	AF067364.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4211	16952	29578	2.14	1.0E-100	4503782	NT	Homo sapiens myoblastin-related protein 1a mRNA, partial cds
4418	17164	29735	1.03	1.0E-100	AF036943.1	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5031	17751	30382	2.86	1.0E-100	5032104	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
5031	17751	30383	2.86	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5207	18015	30637	1.92	1.0E-100	BF244218.1	EST_HUMAN	60186316AF1 NH_MGC_57 Homo sapiens cDNA clone IMAGE:280999 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5421	18220	30931	0.59	1.0E-100	AW075983.1	EST_HUMAN	x8201.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:U12433
5424	18410	31323	1.33	1.0E-100	AU118182.1	EST_HUMAN	PROTEIN PHF-S1-2 (HUMAN);
5424	18410	31323	1.33	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEIMBA1003046 5'
5660	18455	31366	1.28	1.0E-100	AF135118.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
5747	18539	31461	0.8	1.0E-100	X14800.1	NT	Human mRNA for plasma Inter-alpha-1-trypsin inhibitor heavy chain H(3)
6071	18550	31614	0.94	1.0E-100	4557558	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6071	18550	31614	0.94	1.0E-100	4557558	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6343	18613	31815	1.97	1.0E-100	5729897	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6405	18174	32173	5.84	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6457	19224	32224	1.97	1.0E-100	AU136900.1	EST_HUMAN	AU136900 PLACE2 Homo sapiens cDNA clone PLACE1005089 5'
6566	18249	32362	1.37	1.0E-100	R10887.1	EST_HUMAN	X83608.x1 Sources field liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6570	18987	32622	0.9	1.0E-100	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6742	19576	32608	1.19	1.0E-100	AA496841.1	EST_HUMAN	ae33606.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR-G487418
6742	19576	32608	1.19	1.0E-100	AA496841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
6766	19530	32557	1.13	1.0E-100	BF376478.1	EST_HUMAN	MRL-TN0048.060900-004-505 TN0048 Homo sapiens cDNA
6766	19530	32557	1.13	1.0E-100	BF376478.1	EST_HUMAN	MRL-TN0048.060900-004-505 TN0048 Homo sapiens cDNA
6783	19537	32565	6.76	1.0E-100	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8430	21123	34281	7.17	1.0E-100	BF103953.1	EST_HUMAN	601647357F1 NIH MGSC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
8466	21159	34281	4.8	1.0E-100	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C03
8912	21603	34746	0.88	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
8912	21603	34747	0.88	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9132	21920	34986	3.52	1.0E-100	AB040516.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9210	22089	34986	2.78	1.0E-100	AU972388.1	EST_HUMAN	W37G09.x1 NCL CGAP_P228 Homo sapiens cDNA clone IMAGE:246920 3' similar to contains element
9333	22044	33520	1.82	1.0E-100	AW26851.1	EST_HUMAN	MER22 repetitive element ;
9386	22048	33518	7.61	1.0E-100	AU12720.1	EST_HUMAN	PMO-BN0065-103000-001-208 BN0065 Homo sapiens cDNA
9483	22136	35317	2.11	1.0E-100	AB040484.1	NT	AU12720 NT2P2 Homo sapiens cDNA clone NT2P2001918 5'
9483	22136	35317	2.11	1.0E-100	AB040484.1	NT	Homo sapiens mRNA for KIAA1628 protein, partial cds
9743	22394	35598	1.68	1.0E-100	AW630487.1	EST_HUMAN	h835c11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
9743	22394	35598	1.68	1.0E-100	AW630487.1	EST_HUMAN	h835c11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
9805	22554	35749	0.49	1.0E-100	AV732101.1	EST_HUMAN	h835c11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10368	23014	36230	1.47	1.0E-100	BF347519.1	EST_HUMAN	AV732101 HTP Homo sapiens cDNA clone HTFHC001 6'
							602020554F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156165 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10458	23104		2.2	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10558	23419	38598	6.27	1.0E-100	BF327262.1	EST_HUMAN	MRO-BN0070-270300-008-R11 BN0070 Homo sapiens cDNA
11326	24017	37319	4.52	1.0E-100	AF11170.3	EST	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11326	24017	37320	4.52	1.0E-100	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11356	22830	25443	2.11	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11633	24230		1.59	1.0E-100	AW875464.1	EST_HUMAN	QV2-P10012-010300-070-004 P10012 Homo sapiens cDNA
11681	24276		1.48	1.0E-100	AF266285.1	NT	Homo sapiens g91gh-like protein (GLP) gene, complete cds
11749	24340	37698	1.57	1.0E-100	AA115605.1	EST_HUMAN	ZK89a03.1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489984 5'
11749	24340	37698	1.57	1.0E-100	AA115605.1	EST_HUMAN	ZK89a03.1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489984 5'
11907	24471	37806	6.67	1.0E-100	AF240766.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12031	25278		1.51	1.0E-100	BF446549.1	EST_HUMAN	7q88H03.X1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR-Q21997 Q21997
12203	24686	31071	3.67	1.0E-100	BF446549.1	EST_HUMAN	COSMID R151, [2] TR-Q8LJA08:
12792	25044	30668	4.62	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
75	12902	26539	1.75	1.0E-101	11471874	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
75	12902	26540	1.76	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
671	13447	20937	1.62	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
688	13463	26111	5.88	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
688	13463	26112	5.88	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
754	13528	26185	1.99	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
833	13603	26273	1.5	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
904	13671	26335	1.22	1.0E-101	4603914	NT	Homo sapiens phosphatidylglyceride formyltransferase, phosphatidylglyceride synthetase, phosphatidylaminidazole synthetase (GART) mRNA
964	13729	26396	14.28	1.0E-101	Z20658.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1030	13700	26446	1.63	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4267291 6'
1577	14324	27012	1.48	1.0E-101	AI221876.1	EST_HUMAN	qg9a092.X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1577	14324	27013	1.48	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1577	14324	27013	1.48	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1740	14482	27182	1.52	1.0E-101	7682168	NT	Homo sapiens KIAA0589 gene product (KIAA0589), mRNA
1740	14482	27183	1.52	1.0E-101	7682168	NT	Homo sapiens KIAA0589 gene product (KIAA0589), mRNA
1938	14673	27359	1.62	1.0E-101	4602996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2050	14783	27510	1.79	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-016-009 ST0281 Homo sapiens cDNA
2249	15592	27908	1.71	1.0E-101	5728682	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2620	15332	28076	2.8	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 5

Page 425 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2747	15452	28162	1.09	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2747	15452	28163	1.09	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2935	15721		13.73	1.0E-101	AJ262312.1	NT	Homo sapiens genomic downstream Rhesus box
3198	15961	28613	1.99	1.0E-101	4856270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3235	15997		2.27	1.0E-101	BF035327.1	EST_HUMAN	60145531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662086 5'
3375	16134	28700	1.93	1.0E-101	AW085568.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
3395	15452	28162	1.49	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3957	16907	29245	3.59	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4974	17697	30304	1.16	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
4974	17697	30305	1.16	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5235	18041	30669	1.22	1.0E-101	AW665139.1	EST_HUMAN	EST137212 MAGE resequences, MAGI Homo sapiens cDNA
5913	18698	31651	3.88	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5913	18698	31652	3.88	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6595	16258	32372	1.27	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7173	19859		1.01	1.0E-101	11545763	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7220	19905	32977	5.97	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7220	19905	32978	5.97	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7376	20058	33136	7.48	1.0E-101	AW009476.1	EST_HUMAN	w55f12.1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7474	20147		1.78	1.0E-101	BE257364.1	EST_HUMAN	50110321F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3349901 5'
7623	20289	33398	7.43	1.0E-101	BF307599.1	EST_HUMAN	RC1-BT0313-220700-016-R12 BT0313 Homo sapiens cDNA
7813	20508	33631	0.84	1.0E-101	BE276821.1	EST_HUMAN	60112162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345669 5'
7813	20508	33632	0.84	1.0E-101	BE276821.1	EST_HUMAN	60112162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345669 5'
7954	20649	33772	2.88	1.0E-101	BF029174.1	EST_HUMAN	50176468F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3968637 5'
8221	20915	34050	0.97	1.0E-101	AW630070.1	EST_HUMAN	h374g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143
8221	20915	34051	0.97	1.0E-101	AW630070.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8908	21539	34741	1.08	1.0E-101	AA036800.1	EST_HUMAN	h374g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143
9229	21903	35080	0.93	1.0E-101	AB037772.1	NT	PIR29608.1 Scores_pregnant_uterus_Nb-IPU Homo sapiens cDNA clone IMAGE:3968637 5'
9229	21908	35081	0.93	1.0E-101	AB037772.1	NT	PIR29608.1 Scores_pregnant_uterus_Nb-IPU Homo sapiens cDNA clone IMAGE:3968637 5'
9362	20432	33553	17.13	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9362	20432	33554	17.13	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
							Human mRNA for pancreatic gamma-glutamyltransferase
							Human mRNA for pancreatic gamma-glutamyltransferase

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6375	21890	35123	17.01	1.0E-101	9845402	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
6657	22308	35508	6.24	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9557	22309	35507	6.24	1.0E-101	BE919667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9794	22445	35650	0.72	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10308	22955	36171	1.49	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10447	23093	36323	0.94	1.0E-101	BE073648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10447	23093	36324	0.94	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10788	23471	36713	1.98	1.0E-101	S38327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit (human), Genomic, 195 nt, segment 8 of 9
11053	23723	36894	2.11	1.0E-101	AB029626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
11398	24004	37307	2.06	1.0E-101	A1590078.1	EST_HUMAN	tm66d01.xt NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162304 3' similar to gb:M13361
11398	24004	37308	2.06	1.0E-101	A1590078.1	EST_HUMAN	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);
11763	24394	37685	1.31	1.0E-101	A1608168.1	EST_HUMAN	tm66d01.xt NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162304 3' similar to gb:M13361
11763	24394	37687	1.31	1.0E-101	A1608168.1	EST_HUMAN	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);
12491	24929	38266	13.68	1.0E-101	A1929051.1	EST_HUMAN	RC-BT163-290498-085 BT163 Homo sapiens cDNA
38	12866	25485	2	1.0E-102	AF012872.1	NT	QY1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
332	13193	25767	4.35	1.0E-102	AL163303.2	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pIK230) mRNA, complete cds
768	13530	26160	1.59	1.0E-102	4557834	NT	Homo sapiens chromosome 21 segment HS21G103
1095	13853	26512	2.8	1.0E-102	M10276.1	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1245	13994	26560	1.67	1.0E-102	11437146	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
1245	13994	26661	1.67	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1281	14070	26878	0.99	1.0E-102	4826977	EST_HUMAN	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1398	14145	26823	119.7	1.0E-102	BE408447.1	EST_HUMAN	Homo sapiens retin (RELN) mRNA
2307	15032	27769	1.88	1.0E-102	A1124699.1	EST_HUMAN	601268882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629601 5'
2307	15032	27770	1.88	1.0E-102	A1124699.1	EST_HUMAN	sm60c10.xt Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to
3051	15927	28472	1.32	1.0E-102	7681978	NT	SW_GG95_HUMAN Q08379 GOLGIN-95 ;
3131	15895	28539	4.76	1.0E-102	AU141005.1	EST_HUMAN	sm60c10.xt Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to
3130	15895	28539	4.76	1.0E-102	AU141005.1	EST_HUMAN	SW_GG95_HUMAN Q08379 GOLGIN-95 ;
4207	16948	29574	1.97	1.0E-102	BE251310.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4378	17115	29748	2.17	1.0E-102	BE251310.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4008650 5'
							AU141005 PLACE4 Homo sapiens cDNA clone PLACE4008650 5'
							Homo sapiens chromosome 21 segment HS21C007
							60110743F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'

Page 427 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5287	18002	30753	1.87	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5683	19458		9.17	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5688	19462	31414	2.84	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5698	18492	31415	2.84	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5704	18490	31420	0.81	1.0E-102	11433048	NT	Homo sapiens hct domain and RLD 2 (HIERC2), mRNA
6200	18976	31954	2.93	1.0E-102	AI499825.1	EST_HUMAN	Q13137 NDP92.1
7036	19728	32785	0.75	1.0E-102	BE728323.1	EST_HUMAN	601581505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3891241.5'
7065	19756	32821	1.04	1.0E-102	BE386106.1	EST_HUMAN	601272155F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818243.5'
7265	19939	33014	8.23	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7624	20166	33288	2.48	1.0E-102	AV10738.1	EST_HUMAN	AV107383 Cu Homo sapiens cDNA clone CUA-KD03.5'
8122	20810	33962	3.91	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT10025-210800-298-H08 NT0028 Homo sapiens cDNA
8201	20895	34032	1.32	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145.5'
8392	21085	34218	2.21	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11.5'
8392	21085	34219	2.21	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11.5'
8501	21193	34335	1.19	1.0E-102	AB007923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8828	21621	34687	0.63	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536.5'
8828	21621	34688	0.63	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536.5'
8150	21881	35046	0.52	1.0E-102	AT672869.1	EST_HUMAN	W635063X1 NCI_CGAP_K12 Homo sapiens cDNA clone IMAGE:2387971.3' similar to contains MER4.11
9181	21851	35017	0.81	1.0E-102	AV755942.1	EST_HUMAN	MER4 MER4 repetitive element;
9221	21900	35059	2.28	1.0E-102	IT70393.1	EST_HUMAN	AV755942 BM Homo sapiens cDNA clone IMAGE:67021.5'
9221	21900	35070	2.28	1.0E-102	IT70393.1	EST_HUMAN	AV755942 BM Homo sapiens cDNA clone IMAGE:67021.5'
9311	21978	35151	3.78	1.0E-102	AJ124628.1	EST_HUMAN	Y413407.1 Soares fetal liver spleen cDNA clone IMAGE:67021.5'
10281	22029		0.69	1.0E-102	AF165716.1	EST_HUMAN	Y413407.1 Soares fetal liver spleen cDNA clone IMAGE:67021.5'
10387	22013	36228	3.67	1.0E-102	AI905037.1	EST_HUMAN	AU124628 NT2RMA Homo sapiens cDNA clone NT2RMA4000309.5'
10387	22013	36229	3.67	1.0E-102	AI905037.1	EST_HUMAN	AU124628 NT2RMA Homo sapiens cDNA clone NT2RMA4000309.5'
10428	23074	36295	1.24	1.0E-102	AA970788.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
11008	23680	36937	2.90	1.0E-102	4507822	NT	RC-BT074-250499-014 BT074 Homo sapiens cDNA
11008	23680	36938	2.90	1.0E-102	4507822	NT	RC-BT074-250499-014 BT074 Homo sapiens cDNA
11260	23951	37248	1.55	1.0E-102	AA969675.1	EST_HUMAN	RC-BT074-250499-014 BT074 Homo sapiens cDNA
11380	23987	37287	3.01	1.0E-102	BF359243.1	EST_HUMAN	RC-BT074-250499-014 BT074 Homo sapiens cDNA
							onc704.4; Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1560823.3' similar to
							SW-CAV2_HUMAN_P51636 CAVFOLIN-2. [1];
							Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
							Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
							AK0610.61 Soares testis NIH Homo sapiens cDNA clone IMAGE:1409347.3'
							RC06-ET0072-150600-011-F01 ET10072 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11710	24305	37631	3.57	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
11911	24475		3.52	1.0E-102	AL163260.2	NT	Homo sapiens chromosome 21 segment H52C080
12550	24820	31023	4.69	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment H52C080
67	12895	25528	1.19	1.0E-103	BE908158.1	EST_HUMAN	407c12.1x1 NCL CGAP_Co20 Homo sapiens cDNA clone IMAGE:2660338 3'
67	12895	25528	1.19	1.0E-103	BE908158.1	EST_HUMAN	60150405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
68	12924	25561	10.8	1.0E-103	D87078.2	NT	60150405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
203	13016	26560	1.45	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
960	13216	26389	0.79	1.0E-103	AJ278348.1	NT	Homo sapiens nuclear protein (KCED repeat) (NOP56) mRNA
1221	13371	26643	10.23	1.0E-103	BE97541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1801	14337	27026	3.76	1.0E-103	AF012872.1	NT	60148538F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3987870 5'
1807	14644	27354	1.75	1.0E-103	7657592	NT	60148538F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3987870 5'
1988	14704	27420	1.44	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
1988	14704	27421	1.44	1.0E-103	AJ134991.1	EST_HUMAN	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
2303	15028	27785	1.15	1.0E-103	AF060668.1	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
2452	15170	27909	1.33	1.0E-103	AF060668.1	EST_HUMAN	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
2693	15316	28055	1.23	1.0E-103	BF529376.1	EST_HUMAN	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
2693	15316	28055	1.23	1.0E-103	BF529376.1	EST_HUMAN	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
3064	15630	28789	2.68	1.0E-103	BE744722.1	EST_HUMAN	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
3374	16133	28789	4.71	1.0E-103	AW238245.1	NT	U18157-BWD-ql-1b-14-JUI-51 NCL CGAP_Su68 Homo sapiens cDNA clone IMAGE:2733165 3'
3493	16189	28837	0.99	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1456 protein, complete cds
3737	16480		8.65	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3774	16626	29165	1.23	1.0E-103	AA485953.1	EST_HUMAN	4010d12.1x1 Stralagene lung (9337210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element
3810	16592	29195	1.72	1.0E-103	11430876	NT	Homo sapiens neurotrophin 1 (NRP1) mRNA
3885	16733	29397	3.47	1.0E-103	T29883.1	EST_HUMAN	seq440 b4HB3MA-Cot109-10-B10 Homo sapiens cDNA clone b4HB3MA-Cot109-10-B10-7 3'
5844	18632	31587	0.68	1.0E-103	BF596927.1	EST_HUMAN	602186023F1 NIH_MGC_245 Homo sapiens cDNA clone IMAGE:4178429 5'
5952	18639	31577	2.82	1.0E-103	AF178695.1	NT	Homo sapiens scapin 2 (SEP2) mRNA, partial cds
6174	18951	31623	0.89	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6174	18951	31623	0.89	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6368	19137	32132	0.75	1.0E-103	AW954596.1	EST_HUMAN	EST13669333 MAGE resequences, MAGEC Homo sapiens cDNA
6368	19137	32133	0.75	1.0E-103	AW954596.1	EST_HUMAN	EST13669333 MAGE resequences, MAGEC Homo sapiens cDNA
6468	19137	32265	1.50	1.0E-103	AA781442.1	EST_HUMAN	4020603.s1 Soares testis NIH Homo sapiens cDNA clone 1391452 3'
6535	18301	32304	0.94	1.0E-103	AF053480.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6818	19380	32396	1.48	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6818	19380	32397	1.48	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6747	17916	30579	1.53	1.0E-103	6032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6747	17916	30580	1.53	1.0E-103	6032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6872	17049	30544	1.37	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
6935	19070	32718	0.89	1.0E-103	AI286880.1	NT	Homo sapiens KIA0081 gene (partial), X13 gene and LZTFL1 gene
7127	18615	32893	1.83	1.0E-103	AW965776.1	EST_HUMAN	EST137849 MAGE resequences, MAGI Homo sapiens cDNA
7233	18918	32890	6.63	1.0E-103	BE748158.1	EST_HUMAN	601871637F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838546 5'
7671	20335	33448	4.21	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
7671	20335	33447	4.21	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8197	20881	34019	0.77	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
8519	21211	34354	2.22	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8519	21211	34355	2.22	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8804	21296	34439	1.1	1.0E-103	BF108244.1	EST_HUMAN	769b03.x1 Soras NSF F8 SW OT PA P S1 Homo sapiens cDNA clone IMAGE:3525064 3' similar to SWPTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;
8005	21695	34845	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8005	21695	34846	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9046	21738	34891	1.16	1.0E-103	AA581088.1	EST_HUMAN	nd13c02.s1 NCI CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gbl:02428 265
9046	21738	34891	1.16	1.0E-103	AA581088.1	EST_HUMAN	PROTEASE SUBUNIT 1 (HUMAN);
9088	21777	34941	5.04	1.0E-103	AA774880.1	EST_HUMAN	ae8d42.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to g0303747.c1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
9182	21832	34995	0.56	1.0E-103	BE939942.1	EST_HUMAN	QV2-NN0045-230800-322-003 NN0045 Homo sapiens cDNA
9182	21832	34996	0.56	1.0E-103	BE939942.1	EST_HUMAN	QV2-NN0045-230800-322-003 NN0045 Homo sapiens cDNA
9338	22808	35811	1.44	1.0E-103	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
9369	22847	35869	1.89	1.0E-103	AW963676.1	EST_HUMAN	EST1375749 MAGE resequences, MAGI Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10138	22768	35998	9.2	1.0E-103	AJ878966.1	EST_HUMAN	au51904.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:3518328 5' similar to
10634	23326	36663	3.66	1.0E-103	AJ792769.1	EST_HUMAN	TR015048 O15048 KIA00338
10737	23424	36663	2.04	1.0E-103	11424061	NT	002808.95 NCL CGAP L05 Homo sapiens cDNA clone IMAGE:162283 5 similar to TR:Q62084 Q62084
10737	23424	36663	2.04	1.0E-103	11424061	NT	PHOSPHOLIPASE C NEIGHBORING
10748	23434	36677	2.22	1.0E-103	AF148773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10748	23434	36678	2.22	1.0E-103	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10763	23476	36717	1.3	1.0E-103	AB7831.2	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10763	23476	36718	1.3	1.0E-103	AB7831.2	NT	Homo sapiens mRNA for partial OCT1000-A2 protein
11347	24037	37240	2.6	1.0E-103	AJ138283.1	EST_HUMAN	Homo sapiens mRNA for partial OCT1000-A2 protein
11423	25190	36421	10.74	1.0E-103	L4510.1	NT	AJ138283 PLACE1 Homo sapiens cDNA clone IMAGE:1003923 5'
11748	24539	37667	2.41	1.0E-103	BE844611.1	EST_HUMAN	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11937	24484		2.11	1.0E-103	11526281	NT	766810.X1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to
12128	24620	31091	2.83	1.0E-103	AB011389.1	NT	contains MER2813 MER28 repetitive element
227	13039	25676	3.73	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens hypodermal protein FLJ20454 (FLJ20454), mRNA
227	13039	25677	3.73	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens gene for AF-9, complete cds
1881	14618	27328	2.18	1.0E-104	4502428	NT	DKFZp564H1072.11 664 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
2190	14618	27653	3.88	1.0E-104	AA132875.1	EST_HUMAN	DKFZp564H1072.11 664 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
2201	14628	27663	2.57	1.0E-104	BE744628.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2369	15091	27829	1.38	1.0E-104	BF334221.1	EST_HUMAN	z02206.61 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:587626 3' similar to
2369	16001	27830	1.38	1.0E-104	BF334221.1	EST_HUMAN	gb:214116.1_m1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN)
2438	15158	27893	1.08	1.0E-104	5031570.1	EST_HUMAN	601677460.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3026438 5'
2507	15224	27965	1.11	1.0E-104	7682125	NT	RC1-CT0249-110900-214412 CT0249 Homo sapiens cDNA
2507	15224	27968	1.11	1.0E-104	7682125	NT	RC1-CT0249-110900-214412 CT0249 Homo sapiens cDNA
2874	15841	28285	7.41	1.0E-104	M34871.1	NT	Homo sapiens ARP2 (ectin-related protein 2, yeast) homolog (ACTR2), mRNA
2917	15883		2.74	1.0E-104	Y11191.1	NT	Homo sapiens KIA00440 protein (KIA00440), mRNA
3336	16145		2.04	1.0E-104	AA319436.1	EST_HUMAN	Homo sapiens KIA00440 protein (KIA00440), mRNA
3587	16341	28966	0.78	1.0E-104	AB033102.1	NT	Human lymphocyte antigen CD58/MEB43 mRNA, complete cds
3587	16341	28967	0.78	1.0E-104	AB033102.1	NT	Hs sapiens gene encoding phenylpyruvate tautomerase II
3924	16574	29315	0.78	1.0E-104	AB033102.1	NT	EST121658 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17083	28712	3.93	1.0E-104	X02761.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
							Homo sapiens mRNA for KIAA1276 protein, partial cds
							Homo sapiens mRNA for KIAA1172 protein, partial cds
							Human mRNA for fibronectin (FN precursor)

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4570	17305	29932	1.23	1.0E-104	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
4570	17305	29933	1.23	1.0E-104	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
4570	17824	30441	1.06	1.0E-104	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
5850	18637	31573	1.26	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5850	18637	31574	1.26	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5897	18682	31630	1.12	1.0E-104	AB017332.1	NT	Homo sapiens alk mRNA for Aurora/fgfr-related kinase 3, complete cds
6375	18144	32141	9.51	1.0E-104	AJ768787.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6375	18144	32142	9.51	1.0E-104	AJ768787.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6551	18516	32322	0.75	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6706	18621	32663	3.31	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6706	18621	32664	3.31	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7125	18613	32681	2.03	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8495	21187	34330	0.83	1.0E-104	BF509244.1	EST_HUMAN	U147814-acw-b-05-q-11 s1 NCL CGAP_S124 Homo sapiens cDNA clone IMAGE:3086178 3'
8655	21754	34915	5.23	1.0E-104	BF448230.1	EST_HUMAN	hac16711 x1 NCL CGAP_L124 Homo sapiens cDNA clone IMAGE:3365948 3'
9163	21633	34997	0.5	1.0E-104	AA692308.1	EST_HUMAN	z98b05.s1 Soares_Tetraliver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9184	21854	35081	1.31	1.0E-104	T74219.1	EST_HUMAN	yc85102.1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:22440 5'
9214	21893	35080	4.27	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9214	21893	35081	4.27	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9341	20412	35329	4.4	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0818-080900-249-F07 HT0818 Homo sapiens cDNA
9341	20412	35330	4.4	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0818-080900-249-F07 HT0818 Homo sapiens cDNA
9854	22306	35503	0.85	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPOTHETICAL 28.4 KD PROTEIN, ;
9854	22306	35504	0.85	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPOTHETICAL 28.4 KD PROTEIN, ;
9847	22497	35598	0.71	1.0E-104	AF113514.1	NT	KX76602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TRQ24116
9893	22841	35832	2.83	1.0E-104	BE791713.1	EST_HUMAN	Q24116 HYPOTHETICAL 28.4 KD PROTEIN, ;
9893	22841	35833	2.83	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10299	22846	36160	1.28	1.0E-104	AU728070.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10339	22896	36204	4.61	1.0E-104	AU130765.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10450	23096	36327	4.41	1.0E-104	U66535.1	NT	AU728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10464	23110	36327	4.41	1.0E-104	U66535.1	NT	AU728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
11268	23930	37221	2.07	1.0E-104	BE720191.1	EST_HUMAN	Human beta-actin (ACTB) gene, exons 19, 20, 21, 22, 23, 24, and 25
11268	23930	37221	2.07	1.0E-104	BE720191.1	EST_HUMAN	Human beta-actin (ACTB) gene product (KIAA0649), mRNA
11268	23930	37221	2.07	1.0E-104	BE720191.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11268	23930	37221	2.07	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-509 HT0885 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11268	23930	37222	2.07	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0895-310700-021-508 HT0895 Homo sapiens cDNA
11269	37226	37226	4.98	1.0E-104	BF694288.1	EST_HUMAN	602141215F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302807.5'
11290	23959	37250	1.75	1.0E-104	BE731978.1	EST_HUMAN	60156806F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841681.5'
11590	24169	37505	1.75	1.0E-104	BE731978.1	EST_HUMAN	60156806F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841681.5'
11590	24169	37506	1.75	1.0E-104	BE731978.1	EST_HUMAN	60156806F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841681.5'
11761	24381	37712	1.42	1.0E-104	11434128	NT	Homo sapiens fibronectin S6 kinase, 90kD, polypeptide 5 (PSPSG45) mRNA
12702	24982		2.38	1.0E-104	BE93892.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3658976.5'
272	15514	25722	11.13	1.0E-105	4502160	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA
418	12827	28440	8.99	1.0E-105	4505160	NT	Homo sapiens Mest1 (mouse) homolog (MEST) mRNA
580	13360	25987	1.92	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
590	13360	25988	1.92	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1814	14554	27269	0.91	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1919	14059	27365	1.29	1.0E-105	D50918.1	NT	Homo sapiens chromosome 21 segment HS21C080
2168	14915	27549	1.83	1.0E-105	AA318359.1	EST_HUMAN	Human mRNA for KIAA0128 gene, partial cds
2322	15047		1.44	1.0E-105	BE9891768.1	EST_HUMAN	EST20509 Sp1en1 Homo sapiens cDNA 5' end similar to autotransmembrane protein, p70p80 subunit
3306	15772	28759	2.98	1.0E-105	AI22904.1	NT	60144823F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918511.5'
3346	16105	28760	0.88	1.0E-105	7304022	NT	Homo sapiens 959 kb contig between ANK1 and CBR1 on chromosome 21q22, segment 1/3
3346	16105	28760	0.88	1.0E-105	7304022	NT	Homo sapiens 959 kb contig between ANK1 and CBR1 on chromosome 21q22, segment 1/3
4077	16821	29447	2.07	1.0E-105	AW16088.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4377	17428	30058	0.74	1.0E-105	BE989881.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4694	17428	30059	0.74	1.0E-105	BE989881.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4898	17613		4.24	1.0E-105	AL162308.2	NT	Homo sapiens chromosome 21 segment HS21C008
5043	17762	30377	1.19	1.0E-105	AB018339.1	EST_HUMAN	Homo sapiens mRNA for KIAA0760 protein, partial cds
5091	17762	30426	0.94	1.0E-105	AW966016.1	EST_HUMAN	EST378089 MAGC resequences, MAGI Homo sapiens cDNA
5247	18053	30681	0.66	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5917	18116		1.07	1.0E-105	11420134	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
6804	19465	32485	2.16	1.0E-105	BF9314302.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6804	19465	32486	2.16	1.0E-105	BF9314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334.5'
6804	19465	32486	2.16	1.0E-105	BF9314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334.5'
6885	17961	30515	3.95	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6885	17961	30516	3.95	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6927	18053	32709	0.63	1.0E-105	AW951634.1	EST_HUMAN	EST380889 MAGC resequences, MAGB Homo sapiens cDNA
6927	18053	32709	0.63	1.0E-105	AW951634.1	EST_HUMAN	EST380889 MAGC resequences, MAGB Homo sapiens cDNA
7184	19870	32944	0.59	1.0E-105	BE802618.1	EST_HUMAN	601677270F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980019.5'
7722	20286	33500	0.95	1.0E-105	6805894	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
7758	20454	33579	0.97	1.0E-105	X12556.1	NT	Human mRNA for dbi proto-oncogene

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7027	20622	33760	0.55	1.0E-105	U05087.1	EST_HUMAN	EST U02975 Fetal brain, Striatum (cd#838208) Homo sapiens cDNA clone HFB0R32
8297	20891	34129	1.41	1.0E-105	AW07194.1	EST_HUMAN	we5b010.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to SW-620A_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
8329	21516	34663	0.68	1.0E-105	AW640817.1	EST_HUMAN	UC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
8943	21639	34766	2.82	1.0E-105	AW016879.1	EST_HUMAN	UJH-B10P-46b-5-72-Q-UI-1 NCL CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9103	21781	34954	0.9	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0082-140300-083-069 OT0082 Homo sapiens cDNA
9103	21781	34955	0.9	1.0E-105	AW982372.1	EST_HUMAN	QV2-OT0082-140300-083-069 OT0082 Homo sapiens cDNA
9487	22077	35247	0.68	1.0E-105	BE687763.1	EST_HUMAN	601443755F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847884 5'
9487	22077	35248	0.68	1.0E-105	BE687763.1	EST_HUMAN	601443755F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847884 5'
10950	23931	36778	5.73	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11195	23860	37146	1.59	1.0E-105	D63548.1	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11250	23912	37204	2.38	1.0E-105	7705938	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11580	24179	37494	2.58	1.0E-105	AW027554.1	EST_HUMAN	w7487.x1 Scars_thymus_NHFFth Homo sapiens cDNA clone IMAGE:25355001 3' similar to TR-P87892
11675	24270	37592	1.43	1.0E-105	BIF430921.1	EST_HUMAN	P87892 PROTEASE ;
11831	24415	37753	1.73	1.0E-105	AB004924.1	NT	7018c10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR-P97680 P97680
11831	24415	37754	1.73	1.0E-105	AB004924.1	NT	RIN1 ;
147	12882	25654	1.39	1.0E-105	AB004924.1	EST_HUMAN	Homo sapiens gene for Smad 3, exon 2 and 3
200	13013	25947	1.79	1.0E-105	AW603208.1	EST_HUMAN	UHF-BNG-alk-g-07-0-ULT NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
529	13313	25947	2.68	1.0E-105	AI565565.1	EST_HUMAN	U79b01.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2215008 3'
591	13371	26000	0.76	1.0E-106	AI565565.1	EST_HUMAN	EST137623 MAGI resequences, MAGI Homo sapiens cDNA
592	13371	26000	2.06	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psh-hd1)
1515	14262	26948	1.33	1.0E-105	AF145712.1	NT	Human dihydrofolate reductase pseudogene (psh-hd1)
1697	14440	27138	3.48	1.0E-106	U48724.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1766	14536	27245	4.71	1.0E-105	AA527448.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1766	14536	27246	4.71	1.0E-105	AA527448.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
2118	14848	27578	2.31	1.0E-106	BE144268.1	EST_HUMAN	TR3 repetitive element ;
2315	15040	27778	2.89	1.0E-105	4504184	NT	1941c05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element
2610	15322	28084	1.82	1.0E-106	BE260201.1	EST_HUMAN	1941c05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element
2761	15466	28210	3.24	1.0E-106	AI276526.1	EST_HUMAN	1941c05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element
2828	14159	28842	1.91	1.0E-106	4504184	NT	TR3 repetitive element ;

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2828	14159	26843	1.91	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2842	15707	28357	5.23	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2842	15707	28358	5.23	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3178	16939	29598	2.18	1.0E-106	8622965	NT	Homo sapiens hypochlorite protein FLJ11273 (FLJ11273), mRNA
3178	16939	29599	2.18	1.0E-106	8622965	NT	Homo sapiens hypochlorite protein FLJ11273 (FLJ11273), mRNA
3367	16126	28784	0.81	1.0E-106	AB008681.1	NT	Homo sapiens gene for actin receptor type IIB, complete cds
3434	16190	28839	1.18	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3434	16190	28839	1.18	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4017	16763	29391	7.95	1.0E-106	AW974650.1	EST_HUMAN	EST386975 MAGC resequences; MAGN Homo sapiens cDNA
4017	16763	29392	7.95	1.0E-106	AW974650.1	EST_HUMAN	EST386975 MAGC resequences; MAGN Homo sapiens cDNA
4035	16760	29410	1.05	1.0E-106	5729729	NT	Homo sapiens AIP5-like 1 (AIP5L1), mRNA
4562	17297	29924	1.41	1.0E-106	BE144286.1	EST_HUMAN	MRO-H10165-140200-008-410 H10165 Homo sapiens cDNA
5135	17853	30469	1.09	1.0E-106	AL050253.1	NT	H. sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6, Shares domains with BMPs, Teloid, Sushi repeat proteins
5135	17853	30470	1.09	1.0E-106	AL050253.1	NT	H. sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6, Shares domains with BMPs, Teloid, Sushi repeat proteins
5285	18090	30750	2.61	1.0E-106	AA781155.1	EST_HUMAN	PHPS-1-2 (HUMAN);
5764	18555	31480	0.58	1.0E-106	AU130113	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5764	18555	31481	0.58	1.0E-106	AU130113	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5816	18505	31533	0.58	1.0E-106	AA434168.1	EST_HUMAN	2a28d12 s1 Scores every tumor N6HOT Homo sapiens cDNA clone IMAGE:770615 3'
5804	18589	31637	1.3	1.0E-106	AU143428	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
5904	18696	31638	1.3	1.0E-106	AU143428	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6011	18792	31755	4.89	1.0E-106	BF076674.1	EST_HUMAN	602154072F1 NIH MGSC 83 Homo sapiens cDNA clone IMAGE:4295067 5'
6303	18892	31860	0.77	1.0E-106	BE887112.1	EST_HUMAN	601439670F1 NIH MGSC 72 Homo sapiens cDNA clone IMAGE:3924641 5'
6325	19095	32083	17.66	1.0E-106	11546913	NT	Homo sapiens xycosyltransferase II (XT2), mRNA
6325	19095	32084	17.66	1.0E-106	11546913	NT	Homo sapiens xycosyltransferase II (XT2), mRNA
7271	19855	33031	5.16	1.0E-106	AA663779.1	EST_HUMAN	ae72607 s1 Stratiene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gp-X65873
7324	20007	33084	5.33	1.0E-106	11429817	NT	KINESIN HEAVY CHAIN (HUMAN);
7402	20180	33161	1.21	1.0E-106	BE282722.1	EST_HUMAN	Homo sapiens XPMO2 protein (LOC57109), mRNA
7511	20182	33275	9.29	1.0E-106	11425603	NT	601105736F1 NIH MGSC 13 Homo sapiens cDNA clone IMAGE:288345 5'
7511	20182	33276	9.29	1.0E-106	11425603	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7714	20376	33491	0.67	1.0E-106	AU116950.1	EST_HUMAN	AU116950 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'

Page 435 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7884	20579	33707	6.44	1.0E-108 [BE741408.1]	EST_HUMAN	601594333.F1 NIH_MGC	9 Homo sapiens cDNA clone IMAGE:3948463 5'
7884	20579	33708	6.44	1.0E-108 [BE741408.1]	EST_HUMAN	601594333.F1 NIH_MGC	9 Homo sapiens cDNA clone IMAGE:3948463 5'
8074	20768	34387	1.38	1.0E-106 [A5230368.1]	EST_HUMAN	CALGRANULIN B (HUMAN);	ar98407.x1 Barbeded sorna HPLRB6 Homo sapiens cDNA clone IMAGE:227732 3' similar to gb:X06233
8527	21219	34361	0.47	1.0E-108 [BE397950.1]	EST_HUMAN	601282717.F1 NIH_MGC	44 Homo sapiens cDNA clone IMAGE:3604493 5'
8527	21219	34362	0.47	1.0E-108 [BE397950.1]	EST_HUMAN	601282717.F1 NIH_MGC	44 Homo sapiens cDNA clone IMAGE:3604493 5'
8607	21299	34443	3.94	1.0E-108 [A654123.1]	EST_HUMAN	OQ5084.s1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2285932 3' similar to SW10CA8_HUMAN	Y62405.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2285932 3' similar to SW10CA8_HUMAN
8950	21641	34788	0.68	1.0E-108 [AW33893.1]	EST_HUMAN	CMA-LT1006B-150200-068-468 LT0058 Homo sapiens cDNA	
9045	21735	34880	3.28	1.0E-108 [AA625307.1]	EST_HUMAN	cc87c68.x1 NCI CGAP GGB1 Homo sapiens cDNA clone IMAGE:1354760 3'	
9045	21735	34890	3.28	1.0E-108 [AA625307.1]	EST_HUMAN	cc87c68.x1 NCI CGAP GGB1 Homo sapiens cDNA clone IMAGE:1354760 3'	
9186	21855	35021	1.28	1.0E-108 [AT50447.1]	EST_HUMAN	cm03ac4.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTCB_cm03ac4 random	
9329	21886	35169	1.8	1.0E-108 [AT49569.1]	EST_HUMAN	hm41f02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2160689 3' similar to contains MSR1.13	
9329	21886	35170	1.8	1.0E-108 [AT49569.1]	EST_HUMAN	TAR1 PTRS repetitive element;	
9602	22651	35748	1.19	1.0E-108 [BF02334.1]	EST_HUMAN	TAR1 PTRS repetitive element;	
9804	22652	35841	1.08	1.0E-108 [BF02730.1]	EST_HUMAN	601282387.F1 NIH_MGC	44 Homo sapiens cDNA clone IMAGE:3804217 5'
9884	22682	35842	1.08	1.0E-108 [BF02730.1]	EST_HUMAN	601671674.F1 NIH_MGC	20 Homo sapiens cDNA clone IMAGE:3954403 5'
10141	22789	36003	6.22	1.0E-108 [AA604417.1]	EST_HUMAN	np57b10.s1 NCI CGAP B12 Homo sapiens cDNA clone IMAGE:1130395 3'	
10141	22789	36004	6.22	1.0E-108 [AA604417.1]	EST_HUMAN	np57b10.s1 NCI CGAP B12 Homo sapiens cDNA clone IMAGE:1130395 3'	
10185	22843	36047	1.6	1.0E-108 [AV383296.1]	EST_HUMAN	RCP-C10318-201109-031-a11 C10318 Homo sapiens cDNA	
10358	23005	36222	0.53	1.0E-108 [AC039866.1]	EST_HUMAN	DKFZP434F012.1_1.434 (synonym: lited3)	Homo sapiens cDNA clone DKFZP434F012 5'
10479	23125	36354	2.81	1.0E-108 [AL163202.2]	NT	Homo sapiens chromosome 21 segment HS21C002	
10812	23495	36730	7.1	1.0E-108 [BF03765.1]	EST_HUMAN	601453461.F1 NIH_MGC	88 Homo sapiens cDNA clone IMAGE:3857366 5'
10812	23495	36731	7.1	1.0E-108 [BF03765.1]	EST_HUMAN	601453461.F1 NIH_MGC	88 Homo sapiens cDNA clone IMAGE:3857366 5'
10965	23688	36925	2.22	1.0E-108 [J06200.1]	NT	Human pyrimidine receptor mRNA, complete cds	
10965	23688	36926	2.22	1.0E-108 [J06200.1]	NT	Human pyrimidine receptor mRNA, complete cds	
11384	23991	37262	1.81	1.0E-108 [BE27395.1]	EST_HUMAN	601106219.F1 NIH_MGC	16 Homo sapiens cDNA clone IMAGE:3349597 5'
11632	24132	37486	1.35	1.0E-108 [BE010892.1]	EST_HUMAN	RC5-BN0192-100300-021-B02 BN0192 Homo sapiens cDNA	
11632	24132	37487	1.35	1.0E-108 [BE010892.1]	EST_HUMAN	RC5-BN0192-100300-021-B02 BN0192 Homo sapiens cDNA	
11951	25164	37591	6.77	1.0E-108 [AY140405.1]	EST_HUMAN	MCS11.x1 NIH_MGC	17 Homo sapiens cDNA clone IMAGE:2661644 5'
12193	24664	37088	3.32	1.0E-108 [BE894468.1]	EST_HUMAN	601433877.F1 NIH_MGC	72 Homo sapiens cDNA clone IMAGE:3918524 5'

Page 436 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12103	24694	31060	3.32	1.0E-106	BE684488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12408	24791		4.6	1.0E-106	BE685905.1	EST_HUMAN	RC1-CT0249-090800-024-003 CT0249 Homo sapiens cDNA
228	13040		4.42	1.0E-107	AJ271735.1	NT	Homo sapiens Xa pseudocatalase region, segment 1/2
288	13068		1.29	1.0E-107	X60460.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
607	13365		4.03	1.0E-107	4826963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
616	13394	26028	1.89	1.0E-107	AF15103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
866	13635	23305	1.82	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
948	13714	26379	11.55	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1265	14004	26673	0.73	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1662	14309	26966	3.71	1.0E-107	BF087405.1	EST_HUMAN	GV2-HT0540-120900-388-003 HT0540 Homo sapiens cDNA
1746	14468	27187	1.65	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (GTS2) gene, exon 3
1832	14571	27263	0.99	1.0E-107	AB007622.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1832	14571	27284	0.69	1.0E-107	AB007622.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2205	14933	27671	0.95	1.0E-107	U13726.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2362	15084	27822	1.45	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-003 CN0031 Homo sapiens cDNA
2362	15084	27823	1.45	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-003 CN0031 Homo sapiens cDNA
2535	15260	27881	1.2	1.0E-107	BE732460.1	EST_HUMAN	601567616F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2535	15260	27892	1.2	1.0E-107	BE732460.1	EST_HUMAN	601567616F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3007	15773	28421	3.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-003 CN0031 Homo sapiens cDNA
3007	15773	28422	3.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-003 CN0031 Homo sapiens cDNA
3066	15851	28502	2.63	1.0E-107	5802637	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3806	16558	29160	5.14	1.0E-107	AF020871.1	NT	Homo sapiens myoglobin (MTM1) gene, exon 9
5537	18335	31242	0.69	1.0E-107	AW98036.1	EST_HUMAN	EST338111B MAGE resequences, MAGK Homo sapiens cDNA
5775	18569	31485	3.2	1.0E-107	BE967469.1	EST_HUMAN	601442593F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3846494 5'
6923	19484	32506	1.45	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIC, polypeptide 1 (alpha subunit, 220KD) (GTF3C1), mRNA
6923	19484	32507	1.45	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIC, polypeptide 1 (alpha subunit, 220KD) (GTF3C1), mRNA
7263	19947	33023	1.42	1.0E-107	AW503613.1	EST_HUMAN	UJHF-BNG-alf-c-08-O-J1-F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7263	19947	33024	1.42	1.0E-107	AW503613.1	EST_HUMAN	UJHF-BNG-alf-c-08-O-J1-F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7429	20105	33193	1.46	1.0E-107	AF165078.1	EST_HUMAN	W454904.X1 NC1 CGAP Kld11 Homo sapiens cDNA clone IMAGE:2384791 3'
7690	20354	33469	0.6	1.0E-107	AW410861.1	EST_HUMAN	IR08H11.X2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2864524 5'
9267	22041	35213	0.95	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MANM1A1 Homo sapiens cDNA clone MAMMA1002433 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10803	23227	36537	3.18	1.0E-107	AI328550.1	EST_HUMAN	IG10408.x1 NCL CGAP, CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI
10888	23548	36704	14.28	1.0E-107	U67141.1	NT	P05068 ALPHA-ACTININ 3, NON MUSCULAR, .
10880	23560	36807	1.71	1.0E-107	BF60511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11283	23564	37282	6.66	1.0E-107	BE540550.1	EST_HUMAN	602123953F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4281039 5'
11387	23178	36405	5.97	1.0E-107	11419701	NT	60106595F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11387	23178	36406	5.97	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11843	24427	37768	1.36	1.0E-107	4505970	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11843	24427	37769	1.36	1.0E-107	4505970	NT	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
12043	25228	26387	5.86	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
935	13702	26387	2.69	1.0E-108	BE28042.1	EST_HUMAN	ZK43601.k1 Scores retina N2b-4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
1242	13591	26537	1.87	1.0E-108	Y18000.1	NT	THR repetitive element ;
							60117701B1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
							Homo sapiens NF2 gene
2428	15146	27683	4.97	1.0E-108	BE206954.1	EST_HUMAN	b625b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2983899 3' similar to gb:X53777 60S
3344	16103	28755	0.71	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L28 (HUMAN); gb:J06277 Mouse hexokinase mRNA, complete cds (MOUSE);
3344	16103	28756	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4136	16378	28607	1.14	1.0E-108	AW684438.1	EST_HUMAN	HT281.x1 NCL CGAP, GU1 Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW:3BP1_MOUSE
4489	17225	28953	2.18	1.0E-108	U72961.1	NT	P51584 SH3-BINDING PROTEIN 3BP-1 ;
4489	17225	28954	2.18	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4752	17484	30113	1.74	1.0E-108	7661978	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4893	17623	30241	2.8	1.0E-108	AJ068005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5391	18191	30583	1.16	1.0E-108	AW384694.1	EST_HUMAN	RCOHT0372-241199-031-d03 HT0372 Homo sapiens cDNA
5440	18239	30954	1.7	1.0E-108	BE69018.1	EST_HUMAN	60144492F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3848980 5'
5440	18239	30955	1.7	1.0E-108	BE69018.1	EST_HUMAN	60144492F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3848980 5'
5937	18628		0.99	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6048	18628	31790	6.13	1.0E-108	AF29417.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6048	18628	31791	6.13	1.0E-108	AF29417.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

Page 438 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6169	18946	31918	1.27	1.0E-108	AJ133289.1	NT	Homo sapiens carboxin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6285	18907	31950	0.92	1.0E-108	BF334851.1	EST_HUMAN	PMA-CTD403-240700-001-c10 CTD403 Homo sapiens cDNA
6321	18287	32290	0.63	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6521	19287	32290	0.63	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7057	19748	32811	5.82	1.0E-108	11451857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7339	20020	33098	3.55	1.0E-108	47598333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS5D6) mRNA
7371	20057	33137	1.16	1.0E-108	BE262607.1	EST_HUMAN	601134771F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354084 5'
7405	20082	33164	0.84	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7405	20082	33164	0.84	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7663	20658	33655	1.68	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8014	20709	33838	0.48	1.0E-108	AW408694.1	EST_HUMAN	U-HE-BMD-ada-e-12-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8014	20709	33839	0.48	1.0E-108	AW408694.1	EST_HUMAN	U-HE-BMD-ada-e-12-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8945	21636	34781	0.75	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
8984	21674	34823	0.54	1.0E-108	N44974.1	EST_HUMAN	Y95h10.1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:273293 5' similar to PIR-A45773
10565	20368	33481	1.73	1.0E-108	BE53227.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly
10731	17911	30597	1.98	1.0E-108	Y12490.1	NT	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
10998	23871	36928	1.39	1.0E-108	AF223591.1	NT	Homo sapiens mRNA for Gqg-associated microtubule-binding protein (GMAP-210)
11239	23902	37191	3.82	1.0E-108	AW866185.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11294	23955	37293	2.2	1.0E-108	AV708760.1	EST_HUMAN	EST373253 IMAGE: ressequences, MAGI Homo sapiens cDNA
11294	23955	37294	2.2	1.0E-108	AV708760.1	EST_HUMAN	AV708760 ADC Homo sapiens cDNA clone ADCAEE03 5'
11343	24033	37399	1.67	1.0E-108	D63339.1	NT	AV708760 ADC Homo sapiens cDNA clone ADCAEE03 5'
11405	24054	37399	1.68	1.0E-108	D63339.1	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
12204	24871	31072	2.41	1.0E-108	AK024447.1	NT	Homo sapiens COL4A8 gene for alpha(IV) collagen, exon 23
12583	24906	37406	8.32	1.0E-108	BF344596.1	EST_HUMAN	Homo sapiens mRNA for FLJ003037 protein, partial cds
41	12569	25448	0.97	1.0E-108	AW803116.1	EST_HUMAN	Homo sapiens mRNA for KIAA0699 protein, partial cds
62	12569	25523	0.97	1.0E-108	D86974.1	NT	Human mRNA for KIAA0699 protein, partial cds
220	13031	26687	1.39	1.0E-108	11436391	NT	Human mRNA for KIAA0220 gene, partial cds
454	13240	25978	6.59	1.0E-109	4507712	NT	Homo sapiens tetrahydrofolate repeat domain 2 (TH22) mRNA
584	13364	25982	26.8	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
584	13364	25983	26.8	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
1180	13633	26598	10.97	1.0E-109	N29599.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPB23) mRNA, complete cds

Page 439 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1181	13933	26598	4	1.0E-109	M26699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1533	14280	26597	3.31	1.0E-109	BE263673.1	EST_HUMAN	301186022F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1533	14280	26598	3.31	1.0E-109	BE263673.1	EST_HUMAN	301186022F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1857	14605	27315	3.3	1.0E-109	D13543.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2237	14605	27705	1.78	1.0E-109	AL165284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2248	14676	27714	1.89	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/JN1 gene, exon 6
2628	15340	28084	3.68	1.0E-109	AI022328.1	EST_HUMAN	owl56a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.1
2628	15340	28085	3.96	1.0E-109	AI022328.1	EST_HUMAN	owl56a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.1
2629	15341	28086	2.07	1.0E-109	4504206	NT	Homo sapiens quaternary cyclase activator 1A (relina)(GUCY1A1) mRNA
3054	15820	28464	2.22	1.0E-109	N85160.1	EST_HUMAN	J2810F Human fetal heart_Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3383	16142	28799	3.14	1.0E-109	AW583192.1	EST_HUMAN	GM3-NN0009-190400-150-F10 NN0009 Homo sapiens cDNA
3383	16142	28800	3.14	1.0E-109	AW583192.1	EST_HUMAN	GM3-NN0009-190400-150-F10 NN0009 Homo sapiens cDNA
3508	16284	28918	1.21	1.0E-109	AF240598.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3548	16303	28933	0.9	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3548	16303	28934	0.9	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3823	16573	29357	2.59	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
3974	16723	29357	1.42	1.0E-109	A5011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3974	16723	29358	1.42	1.0E-109	A5011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4127	16869	29497	3.88	1.0E-109	AI656417.1	EST_HUMAN	ts96a03.x1 NCI_CGAP_PG22 Homo sapiens cDNA clone IMAGE:2238330 3' similar to WIP-F55A2.8
4141	16893	29512	1.02	1.0E-109	AA692274.1	EST_HUMAN	CE16100.1
4141	16893	29513	1.02	1.0E-109	AA692274.1	EST_HUMAN	CE16100.1
4371	17109	29744	2.48	1.0E-109	4504206	NT	P30712 GLUTHATHIONE S-TRANSFERASE THETA 2
4591	17286	29923	1.69	1.0E-109	R15400.1	EST_HUMAN	P30712 GLUTHATHIONE S-TRANSFERASE THETA 2
4591	17286	29923	1.69	1.0E-109	R15400.1	EST_HUMAN	P30712 GLUTHATHIONE S-TRANSFERASE THETA 2
4857	17595	30218	1.21	1.0E-109	BE263673.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377) mRNA
4892	17715	30320	1.39	1.0E-109	BE263673.1	EST_HUMAN	ys48a06.r1 Soares infant brain_11N1B Homo sapiens cDNA clone IMAGE:55057 5'
4892	17715	30321	1.39	1.0E-109	BE263673.1	EST_HUMAN	ys48a06.r1 Soares infant brain_11N1B Homo sapiens cDNA clone IMAGE:55057 5'
4892	17715	30321	1.39	1.0E-109	BE263673.1	EST_HUMAN	ys48a06.r1 Soares infant brain_11N1B Homo sapiens cDNA clone IMAGE:55057 5'
5167	17976	30534	0.81	1.0E-109	AU137282.1	EST_HUMAN	601186022F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5179	17988	30593	1.06	1.0E-109	BF673718.1	EST_HUMAN	601186022F2 NIH_MGC_15 Homo sapiens cDNA clone PLACE1006159 5'
5179	17988	30593	1.06	1.0E-109	BF673718.1	EST_HUMAN	601186022F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4272922 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5230	18038	30682	3.09	1.0E-109	5174822	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5520	18018		1.11	1.0E-109	BE178836.1	EST_HUMAN	RCH-UT015-200400-022-004 HT0615 Homo sapiens cDNA
5838	26078	31580	0.84	1.0E-109	BF76988.1	EST_HUMAN	CMT-UT0038-059500-399-007 UT0038 Homo sapiens cDNA
5907	18318		1.6	1.0E-109	BE178356.1	EST_HUMAN	RCH-UT0615-200400-022-004 HT0615 Homo sapiens cDNA
7140	19827	32896	0.97	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7484	20158	33230	3.99	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (AT-BTF1), mRNA
7486	20140	33232	6.28	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC, 18 Homo sapiens cDNA clone IMAGE:4040279 5'
7488	20140	33233	5.28	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC, 18 Homo sapiens cDNA clone IMAGE:4040279 5'
7874	20338	33451	0.97	1.0E-109	BE263297.1	EST_HUMAN	601145017F2 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3160228 5'
8073	20767	33898	1.48	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8183	20877	34014	0.99	1.0E-109	AW749130.1	EST_HUMAN	PMO-BT0340-091299-002-405 BT0340 Homo sapiens cDNA
8555	21247		2.77	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8633	21325	34466	8.42	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC, 88 Homo sapiens cDNA clone IMAGE:3882124 5'
8633	21325	34487	8.42	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC, 88 Homo sapiens cDNA clone IMAGE:3882124 5'
8876	21867	34711	0.56	1.0E-109	BE145872.1	EST_HUMAN	IL0-HT0205-071189-142-g01 HT0205 Homo sapiens cDNA
9137	21825	34980	1.81	1.0E-109	H84680.1	EST_HUMAN	y68g08.r1 Soares retina N265R Homo sapiens cDNA clone IMAGE:2221170 5' similar to SP.A53491
9250	21929	35101	0.83	1.0E-109	BE397058.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPIN;Y
9250	21929	35102	0.83	1.0E-109	BE397058.1	EST_HUMAN	601289760F1 NIH_MGC, 8 Homo sapiens cDNA clone IMAGE:3620030 5'
9384	22346		2.94	1.0E-109	F08604.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
10873	23364	36806	1.71	1.0E-109	BE540609.1	EST_HUMAN	601063030F1 NIH_MGC, 10 Homo sapiens cDNA clone IMAGE:3449599 5'
10873	23364	36807	1.71	1.0E-109	BE540609.1	EST_HUMAN	601063030F1 NIH_MGC, 10 Homo sapiens cDNA clone IMAGE:3449599 5'
10710	23369	36838	15.79	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC, 81 Homo sapiens cDNA clone IMAGE:4245341 5'
10888	23568	36818	1.85	1.0E-109	7682278	NT	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
10888	23568	36819	1.85	1.0E-109	7682278	NT	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
11069	23739	37013	1.8	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11342	24032	37336	2.72	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11383	23690	37291	11.6	1.0E-109	W16510.1	EST_HUMAN	z80B12.r1 Soares fetal lung, NIH-L19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
11685	24280	37802	1.48	1.0E-109	11148618	NT	PR-S43968 S43968 p54-beta stress-activated protein kinase - ret;
11848	24432	37773	1.27	1.0E-109	BF339540.1	EST_HUMAN	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
11848	24432	37774	1.27	1.0E-109	BF339540.1	EST_HUMAN	602039003F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4186753 5'
12112	14970	27714	2.71	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12328	14976	27714	2.73	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6

Page 441 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12443	24813	31047	2.08	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	12831	26444	1.65	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
36	12884	25482	4.71	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
36	12884	25483	4.71	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
36	12884	25483	4.71	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
79	12905	25543	0.7	1.0E-110	C04468.1	EST_HUMAN	C04468 Human heart cDNA (YNAkamure) Homo sapiens cDNA clone 3NH-C3467
107	12831	25444	2.28	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
514	13298	25930	1.54	1.0E-110	U64950.1	NT	Human dyshibelin (DTN) gene, exon 20
1157	13912	26575	0.8	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALGRU) mRNA
1258	14005	26374	0.8	1.0E-110	AB032263.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1914	14851	27361	1.18	1.0E-110	BE378477.1	EST_HUMAN	601237546F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609863 5'
2051	14784		1.6	1.0E-110	BF508858.1	EST_HUMAN	U11814-acc-b5-0-J1 st NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2843	19513		1	1.0E-110	4503088	NT	Homo sapiens chondralin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3189	15652	26803	1.49	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3189	15652	26804	1.49	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4031	16776	29407	1.09	1.0E-110	BE018558.1	EST_HUMAN	b582a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:060312 O60312 KIAA0596 PROTEIN ;
4591	17326	29551	2.14	1.0E-110	AB017213.1	EST_HUMAN	cc32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627683 3' similar to SW:NIH121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4608	17341	29572	3.6	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBAT Homo sapiens cDNA clone HEMBA1002241 5'
4916	17644		2.7	1.0E-110	7692441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5212	18020	30642	2.63	1.0E-110	BE289408.1	EST_HUMAN	601118170F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5639	18434	31347	0.8	1.0E-110	BE621069.1	EST_HUMAN	601118170F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3895795 5'
5656	18451	31384	8.61	1.0E-110	11416223	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5656	18451	31386	8.61	1.0E-110	11416223	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6617	25068	32395	8.08	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7002	16994	32746	0.8	1.0E-110	U06888.1	NT	Human GS2 gene, exon 2
7002	16994	32747	0.8	1.0E-110	U06888.1	NT	Human GS2 gene, exon 2
7224	19009	32983	0.74	1.0E-110	AJ660280.1	EST_HUMAN	U12608.x1 NCL_CGAP_Bro25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7326	20008	33085	6.9	1.0E-110	AU714276.1	EST_HUMAN	P90649 E1S TRANSLOCATION VARIANT 1 ;
7326	20008	33086	6.9	1.0E-110	AU714276.1	EST_HUMAN	AV1714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7355	20036	33114	3.21	1.0E-110	AB020875.1	NT	AV1714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7355	20036	33114	3.21	1.0E-110	AB020875.1	NT	Homo sapiens mRNA for KIAA0368 protein, partial cds
7469	20143	33235	0.83	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007811 5'

Page 442 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9234	21913	35087	7.88	1.0E-110	BE302564.1	EST_HUMAN	366801.v1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:07258 07258
9478	22129	35308	2.39	1.0E-110	AW83394.1	EST_HUMAN	EG-114D9.2 PROTEIN. ;
10221	22869	36081	3.45	1.0E-110	11432732	NT	QVZ1-T0053-020400-119-041 T0053 Homo sapiens cDNA
10648	23339	36578	3.64	1.0E-110	Y1237.1	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10887	23567	36816	3.75	1.0E-110	BE734337.1	EST_HUMAN	H sapiens mRNA for myotonic dystrophy protein kinase like protein
10887	23567	36817	3.75	1.0E-110	BE734337.1	EST_HUMAN	601555904.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11420	23187	36418	2.45	1.0E-110	AA445529.1	EST_HUMAN	601555904.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11839	24498		4.54	1.0E-110	BE897218.1	EST_HUMAN	zw67602.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781258 5' similar to TR:G1145816
12081	24576		11.71	1.0E-110	AW062258.1	EST_HUMAN	G1145816 FKBP54 ;
12280	24720		1.44	1.0E-110	AB011359.1	NT	601439784.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924948 5'
12346	24753		1.35	1.0E-110	AI27761.1	EST_HUMAN	10-070163-040989-094-010 BT0163 Homo sapiens cDNA
12429	25339		3.25	1.0E-110	BF364466.1	EST_HUMAN	Homo sapiens gene for AF-8, complete cds
12701	14784		1.45	1.0E-110	BF508896.1	EST_HUMAN	gc31c12.x1 Soares_pregnant_uterus_NbRPU Homo sapiens cDNA clone IMAGE:1711222 3'
1701	12883		10.84	1.0E-111	UA3701.1	NT	PM3-NHT082-140900-008-f12 NN1082 Homo sapiens cDNA
181	13004	25045	1.05	1.0E-111	BF035327.1	EST_HUMAN	U-H-BJ4-mos-b-05-o-UJLat NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
718	13492		2.35	1.0E-111	BF035327.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
728	13500	25154	5.13	1.0E-111	M25142.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
908	13673	26338	3.82	1.0E-111	M25142.1	NT	60145831.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662098 5'
1624	14371	27050	1.43	1.0E-111	F652177.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CEGR1), mRNA
2234	14992	27701	1.02	1.0E-111	AF036126.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4150	16592	29522	1.08	1.0E-111	K02268.1	NT	Homo sapiens KIAA0556 gene product (KIAA0556), mRNA
4295	17034	29662	4.38	1.0E-111	K02268.1	NT	Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene, exons 28, 30, 31, and 32
4581	17425	30057	8.36	1.0E-111	4505778	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
5544	18341	31249	1.09	1.0E-111	BE567039.1	EST_HUMAN	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
5942	18724	31683	1.98	1.0E-111	AI844876.1	EST_HUMAN	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PTK1A1), mRNA
6550	18849	32357	1.16	1.0E-111	AL040762.1	EST_HUMAN	601443590.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
6709	19624	32958	1.06	1.0E-111	AIW284648.1	EST_HUMAN	qp09g12.x1 NCI CGAP_Kids Homo sapiens cDNA clone IMAGE:1617574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
7347	20028	33104	2.69	1.0E-111	BF366228.1	EST_HUMAN	DKFZP434C1815.1 1341 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
7433	20110	33189	0.92	1.0E-111	AI781228.1	EST_HUMAN	UHL-BWO-aid-03-o-UJ1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729525 3'
							IL2-NT0101-289700-114-E03 NT10101 Homo sapiens cDNA
							w65d01.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813
							CYTCHROME P450 IIIA5 (HUMAN);

Page 443 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7514	20185	33279	0.6	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p47 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
7993	20688	33815	0.73	1.0E-111	AA278868.1	EST_HUMAN	G12694.0 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
7993	20688	33815	0.73	1.0E-111	AA278868.1	EST_HUMAN	G12694.0 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
8088	20782	33912	0.82	1.0E-111	11431896	NT	Homo sapiens protein x 0001 (LOC51185) mRNA
8138	20833	33967	3.28	1.0E-111	U66533.1	NT	Homo sapiens integrin (ITGB4) gene, exon 13
8579	21271	34409	0.79	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2) mRNA
8674	21365	34513	0.73	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
8707	21399		1.57	1.0E-111	AF177987.1	NT	Homo sapiens cone sodium-calcium potassium exchanger splice variant (NCKX) mRNA, complete cds
8708	21400		8.85	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIP1_MGC_58 Homo sapiens cDNA clone IMAGE:4078303 5'
8782	21474	34620	12.9	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8782	21474	34621	12.9	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8866	21676	34825	2.8	1.0E-111	AF091395.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
8217	21898	35056	0.49	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-065 BT0817 Homo sapiens cDNA
10062	22700	35917	3.21	1.0E-111	AA604160.1	EST_HUMAN	ae58g02.61 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:U09235
10080	22728		2.4	1.0E-111	DT0083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10172	22820	36036	5.24	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10973	23849	36902	4.25	1.0E-111	U88156.1	NT	723101.r1 Scores_Pregnant_Uterus_NHPHU Homo sapiens cDNA clone IMAGE:503545 5'
11465	24068	37376	2.74	1.0E-111	AJ761071.1	EST_HUMAN	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11987	24464	37802	3.72	1.0E-111	11417801	NT	cn07a11.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn07a11 random
12424	24800	31040	1.51	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT), mRNA
12672	17814	30589	1.56	1.0E-111	AB033559.1	NT	AV708482 ADC Homo sapiens cDNA clone ADCA0809 5'
594	13372	28001	1.29	1.0E-112	4501854	NT	Homo sapiens mRNA for neuroxin 1-alpha protein, complete cds
595	13374	28003	12.95	1.0E-112	U28103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
596	13374	28004	12.95	1.0E-112	U28103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
598	13374	28004	1.86	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
617	13385	28029	1.86	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
617	13395	28030	1.86	1.0E-112	BF509039.1	EST_HUMAN	U1-HB4-act-g-04-U1.g1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
981	13746	28408	8.84	1.0E-112	AF157823.1	NT	U1-HB4-act-g-04-U1.g1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1040	13800	28446	2.2	1.0E-112	IP52742	SWISSPROT	Homo sapiens HTRA serine protease (FRS311) gene, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1879	14423	27117	4.39	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1879	14423	27118	4.39	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2194	14823	27657	1.37	1.0E-112	A1766525.1	EST_HUMAN	w60106.x1 NCI CGAP_KR12 Homo sapiens cDNA clone IMAGE:2400811 3'
2612	18226	27989	1.1	1.0E-112	BE66859.1	EST_HUMAN	6011442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3076	15842		1.15	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3955	18116	28770	0.7	1.0E-112	A1825511.1	EST_HUMAN	wk45b12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb181650_rnet SEMNENGEIN 1 PROTEIN PRECURSOR (HUMAN);
3984	18014	29233	0.74	1.0E-112	BE076073.1	EST_HUMAN	MR2-B10500-090300-113-09 BT0560 Homo sapiens cDNA
4565	17300	29827	1.39	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4704	17437	30068	4.9	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4704	17437	30069	4.9	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5681	18378	31291	40.71	1.0E-112	N46046.1	EST_HUMAN	w35407.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273229 5'
5985	18768	31730	1.04	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6155	18832	31699	1.43	1.0E-112	BE741660.1	EST_HUMAN	6011594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6989	19138	32134	0.68	1.0E-112	BF672815.1	EST_HUMAN	802152648F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293420 5'
6939	18304	32308	0.71	1.0E-112	BE273103.1	EST_HUMAN	601142765F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6939	18304	32309	0.71	1.0E-112	BE273103.1	EST_HUMAN	601142765F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6741	18575	32607	1.13	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7235	18921	32995	1.87	1.0E-112	11418777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7235	18921	32995	1.87	1.0E-112	11418777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7729	25120	33507	0.56	1.0E-112	BF213358.1	EST_HUMAN	601845039F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070302 5'
8093	20787	33919	1.73	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBAT1 Homo sapiens cDNA clone HEMBAT1002773 5'
8556	21647	34694	2.09	1.0E-112	BE887835.1	EST_HUMAN	6011443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8556	21647	34695	2.09	1.0E-112	BE887835.1	EST_HUMAN	6011443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9793	22444	35649	2.15	1.0E-112	BF114413.1	EST_HUMAN	730097.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TRCQVHV135 Q9VHV35 CG8743 PROTEIN;
10677	23368	36511	2.86	1.0E-112	AW683327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
10898	23548	36796	3.37	1.0E-112	AJ246900.1	NT	TRCQVHV135 Q9VHV35 CG8743 PROTEIN for secreted calcium-binding protein (smoc1 gene)
11040	23711	36981	1.92	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3713898 5'
11109	23779	37053	1.59	1.0E-112	A1762803.1	EST_HUMAN	q124608.y6 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TRCQ64362 Q64362 FUSED 102;

Page 445 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11109	23779	37054	1.59	1.0E-112	AI792903.1	EST_HUMAN	qk24c08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11139	23905	37085	6.6	1.0E-112	AW377670.1	EST_HUMAN	PMO-CT0237.141099.001-h02 CT0237 Homo sapiens cDNA
11810	24599	37734	1.82	1.0E-112	AI792903.1	EST_HUMAN	FUSED TOES ;
11810	24599	37735	1.92	1.0E-112	AI792903.1	EST_HUMAN	qk24c08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
725	13499	29152	5.37	1.0E-113	AI395586.1	EST_HUMAN	ac95101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
725	13499	29153	5.37	1.0E-113	AI395586.1	EST_HUMAN	ac95101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
921	13968	26352	7.89	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1532	14279	26966	2.86	1.0E-113	AI395586.1	EST_HUMAN	ac95101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1832	15524	27382	1.44	1.0E-113	AF240775.1	NT	Homo sapiens eIF-4E-transporter mRNA, complete cds
2088	14820	27551	1.02	1.0E-113	BF616218.1	EST_HUMAN	U1H-BW1-antF-03-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
2456	15174	27813	26.34	1.0E-113	AI006978.1	NT	Homo sapiens PLP gene
3127	15892	28536	1.82	1.0E-113	AI223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
4968	17691	30300	0.91	1.0E-113	D85606.1	NT	Homo sapiens gene for cholesteryloligolipin type-A receptor, complete cds
5008	17731	30335	2.16	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5008	17731	30336	2.16	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5165	25178	30393	2.97	1.0E-113	BE760958.1	EST_HUMAN	601469465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3872538 5'
5405	18205	30509	7.66	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP200607 5'
5832	18821	31554	4.17	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
5981	18548	31559	1.47	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
5978	18761	31725	2.92	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GALNAc-T8) (GALNT8), mRNA
6064	18943	31806	0.88	1.0E-113	5961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR7/TFAP), member 4 (ABCB4), transcript variant B, mRNA
6064	18943	31807	0.88	1.0E-113	5961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR7/TFAP), member 4 (ABCB4), transcript variant B, mRNA
6224	18998	31974	0.8	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6224	18998	31975	0.8	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7221	18906	32979	0.78	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503862 5'
7221	18906	32980	0.78	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503862 5'
7573	20242	33347	0.56	1.0E-113	AW959890.1	EST_HUMAN	EST371030 MAGE cDNAs, MAGE
8790	21482	34629	0.46	1.0E-113	8622819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8992	21882	34830	3.06	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
8992	21882	34831	3.06	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
9301	21868	34831	0.93	1.0E-113	BE772667.1	EST_HUMAN	RC1-F10134-280600.021-402 F10134 Homo sapiens cDNA
9730	22381	35593	1.4	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
9830	22381	35693	0.46	1.0E-113	M21535.1	NT	Human erg protein (steroid-related gene) mRNA, complete cds
9850	22598	35902	0.81	1.0E-113	5453907	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9850	22598	35903	0.81	1.0E-113	5453907	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10514	23160	36389	0.61	1.0E-113	AW600517.1	EST_HUMAN	UI-HF-BND-alk-b-10-Q-UI1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
10515	23161	36387	0.55	1.0E-113	BF691687.1	EST_HUMAN	602247740F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333280 5'
10516	23161	36398	0.55	1.0E-113	BF691687.1	EST_HUMAN	602247740F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333280 5'
11067	23737	37011	1.83	1.0E-113	AW600518.1	EST_HUMAN	UI-HF-BND-alk-b-12-Q-UI1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077328 5'
11076	23746	37016	2.84	1.0E-113	AW630281.1	EST_HUMAN	hh81a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11076	23748	37020	2.84	1.0E-113	AW630281.1	EST_HUMAN	hh81a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11181	18998	31974	1.39	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA
11181	18998	31976	1.39	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA
11227	23990	37177	2.81	1.0E-113	BE262688.1	EST_HUMAN	601105029F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
11481	24082	37393	1.32	1.0E-113	AA580720.1	EST_HUMAN	nc80903.r1 NCI_CGAP_GG1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P38748 FLAP ENDONUCLEASE-1 ;
11481	24082	37394	1.32	1.0E-113	AA580720.1	EST_HUMAN	nc80903.r1 NCI_CGAP_GG1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P38748 FLAP ENDONUCLEASE-1 ;
630	13409	26045	6.8	1.0E-114	T70551.1	EST_HUMAN	yd15d01.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN) contains Alu repetitive element;
1046	13808	26468	1.7	1.0E-114	8923087	NT	Homo sapiens hypothelial protein FUJ20080 (FUJ20080), mRNA
1290	14039	26712	5.09	1.0E-114	7657529	NT	Homo sapiens nucleolin-like protein 1 (NLP_1), mRNA
1667	14413	27104	4.27	1.0E-114	6678073	NT	Homo sapiens nucleolin-like protein 1 (NLP_1), mRNA
2807	12871	25491	1.28	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2807	12871	25492	1.28	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3128	15893	26337	2.76	1.0E-114	X04086.1	NT	Human gene for cathepsin (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3169	15932	26581	1.02	1.0E-114	BF206374.1	EST_HUMAN	601189932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3987	16745	28971	2.61	1.0E-114	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4388	17096	29731	0.72	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rac) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5064	17783	30420	1.05	1.0E-114	BE275324.1	EST_HUMAN	60122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345089 5'
5315	18119	30775	1.28	1.0E-114	4506890	NT	Homo sapiens scna domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5315	18119	30776	1.26	1.0E-114	4506880	NT	Homo sapiens scna domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5508	18308	31207	0.97	1.0E-114	9257201	NT	Homo sapiens calinin, heavy polypeptide-like 1 (GLTCL1), transcript variant 2, mRNA
6134	18912	31881	0.84	1.0E-114	Z26288.1	NT	H. sapiens Isodorm 1 gene for L-type calcium channel, exon 20
6898	17974	30531	0.62	1.0E-114	4750163	NT	Homo sapiens sparc/osteonectin, ovcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6977	19459	32594	1.02	1.0E-114	AU134187.1	EST_HUMAN	Homo sapiens HOMO1GT-1 mRNA for sperm antigen, complete cds
7139	18628	32594	1.02	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARG1 Homo sapiens cDNA clone OVARG1001444 5'
7139	18628	32595	1.02	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARG1 Homo sapiens cDNA clone OVARG1001444 5'
7182	18668	32941	8.3	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7182	18668	32942	8.3	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7182	20487	33610	2.92	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutylic acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8067	20761	33589	1.92	1.0E-114	A393139.1	EST_HUMAN	gy88d06.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8067	20761	33590	1.92	1.0E-114	A393139.1	EST_HUMAN	gy88d06.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8602	21284	34437	3.81	1.0E-114	U83041.1	NT	Homo sapiens cDNA for KIAA0561 protein, partial cds
8695	21357	34505	6.93	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8695	21357	34508	6.93	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9081	21770	34933	0.49	1.0E-114	BF109832.1	EST_HUMAN	718912.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR-040988 Q80UH9 TRANSMEMBRANE PROTEIN 2.1
9314	21881	35171	6.83	1.0E-114	AW327455.1	EST_HUMAN	dc03105.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9363	20433	33555	2.8	1.0E-114	AF07754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9448	22987	33505	1.03	1.0E-114	M13536.1	NT	Homo sapiens cDNA clone IMAGE:3853500 5'
10039	22987	33505	1.03	1.0E-114	BE870004.1	EST_HUMAN	601448752F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3853500 5'
10061	22709	33527	1.5	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10439	22085	36313	0.7	1.0E-114	BE171694.1	EST_HUMAN	MRO-H10559-250200-002-007 H10559 Homo sapiens cDNA
							bat7ag12Y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3206086 5' similar to gb:X17209 40S RIBOSOMAL PROTEIN S4 (HUMAN); gi:M20032 Mouse LLRpp3 protein mRNA from a repetitive element, complete (MOUSE)
10697	23378	38714	3.15	1.0E-114	BE302866.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CAON1E) gene, exons 7-49, and partial cds, alternatively spliced
10789	23472	38714	1.71	1.0E-114	AF22391.1	NT	

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10789	23472	36715	1.71	1.0E-114	AF22391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11145	23812	37094	3	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cDABA08 5'
11145	23812	37094	3	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cDABA08 5'
11796	24386	37719	1.7	1.0E-114	4758673	NT	Homo sapiens LIM HOX gene 2 (LHX2) mRNA
11834	24418	37769	1.32	1.0E-114	11526317	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), mRNA
12354	24502	30998	3.42	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein G12-1 (CG12-1), mRNA
12577	24602	30998	4.63	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12577	24602	30999	4.93	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
21	12849	25464	2.89	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
127	12842	26885	2.03	1.0E-115	4505988	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	12846	25733	2.33	1.0E-115	4557897	NT	Homo sapiens keratin 18 (KRT18) mRNA
288	13062	25733	2.23	1.0E-115	AW804759.1	EST_HUMAN	QV4UM0094-300300-155-508 Homo sapiens cDNA clone IMAGE:1946803 3' similar to TR:000336 000536
523	13307	26639	0.99	1.0E-115	A139206.1	EST_HUMAN	q0601.x1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946803 3' similar to TR:000336 000536
523	13307	25940	0.99	1.0E-115	A139206.1	EST_HUMAN	q0601.x1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946803 3' similar to TR:000336 000536
523	13307	25940	0.99	1.0E-115	A139206.1	EST_HUMAN	q0601.x1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946803 3' similar to TR:000336 000536
769	13541	28201	1.38	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
769	13541	28202	1.38	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
771	13543	25204	40.4	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1552	14298	26995	1.26	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidase semialdehyde synthase mRNA, complete cds
1552	14298	26996	1.26	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidase semialdehyde synthase mRNA, complete cds
1633	14572	27285	1.01	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2078	14810	27541	0.96	1.0E-115	AB007602.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2298	15023	27768	2.13	1.0E-115	AF231124.1	EST_HUMAN	Homo sapiens KIAA0442 mRNA, partial cds
2655	15623	28518	1.39	1.0E-115	AW804759.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
3113	16978	28519	8.22	1.0E-115	AJ245922.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
3113	16978	28519	8.22	1.0E-115	AJ245922.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
3465	16221	28875	1.6	1.0E-115	AJ271692.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
4021	16767	29397	3.67	1.0E-115	AB002348.2	NT	Homo sapiens KIAA0442 mRNA, partial cds
4389	17107	29742	3.27	1.0E-115	6812659	NT	Homo sapiens KIAA0442 mRNA, partial cds
4403	17140	29768	3.5	1.0E-115	4758279	NT	Homo sapiens KIAA0442 mRNA, partial cds
4428	17363	28996	2.64	1.0E-115	AL096957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

Page 449 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4628	17363	29597	2.64	1.0E-115	AL095957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4848	17578	30201	3.51	1.0E-115	AL163283.2	NT	Human sapiens chromosome 21 segment HS21C068
4848	17578	30202	3.51	1.0E-115	AL163283.2	NT	Human sapiens chromosome 21 segment HS21C068
5263	18069	30992	1.02	1.0E-115	AW970335.1	EST_HUMAN	ES1392410 MAGE resequences, MAGEK Homo sapiens cDNA
5338	18141	30992	0.78	1.0E-115	BF665367.1	EST_HUMAN	602118246F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5454	18253	31143	1.08	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433). mRNA
5454	18253	31144	1.08	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433). mRNA
5604	18400	31313	1.34	1.0E-115	AI928766.1	EST_HUMAN	au94g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519593 3' similar to gbL07807 DYNAMIN-1 (HUMAN);
5604	18400	31314	1.34	1.0E-115	AI928769.1	EST_HUMAN	au94g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519593 3' similar to gbL07807 DYNAMIN-1 (HUMAN);
6168	18945	31816	0.97	1.0E-115	11428788	NT	Homo sapiens sperm surface protein (HSS). mRNA
6168	18945	31817	0.97	1.0E-115	11428788	NT	Homo sapiens sperm surface protein (HSS). mRNA
6302	18076	32061	0.84	1.0E-115	11428938	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63435). mRNA
6434	18202	32189	2.04	1.0E-115	7861883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054). mRNA
6434	18202	32190	2.04	1.0E-115	7861883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054). mRNA
6835	18497	32521	0.83	1.0E-115	T86774.1	EST_HUMAN	y86b08.r1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:118095 5' similar to SP-DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7178	18864	32835	1.54	1.0E-115	AI076598.1	EST_HUMAN	cc231a06.x1 Scores, total, fetus_N52HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7178	18864	32836	1.54	1.0E-115	AI076598.1	EST_HUMAN	cc231a06.x1 Scores, total, fetus_N52HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7308	18991	33069	8.22	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
8060	20764	33885	13.71	1.0E-115	BE630187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8060	20764	33886	13.71	1.0E-115	BE630187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8712	21404	34548	2.16	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B). mRNA
9075	23237	35522	0.6	1.0E-115	BF382029.1	EST_HUMAN	601816352F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050108 5'
9809	22549	35743	2.25	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0938 gene, partial cds
9809	22549	35744	2.25	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0938 gene, partial cds
10418	23064	36284	1	1.0E-115	AI221878.1	EST_HUMAN	qq9e009.x1 Scores_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10418	23064	36285	1	1.0E-115	AI221878.1	EST_HUMAN	qq9e009.x1 Scores_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10426	23072	36293	0.82	1.0E-115	AI524887.1	EST_HUMAN	h112407.x1 NCL CGAP_CLI1 Homo sapiens cDNA clone IMAGE:2118036 3' similar to TRC16129 O16129 PHENYLALANINE TRNA SYNTHETASE ;
10617	23310	36549	7.62	1.0E-115	AW571644.1	EST_HUMAN	xx3208.x1 NC1 CGAP_UR Homo sapiens cDNA clone IMAGE:2836239 3' similar to SW:CAYP_CANFA P10463 CALYPHOSINE ;
10859	23549	36797	1.33	1.0E-115	9810279	NT	Homo sapiens UDP-glucose 6-epimerase 1 (HUGT1). mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11225	23698	37174	1.54	1.0E-116	BE045890.1	EST_HUMAN	hg54c10.x1 NCI CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378
11225	23698	37175	1.54	1.0E-116	BE045890.1	EST_HUMAN	PRP4 PROTEIN KINASE HOMOLOG ;
11374	23981	37281	2.27	1.0E-115	4502528	NT	hg54c10.x1 NCI CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378
11775	24368	37659	2.53	1.0E-115	BE265649.1	EST_HUMAN	PRP4 PROTEIN KINASE HOMOLOG ;
11842	24426	37767	1.63	1.0E-116	AW884376.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
11920	24481		2.16	1.0E-115	AF240786.1	NT	60111744F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352379 5'
559	13341	25660	1.08	1.0E-116	BE275502.1	EST_HUMAN	QV5-OT0035-290300-137-112 OT0065 Homo sapiens cDNA
783	13355	26216	2.21	1.0E-116	4507334	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
839	13609		1.76	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988975 5'
1990	14726	27447	2.55	1.0E-116	5174478	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
1990	14726	27448	2.65	1.0E-116	5174478	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
2090	15585	27552	2.6	1.0E-116	M19824.1	NT	Homo sapiens pericentriolar (PCNT) mRNA
2090	15585	27553	2.6	1.0E-116	M19824.1	NT	Homo sapiens pericentriolar (PCNT) mRNA
2305	16030	27767	1.95	1.0E-116	6463941	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2340	16063		1.36	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo, olfr17-01 (OR17-01) pseudogene, complete cds
2468	16176	27915	2.84	1.0E-116	AB018333.1	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2739	15533	28183	1.53	1.0E-116	BE889256.1	EST_HUMAN	Human olfactory receptor pseudo, olfr17-01 (OR17-01) pseudogene, complete cds
3171	15634	28592	4.87	1.0E-116	L77570.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
3171	15634	28593	4.87	1.0E-116	L77570.1	NT	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
4545	17084	29713	2.43	1.0E-116	5031954	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4803	17534	30156	1.57	1.0E-116	AB070988.1	EST_HUMAN	Homo sapiens DiGeorge syndrome critical region, centromeric end
5197	18005	30627	0.87	1.0E-116	A1302062.1	EST_HUMAN	Homo sapiens sodium phosphate transporter 3 (NP73) mRNA
5889	18674	31619	4.4	1.0E-116	W42822.1	EST_HUMAN	PM-BT135-070469-016 BT135 Homo sapiens cDNA
6117	18895	31862	1.8	1.0E-116	AB046856.1	NT	q116d04.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element MER25 repetitive element ;
6117	18895	31863	1.8	1.0E-116	AB046856.1	NT	2624d07.r1 Soares_senescent_fibroblasts NIH-SF Homo sapiens cDNA clone IMAGE:32245 5' similar to SW-MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6184	18961	31934	0.76	1.0E-116	BE408097.1	EST_HUMAN	Homo sapiens mRNA for KIAA1635 protein, partial cds
6421	19189		1.55	1.0E-116	BE158133.1	EST_HUMAN	Homo sapiens mRNA for KIAA1635 protein, partial cds
							601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636764 5'
							MR2-HT0379-210200-102-604 HT0379 Homo sapiens cDNA

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	18544	32572	1.18	1.0E-116	C02844.1	EST_HUMAN	C02844 Human heart cDNA (Nidamura) Homo sapiens cDNA clone 3NHCO667
7102	19780	32856	5.74	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBBCG06 5'
8267	20891	34451	1.37	1.0E-116	AA345426.1	EST_HUMAN	AF162685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8267	20881	34102	1.37	1.0E-116	AA345426.1	EST_HUMAN	AF162685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8378	21071	34209	0.88	1.0E-116	AB04151.1	EST_HUMAN	CM187043 c9c2289-075 BT043 Homo sapiens cDNA
8836	21528	34674	1.66	1.0E-116	BE565607.1	EST_HUMAN	601333268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680880 5'
8997	21687	34837	1.61	1.0E-116	AZ16352.1	EST_HUMAN	q00c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1944188 3' similar to gp16X8741_rnse1 PIBULIN-1 ISOFORM A PRECURSOR (HUMAN)
8873	22226	35411	1.52	1.0E-116	11418846	NT	Homo sapiens laminin, alpha 2 (laminin, congenital muscular dystrophy) (LAMA2), mRNA
10170	22818	36038	0.74	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylotransferase (XT-1 gene)
10170	22818	36037	0.74	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylotransferase (XT-1 gene)
10245	22894	36104	0.78	1.0E-116	BF158913.1	EST_HUMAN	QMA-HT0401-281-299-063-c09 HT0401 Homo sapiens cDNA
10586	23281	36519	2.4	1.0E-116	BF135549.1	EST_HUMAN	C62-GT0483-300800-349-c06 GT0482 Homo sapiens cDNA
11080	23760	37025	2.85	1.0E-116	AB987140.1	EST_HUMAN	q441c04.x1 Soares_NHMKP_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP30495.7
12825	25287		1.86	1.0E-116	AL144889.1	EST_HUMAN	DE01765 ;
545	13328	25949	1.67	1.0E-117	4826838	NT	CKFZ7621.110.T1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp7632.1110 5'
1055	15559	26474	0.96	1.0E-117	AF124383.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1747	14498	27188	1.02	1.0E-117	AF123320.1	NT	Mus musculus lymphocyte activation-associated protein 1 (Fath) gene, exons 13a through 15
1823	14592	27274	1.51	1.0E-117	M19816.1	NT	Homo sapiens triphosphate activation-associated protein mRNA, complete cds
2208	14836	27674	1.54	1.0E-117	AW557698.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
3262	16024	28674	1.84	1.0E-117	AA078114.1	EST_HUMAN	U51369/69 MAGE rescuees, MAGE Homo sapiens cDNA
3971	19720	29335	2.1	1.0E-117	AA316723.1	EST_HUMAN	op3211.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4310	17048	29874	2.03	1.0E-117	8693664	NT	EST188414 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to ribosomal protein L29
4538	17273	29805	2.95	1.0E-117	AL042120.1	EST_HUMAN	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4874	17408	30043	1.27	1.0E-117	X80670.1	NT	DKFZ3434C1120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ3434C1120 5'
4874	17408	30044	1.27	1.0E-117	X80670.1	NT	H sapiens mRNA for TPCP16 protein
4759	17491	30119	10.03	1.0E-117	AF134304.2	NT	H sapiens mRNA for TPCP16 protein
4759	17491	30120	10.03	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4887	17614	30233	3.57	1.0E-117	AB020673.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5138	17854	30471	0.73	1.0E-117	BE724681	EST_HUMAN	Homo sapiens mRNA for KIAA0368 protein, complete cds
5284	18070	30699	3.01	1.0E-117	BE730508.1	NT	Homo sapiens atrophin-1 Interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
601562657	F1 NIH_MGC_20	Homo sapiens cDNA clone IMAGE:3832214 5'					

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	17637	30574	0.86	1.0E-117	AA323348.1	EST_HUMAN	EST28111 Cerebellum II Homo sapiens cDNA 5' end similar to zinc finger domain
7350	20031	33108	5.01	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7350	20031	33109	5.01	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7446	20122	33212	1.75	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DOB Homo sapiens cDNA clone DCBBAB01 5'
7446	20122	33213	1.75	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DOB Homo sapiens cDNA clone DCBBAB01 5'
7878	20573	33699	3.39	1.0E-117	AI850145.1	EST_HUMAN	OT8065 KIAA0477 PROTEIN ;
8210	20904	34039	2.29	1.0E-117	10834689	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8210	20904	34040	2.29	1.0E-117	10834689	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8310	21004	34141	0.59	1.0E-117	AI804151.1	EST_HUMAN	CV4BT043-090299-075 BT043 Homo sapiens cDNA
8310	21004	34142	0.59	1.0E-117	AI804151.1	EST_HUMAN	CV4BT043-090299-075 BT043 Homo sapiens cDNA
9199	21868	35033	2.25	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
9886	22338	35532	2.07	1.0E-117	BE733922.1	EST_HUMAN	601568317-1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3843748 5'
9846	25127	35997	2.91	1.0E-117	AF069033.1	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
10469	23115	36345	1.11	1.0E-117	D83778.1	NT	Homo sapiens Drosophila-like protein (DROELOH), mRNA
10765	23449	36691	1.77	1.0E-117	D83778.1	NT	Human mRNA for KIAA0181 gene, partial cds
10984	23540	36891	2.68	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl isomerase) NIMA-interacting 1 (PINT), mRNA
10984	23540	36892	2.68	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl isomerase) NIMA-interacting 1 (PINT), mRNA
11243	23905	37195	3.32	1.0E-117	AB011641.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11243	23905	37197	3.32	1.0E-117	AB011641.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11369	23976	37501	14.73	1.0E-117	BE268956.1	EST_HUMAN	601168203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE3644286 5'
11587	24166	37501	2.02	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11587	24166	37502	2.02	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
68	12996	25530	5.98	1.0E-118	AF161600.1	NT	Homo sapiens HSPC151 mRNA, complete cds
94	12920	25557	2.13	1.0E-118	AL045854.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
504	13289	25922	5.67	1.0E-118	7657016	NT	DKFZP434I056.1 t34 (synonym: t3e3) Homo sapiens cDNA clone DKFZp434I056 5'
894	15555	26328	0.95	1.0E-118	5174680	NT	Homo sapiens hypothetical protein (Drosophila) homolog 1 (SIX1) mRNA
2227	14955	27693	2.04	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2227	14955	27694	2.04	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3604019 5'
2227	14955	27695	2.04	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3604019 5'
2329	15054	28169	1.68	1.0E-118	AW951728.1	EST_HUMAN	EST333769 MAGE resequences, MAGE Homo sapiens cDNA
2744	15450	28169	2.61	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2744	15450	28190	2.61	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3102	15937		4.64	1.0E-118	Y13632.1	NT	Homo sapiens PRKY exon 7

Table 4

Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3180	15953	28605	4.67	1.0E-118	A1347694.1	EST_HUMAN	qp0105.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3180	15953	28606	4.67	1.0E-118	A1347694.1	EST_HUMAN	qp0105.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
4067	16811	29439	4.77	1.0E-118	D23690.1	NT	Human mRNA for ribosomal protein, complete cds
4659	17393	30028	0.9	1.0E-118	11425793	NT	Homo sapiens KIA0478 gene product (KIA0478), mRNA
5337	18140	30800	1.87	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5337	18140	30801	1.87	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5337	18140	30802	1.87	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5543	18340	31247	0.94	1.0E-118	11422054	NT	Homo sapiens retin (RELN), mRNA
5543	18340	31248	0.94	1.0E-118	11422054	NT	Homo sapiens retin (RELN), mRNA
5694	18477	31935	1.24	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5694	18477	31936	1.24	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5694	18477	31937	1.24	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5772	18553	31462	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31578	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31579	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31580	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31581	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31582	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31583	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31584	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31585	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31586	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31587	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31588	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31589	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31590	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31591	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31592	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31593	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31594	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31595	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31596	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31597	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31598	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31599	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31600	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31601	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31602	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31603	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31604	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31605	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31606	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31607	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31608	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31609	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31610	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31611	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31612	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31613	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31614	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31615	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31616	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31617	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31618	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31619	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31620	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31621	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31622	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31623	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31624	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31625	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31626	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31627	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31628	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31629	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31630	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31631	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31632	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31633	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31634	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31635	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31636	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31637	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31638	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31639	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31640	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31641	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31642	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31643	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31644	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31645	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31646	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31647	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31648	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31649	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31650	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31651	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31652	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31653	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31654	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31655	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31656	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31657	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31658	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31659	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31660	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31661	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31662	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31663	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31664	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31665	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31666	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31667	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31668	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31669	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31670	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31671	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31672	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31673	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31674	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31675	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31676	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31677	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31678	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31679	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31680	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31681	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31682	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31683	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31684	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31685	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31686	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31687	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31688	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31689	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31690	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31691	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31692	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31693	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31694	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31695	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31696	0.83	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5853	18640	31697					

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10365	23012	36227	0.48	1.0E-118	AW271289.1	EST_HUMAN	xx46a10.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772668 3' similar to SW15008 HUMAN OT588 GAMMA-BUTYROBETAINE 2-OXOGLUTARATE DIOXYGENASE ;
10431	23077	36300	0.65	1.0E-118	AW296351.1	EST_HUMAN	UIH-BW0-aio-a07-Q-U1.s1 NCI CGAP_Sub0 Homo sapiens cDNA clone IMAGE:2729772 3'
11209	23669	37165	1.61	1.0E-118	BF686214.1	EST_HUMAN	602141626F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302788 5'
11286	23896	37168	1.8	1.0E-118	11065988	NT	Homo sapiens protein with polyglutamine repeat: calcium (ca2+) homeostasis endoplasmic reticulum protein (ERP)P07213-21. mRNA
11246	23908	37201	10.23	1.0E-118	AA315007.1	EST_HUMAN	EST188814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11548	24147	37457	1.68	1.0E-118	BE008876.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11548	24147	37458	1.68	1.0E-118	BE008876.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11551	24150	37461	1.61	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-512 UM0091 Homo sapiens cDNA
11551	24150	37462	1.61	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-512 UM0091 Homo sapiens cDNA
741	13514	28173	0.97	1.0E-119	AF170462.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1014	16558	26433	1.61	1.0E-119	7705807	NT	Homo sapiens GSH-105 protein (LOC51011). mRNA
1928	14682	27374	5.97	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3099	18894	28506	1.57	1.0E-119	8622205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052). mRNA
3234	15996		0.8	1.0E-118	AA916760.1	EST_HUMAN	on10605.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1559241 3' similar to WP:ED04F6.2
3234	15996		0.8	1.0E-118	AA916760.1	EST_HUMAN	CEC1214.1
3934	19694	26325	1.42	1.0E-119	4604116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5253	18068	30688	2.5	1.0E-119	AU133369.1	EST_HUMAN	AUT33369 NT2RP4 Homo sapiens cDNA clone NT2RP4001691 5'
5268	18072	30701	21.82	1.0E-118	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5270	18076	30706	3.11	1.0E-118	BE936121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5347	18150	30830	1.63	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GK-G Homo sapiens cDNA clone GKCDH803 5'
5503	18201	31201	0.53	1.0E-119	AL134803.1	EST_HUMAN	DKFZ762M0710.1 1762 (synonym: lme2) Homo sapiens cDNA clone DKFZ762M0710 5'
5503	18301	31202	0.63	1.0E-119	AL134803.1	EST_HUMAN	DKFZ762M0710.1 1762 (synonym: lme2) Homo sapiens cDNA clone DKFZ762M0710 5'
6036	18816	31778	7.67	1.0E-119	AI150703.1	EST_HUMAN	SW-K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6180	18967	31940	0.92	1.0E-118	AF315883.1	NT	Human c-fes/bpa proto-oncogene
6180	18967	31941	0.92	1.0E-119	AF315883.1	NT	Human c-fes/bpa proto-oncogene
6239	19013	31687	0.85	1.0E-119	AI476732.1	EST_HUMAN	Human c-fes/bpa proto-oncogene
6370	19138	32135	2.62	1.0E-118	X06262.1	NT	Human c-fes/bpa proto-oncogene
6380	19148	32148	4.69	1.0E-119	AW974193.1	EST_HUMAN	EST336236 MAGC resequences, MAGM Homo sapiens cDNA
7310	19693	33070	1.5	1.0E-119	BE766814.1	EST_HUMAN	601562005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946091 5'
8560	21252	34360	1.19	1.0E-119	BE616150.1	EST_HUMAN	601280594F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622328 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	22458	35693	1.15	1.0E-119	11036343	NT	Homo sapiens KIA0477 gene product (KIA0477), mRNA
10008	22654	39987	0.65	1.0E-119	A149796.1	EST_HUMAN	q143a1.1, X1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1792784, 3' similar to TR:Q13458
10149	22764	36008	3.35	1.0E-119	AA465124.1	EST_HUMAN	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10401	23047	36293	1.29	1.0E-119	AJ297701.1	NT	aa3205.1 [NCI] CGAP_GGB1 Homo sapiens cDNA clone IMAGE:814977 5'
10443	23069	36317	0.71	1.0E-119	11425937	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10443	23069	36318	0.71	1.0E-119	11425937	NT	Homo sapiens hypothetical protein FLJ10208 (FLJ10208), mRNA
10517	23163	36390	4.18	1.0E-119	AB032261.1	NT	Homo sapiens Sod mRNA for silaroy-CoA desaturase, complete cds
10385	23680	36913	2.38	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10385	23680	36914	2.38	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11159	23828		0.31	1.0E-119	BF596571.1	EST_HUMAN	G02186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310833 5'
12198	25326		2.16	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240899-011-f03 CT0212 Homo sapiens cDNA
294	13100	26741	1.43	1.0E-120	4607334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1018	13778	26439	2.49	1.0E-120	AF248540.1	NT	Homo sapiens intercedin 2 (SH3D1B), mRNA, complete cds
1018	13778	26440	2.49	1.0E-120	AF248540.1	NT	Homo sapiens intercedin 2 (SH3D1B), mRNA, complete cds
1405	14152	26832	2.31	1.0E-120	N44873.1	EST_HUMAN	Y40g12.r1 Soares melanocytes 2NHHM Homo sapiens cDNA clone IMAGE:273769 5'
1597	14343	27033	3.08	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1789	14539	27250	1.21	1.0E-120	4657250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2100	14831	27595	0.92	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2100	14831	27596	0.92	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2831	15247	27885	5.24	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3302	13100	25741	1.59	1.0E-120	4607334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4325	17064	26992	1.95	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4325	17064	26993	1.95	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4814	17349	26983	2.22	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4814	17349	26984	2.22	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5095	17784	30401	1.36	1.0E-120	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5133	17851	30458	0.9	1.0E-120	A1190903.1	EST_HUMAN	q62f103.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:173981 3'
6949	18444	31357	16.61	1.0E-120	BF596222.1	EST_HUMAN	60218394F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5949	18444	31358	16.61	1.0E-120	BF596222.1	EST_HUMAN	60218394F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6350	19120	32110	0.97	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
6350	19120	32111	0.97	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
7471	20144	33236	1.77	1.0E-120	D34619.1	NT	Human TBXA1S gene for thromboxane synthase, exon 7
7795	20490	33612	5.22	1.0E-120	Y00057.1	NT	Human gene for neurofilament subunit M (NF-M)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7795	20460	33813	5.22	1.0E-120	Y00087.1	NT	Human gene for neurofilament subunit M (NF-M)
8230	20924	34063	2.43	1.0E-120	BF337596.1	EST_HUMAN	602035552P1 NC1 CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4189333 5'
8903	20997	34195	0.85	1.0E-120	A0303057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8303	20597	34195	0.85	1.0E-120	A0303057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8307	21001	34198	2.33	1.0E-120	A0707864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8307	21001	34198	2.33	1.0E-120	A0707864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8307	21001	34198	2.33	1.0E-120	A0707864.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
8302	21045	34182	1.17	1.0E-120	A070784.1	EST_HUMAN	601307739P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9401	22063	35233	5.26	1.0E-120	BE392102.1	EST_HUMAN	601307739P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9401	22063	35234	5.26	1.0E-120	BE392102.1	EST_HUMAN	601307739P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9845	22297	35492	3.75	1.0E-120	BF306541.1	EST_HUMAN	601588958P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9845	22297	35492	3.75	1.0E-120	BF306541.1	EST_HUMAN	601588958P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9680	22312	35510	8.25	1.0E-120	AL132035.1	EST_HUMAN	AU133208 NT2R24 Homo sapiens cDNA clone NT2R2401541 5'
8671	22329	35525	0.79	1.0E-120	AL049801.1	NT	Newly human gene mapping to chromosome 13, similar to rat RhoGAP
8762	22443	35525	0.79	1.0E-120	AL049801.1	EST_HUMAN	CNP-BTD43-060239-075 BT043 Homo sapiens cDNA
8976	22824	35881	2.55	1.0E-120	AI604151.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11071	23741	37015	3.72	1.0E-120	BE265387.1	EST_HUMAN	601176727P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11316	24007	37311	2.06	1.0E-120	BE867619.1	EST_HUMAN	601443135P1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3847281 5'
11316	24007	37312	2.06	1.0E-120	BE867619.1	EST_HUMAN	601443135P1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3847281 5'
11650	24247	37667	1.38	1.0E-120	U64774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
71	12898	25634	1.08	1.0E-121	Y16000.1	NT	Homo sapiens NF2 gene
369	13165	28808	0.83	1.0E-121	AF149683.1	EST_HUMAN	AU134683 PLACET Homo sapiens cDNA clone PLACE1000699 5'
707	15549	28130	1.31	1.0E-121	AF032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1568	14316	27001	2.81	1.0E-121	AB011163.1	NT	Homo sapiens mRNA for KIAAC581 protein, partial cds
1958	14894	27407	1.33	1.0E-121	4755139	NT	Homo sapiens insectal polyphosphate-4-phosphatase, type I, 107MD (INPP4A), splice variant a, mRNA
1958	14894	27408	1.33	1.0E-121	4755139	NT	Homo sapiens insectal polyphosphate-4-phosphatase, type I, 107MD (INPP4A), splice variant a, mRNA
1958	14894	27408	1.33	1.0E-121	4755139	NT	Homo sapiens insectal polyphosphate-4-phosphatase, type I, 107MD (INPP4A), splice variant a, mRNA
1964	14700	27416	1.18	1.0E-121	M95968.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 9
1964	14700	27416	1.18	1.0E-121	M95968.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 9
2095	14926	27559	3.51	1.0E-121	L75693.1	NT	Homo sapiens melastophilin glutamate receptor 1 beta (mGlur1beta) mRNA, complete cds
2095	14926	27559	3.51	1.0E-121	L75693.1	NT	Homo sapiens mGlur1beta mRNA, complete cds
3078	15944	28466	3.51	1.0E-121	Y16208.1	NT	Homo sapiens HMB3 gene for hair keratin, exons 1 to 9
3078	15944	28467	3.51	1.0E-121	Y16208.1	NT	Homo sapiens HMB3 gene for hair keratin, exons 1 to 9
3078	15944	28467	3.51	1.0E-121	Y16208.1	NT	Homo sapiens HMB3 gene for hair keratin, exons 1 to 9
3525	16231	29937	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3525	16231	29937	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3525	16231	29937	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3525	16231	29937	1.19	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4296	17036	28653	2	1.0E-121	AJ263294.1	EST_HUMAN	q457601.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2005417 3'
4919	17647	30258	3.24	1.0E-121	X91031.1	NT	H.sapiens ECE-1 gene (exon 17)
5169	17594	30510	0.97	1.0E-121	BE222280.1	EST_HUMAN	h009038.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168119 3'
5474	18273	31187	0.85	1.0E-121	BE271424.1	EST_HUMAN	60144045F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6524	18290	32294	0.91	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
6788	18932	30537	0.98	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region, segment 2/2
6869	17943	30538	1.78	1.0E-121	AW89086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
6869	17943	30538	1.78	1.0E-121	AW89086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
7838	20533	33580	2.11	1.0E-121	11430217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
7842	20537	33584	2.45	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
7842	20537	33585	2.45	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
9758	22409	35615	1.21	1.0E-121	AW58358.1	EST_HUMAN	PHOSPHOLIPASE A2-GAMMA.1
9788	22409	35616	1.21	1.0E-121	AW58358.1	EST_HUMAN	PHOSPHOLIPASE A2-GAMMA.1
10675	23368	36009	2.95	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
10683	23374	36816	1.28	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
10889	23569	36820	3.46	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10917	23597	36844	2.53	1.0E-121	NS9524.1	EST_HUMAN	Y74260.1.s1 Soares fetal liver spleen cDNA clone IMAGE:249448 3'
11309	23968	37269	2.83	1.0E-121	AU118320.1	EST_HUMAN	AU118320 HEMBAT Homo sapiens cDNA clone HEMBA1006538 5'
281	13069	25707	2.29	1.0E-121	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
327	13128	25763	2.63	1.0E-121	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
348	13147	25787	2.14	1.0E-121	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
892	13631	28502	3.99	1.0E-121	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
11195	13350	26614	4.29	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1688	14432	27128	1.28	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S22 precursor, mRNA, complete cds
1707	14450	27150	1.35	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1707	14450	27151	1.35	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1807	14547	27282	4.34	1.0E-122	BE09024.1	EST_HUMAN	601487032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3866358 5'
2495	15212	27694	6.21	1.0E-122	BF316170.1	EST_HUMAN	601889173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2495	15212	27694	6.21	1.0E-122	BF316170.1	EST_HUMAN	601889173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2495	15212	27695	5.21	1.0E-122	BF316170.1	EST_HUMAN	601889173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2844	15812	28260	1.41	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4795	17528	30148	5.04	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4930	17658		1.46	1.0E-122	AW504645.1	EST_HUMAN	U1HF-BNG-ali-a-03-QJL1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076948 5'
5476	18276	31170	1.36	1.0E-122	BE256039.1	EST_HUMAN	801113697F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3354232 5'
6588	18276	31170	7.1	1.0E-122	BE256039.1	EST_HUMAN	801113697F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3354232 5'
7113	19801	32855	0.73	1.0E-122	AA898671.1	EST_HUMAN	ak49h08.st Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408339 3'
8695	21387	34530	0.66	1.0E-122	AJ278801.1	EST_HUMAN	Homo sapiens mRNA for doublesex and male-3 related transcription factor 1 (DMRT1)
8826	21617	34761	1.21	1.0E-122	11424218	NT	Homo sapiens initial giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9223	21902	35073	1.19	1.0E-122	AJ356818.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Bnc23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
9223	21902	35074	1.19	1.0E-122	AJ356818.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Bnc23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
10034	22682	35899	1.05	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbi (proto-oncogene)
10908	23558	36834	2.17	1.0E-122	AW955834.1	EST_HUMAN	EST367904 IMAGE resequences, MAGD Homo sapiens cDNA
11368	24046	37349	1.88	1.0E-122	AB024088.1	NT	Homo sapiens gene for B120, exon 10
11958	24509		6.8	1.0E-122	11418187	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
751	13523	26181	1.74	1.0E-123	BF345274.1	EST_HUMAN	602018059F1 NCL_CGAP_Bnc67 Homo sapiens cDNA clone IMAGE:4153670 5'
751	13523	26182	1.74	1.0E-123	BF345274.1	EST_HUMAN	602018059F1 NCL_CGAP_Bnc67 Homo sapiens cDNA clone IMAGE:4153670 5'
892	13754	28415	5.4	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1001	13761	28422	2.5	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1219	13966	28684	5.58	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1216	13986	28635	6.59	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1438	14185	28871	0.91	1.0E-123	AJ388341.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GND2
2002	14823	27555	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2092	14823	27556	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2092	14823	27557	2.7	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2313	16038		3.62	1.0E-123	7705862	NT	Homo sapiens RAB-like protein (LOC51209), mRNA
3245	16007	28657	0.95	1.0E-123	6812817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5361	18163	30847	1.59	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5381	18163	30848	1.58	1.0E-123	U34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5484	18283	31191	1.82	1.0E-123	BE789746.1	EST_HUMAN	601181108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948433 5'
6377	19146	32145	2.59	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6805	19043	32888	1.2	1.0E-123	H53198.1	EST_HUMAN	Xp4403.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1_YEAST P1-680 PROTEIN KINASE YAK1
6916	19852	32898	1.25	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7084	19783	32849	2.87	1.0E-123	U55288.1	NT	Human HBAVONIC-CAM precursor (HBAVONIC-CAM) gene, complete cds
7302	19885	33081	1.82	1.0E-123	11328833	NT	Homo sapiens heparan sulfate (glucosaminase) 2 (OAS2), mRNA
7542	20212	33312	1.3	1.0E-123	11436439	NT	Homo sapiens 2-5-difluoroadenylate synthetase 2 (OAS2), mRNA
7651	20221	33324	2.18	1.0E-123	BE269001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509182 5'
7816	20511	33636	0.87	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP-3003409 5'
8433	21126	33637	0.87	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP-3003409 5'
8433	21126	33637	1.13	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251199-012-407 BT0311 Homo sapiens cDNA
9289	22023	35185	2.43	1.0E-123	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9405	22067	35239	15.48	1.0E-123	U08823.1	NT	Oryzopsis cuniculatus New Zealand white elongation factor 1 alpha (Rabefad) mRNA, complete cds
11720	24314	37637	4.86	1.0E-123	BF07292.1	EST_HUMAN	602085791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11720	24314	37638	4.86	1.0E-123	BF07292.1	EST_HUMAN	602085791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
202	13070	25708	2.19	1.0E-124	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
262	13070	25709	2.19	1.0E-124	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	13076	25709	2.99	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
473	13259	25898	2.84	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
675	13450	26092	2.68	1.0E-124	AA397551.1	EST_HUMAN	281104.11 Svalbard schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR-G300482
675	13450	26093	2.68	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
742	13515	26173	7.84	1.0E-124	AF159554.1	NT	281104.11 Svalbard schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR-G300482
790	13562	26223	1.81	1.0E-124	4507500	NT	Human putative ribosomal protein S1 mRNA
884	13563	26321	1.84	1.0E-124	7705446	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1325	14074	26747	4.85	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC988), mRNA
1325	14074	26748	4.85	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1808	14548	27263	2.20	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2054	14788	27512	3.05	1.0E-124	BE878524.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (nHL81 gene)
3358	16118	28774	0.85	1.0E-124	4504116	NT	601481715F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3893954 5'
							Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

Page 480 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3482	16239	28805	1.25	1.0E-124	S76884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6BIR1) gene, exon
3482	16239	28806	1.25	1.0E-124	S76884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6BIR1) gene, exon
3490	16393	28033	1.54	1.0E-124	X13794.1	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (end joined CDS)
3890	16930	29259	1	1.0E-124	4507300	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4058	16801	23432	1.34	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4898	17430	30081	1.94	1.0E-124	A8024069.1	NT	Homo sapiens gene for P120, exon 11
4931	17608		1.13	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x-1
5216	18023	30647	12.12	1.0E-124	8922337	NT	Homo sapiens hypophthal protein FLJ10300 (FLJ10300), mRNA
5598	18333	31293	0.82	1.0E-124	4509786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
5797	18588	31514	8.94	1.0E-124	BF696135.1	EST_HUMAN	602124544F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6077	18868	31823	0.91	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CUAAD707 5'
6339	19109	32039	0.98	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
6912	19849	32695	2.65	1.0E-124	Y11717.1	NT	M.musculus mRNA for hox3 gene
7037	19729	32798	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2968585 5'
7037	19729	32797	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2968585 5'
7452	20128	33220	0.92	1.0E-124	AA690331.1	EST_HUMAN	ac08105.61 Stragano HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8156	20850	33982	6.07	1.0E-124	4608654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8392	21055	34195	1.28	1.0E-124	AW612108.1	EST_HUMAN	hg94469.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR_095162
8392	21055	34196	1.26	1.0E-124	AW612106.1	EST_HUMAN	hg94469.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR_095162
9060	21749	34907	0.61	1.0E-124	A1799864.1	EST_HUMAN	O69162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9060	21749	34908	0.61	1.0E-124	A1799864.1	EST_HUMAN	wc43g03.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9390	22032	35223	2.31	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9390	22032	35224	2.31	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCA0604 3'
9477	22130	35309	0.62	1.0E-124	AF022655.1	NT	Homo sapiens c2350 centromere associated protein mRNA, complete cds
9477	22130	35310	0.52	1.0E-124	AF022655.1	NT	Homo sapiens c2350 centromere associated protein mRNA, complete cds
9508	22161	35342	7.57	1.0E-124	A1767133.1	EST_HUMAN	w63802.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9508	22161	35343	7.57	1.0E-124	A1767133.1	EST_HUMAN	w63802.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9771	22422	35530	1.57	1.0E-124	AW603755.1	EST_HUMAN	U1-HF-BNO-alc-04-04-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078848 5'
10304	22487		1.44	1.0E-124	11432087	NT	Homo sapiens leucine-rich, glioma inactivated 1 (LGI1), mRNA
10978	23652	36905	1.61	1.0E-124	U94776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11305	23964	37265	3.51	1.0E-124	AW656663.1	EST_HUMAN	h105406.x1 Scores_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2969308 3'

Page 461 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11452	23218	36452	3	1.0E-124	AI440455.1	EST_HUMAN	(19603.x1) NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:Q31662 Q31662 YKRS PROTEIN ;
11452	23219	36453	3	1.0E-124	AI446455.1	EST_HUMAN	(19603.x1) NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:Q31662 Q31662 YKRS PROTEIN ;
12028	13480	26092	4.1	1.0E-124	AA387551.1	EST_HUMAN	Z81604.r1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12029	13450	26093	4.1	1.0E-124	AA397551.1	EST_HUMAN	Z81604.r1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12454	24823	31026	1.61	1.0E-124	AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12706	25279	30729	1.44	1.0E-124	11417862	NT	Homo sapiens calneutrin binding protein 1 (KIAA0330), mRNA
12706	25278	30730	1.44	1.0E-124	11417862	NT	Homo sapiens calneutrin binding protein 1 (KIAA0330), mRNA
148	12981	25603	1.74	1.0E-125	BE219510.1	EST_HUMAN	(19603.x1) NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELIN IA ;
146	12981	25604	1.74	1.0E-125	BE219510.1	EST_HUMAN	(19603.x1) NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELIN IA ;
311	13115		5.49	1.0E-125	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
417	12828	25441	5.47	1.0E-125	BE749922.1	EST_HUMAN	601577881F1 NIH_JMGC_9 Homo sapiens cDNA clone IMAGE:3626865 5'
629	13408	26043	1.18	1.0E-125	AI110659.1	EST_HUMAN	HA00065 Human fetal liver cDNA library Homo sapiens cDNA
629	13408	26044	1.18	1.0E-125	AI110659.1	EST_HUMAN	HA00066 Human fetal liver cDNA library Homo sapiens cDNA
711	13485	26134	1.66	1.0E-125	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
840	13610	26280	2.29	1.0E-125	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregment, uterus, NHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:XB6857.cdsl OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
978	13743	26405	1.22	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1131	13887	26545	1.76	1.0E-125	7662276	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1668	15375	27105	0.89	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1793	14533	27242	0.91	1.0E-125	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
1804	14544	27256	1.59	1.0E-125	AF015450.1	NT	Homo sapiens Uesurin-alpha mRNA, complete cds
1804	14544	27259	1.59	1.0E-125	AF015450.1	NT	Homo sapiens Uesurin-alpha mRNA, complete cds
2358	15080	27816	1.68	1.0E-125	AA011278.1	EST_HUMAN	201g06.r1 Soares_fetal liver spleen, NHFCS, S1 Homo sapiens cDNA clone IMAGE:429658 5'
2508	15225	27867	0.99	1.0E-125	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregment, uterus, NHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:XB6857.cdsl OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2604	15317	28057	1.3	1.0E-125	4504606	NT	Homo sapiens inhibin, alpha (INH) mRNA
2604	15317	28058	1.3	1.0E-125	4504606	NT	Homo sapiens inhibin, alpha (INH) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3009	17674	28425	0.94	1.0E-126	BE018009.1	EST_HUMAN	b57406.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:Q56004 Q95604 ZINC FINGER PROTEIN 1;
3839	16590	29228	0.92	1.0E-125	AA042813.1	EST_HUMAN	Z559c07.a1 Scarsa_pregmat_uterus_NNHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gpX66897_c061 OLFACTORY RECEPTOR-LIKE PROTEIN HGM07E (HUMAN);
4513	17248	29883	2.09	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4513	17248	29884	2.08	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4871	12661	25603	1.48	1.0E-125	BE218510.1	EST_HUMAN	h569a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177688 3' similar to TR:Q25058 Q25058 FIBROPELIN A;
4971	12661	25604	1.48	1.0E-125	BE218510.1	EST_HUMAN	h569a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177688 3' similar to TR:Q25058 Q25058 FIBROPELIN A;
5783	18574	31503	3.16	1.0E-125	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
5802	19592	31517	0.91	1.0E-125	BE176169.1	EST_HUMAN	QV2-HT0577-070500-165-505 HT0577 Homo sapiens cDNA
5842	19530	31555	3.76	1.0E-125	BE862980.1	EST_HUMAN	607433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2255108 3' similar to WP:C4639.2
5884	18970	31611	0.74	1.0E-125	AI670904.1	EST_HUMAN	CE01854;
6188	18995	31938	0.8	1.0E-125	BE736055.1	EST_HUMAN	607306670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
6486	19253	32253	1.63	1.0E-125	BE692328.1	EST_HUMAN	607335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689760 5'
6486	19253	32254	1.53	1.0E-125	BE592528.1	EST_HUMAN	607335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689760 5'
6891	19443	32469	5.28	1.0E-125	X03427.1	NT	Homo sapiens GF-II gene, exon 5
6891	19443	32469	5.28	1.0E-125	X03427.1	NT	Homo sapiens GF-II gene, exon 5
6891	19443	32469	5.28	1.0E-125	X03427.1	NT	Homo sapiens GF-II gene, exon 5
7706	20370	33483	0.55	1.0E-125	BE515100.1	EST_HUMAN	601236183F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603084 5'
8444	21136	34273	0.99	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8444	21136	34274	0.99	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8016	21709	34856	6.93	1.0E-125	BE181940.1	EST_HUMAN	QV1-HT0638-070500-191-412 HT0638 Homo sapiens cDNA
8016	21709	34857	6.93	1.0E-125	BE181940.1	EST_HUMAN	QV1-HT0638-070500-191-412 HT0638 Homo sapiens cDNA
9281	22035	36207	0.98	1.0E-125	AI656996.1	EST_HUMAN	h525b03.y1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089 HYPOPHYSICAL PROTEIN 1;
10350	22997	36215	0.53	1.0E-125	BE794576.1	EST_HUMAN	607169346F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'
10391	23037	36263	1.06	1.0E-125	AB002288.1	NT	Human mRNA for KIAA0300 gene, partial cds
10391	23276	36514	3.23	1.0E-125	AF043458.1	NT	Homo sapiens I-RRE gene, exon 6
10758	23443	36688	1.61	1.0E-125	AB014567.1	NT	Homo sapiens ryanodine receptor 1 (skatela) (RYR1), mRNA
11091	23751	37026	3.94	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11259	23921	37213	1.74	1.0E-126	7686505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11259	23921	37218	4.84	1.0E-126	AF260293.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11265	23927	37284	1.92	1.0E-126	AW 812899.1	EST_HUMAN	RC3-ST189-26200-019-211 ST0188 Homo sapiens cDNA
11377	23984	37284	3.58	1.0E-126	BE074267.1	EST_HUMAN	QV8-BT0569-020200-075-005 BT0569 Homo sapiens cDNA
11486	24087	37397	3.58	1.0E-126	BE074267.1	EST_HUMAN	QV8-BT0569-020200-075-005 BT0569 Homo sapiens cDNA
11486	24087	37398	3.58	1.0E-126	BE074267.1	EST_HUMAN	Homo sapiens CDC-like kinase (CLK) mRNA
757	33528	26189	1.48	1.0E-126	4758007	NT	H. sapiens gene for alpha1-antitrypsin, exon 3
889	13687	26331	1.45	1.0E-126	X68735.1	NT	Homo sapiens hypothetical protein FL20048 (FLJ20048), mRNA
2344	15097	27804	1.17	1.0E-126	8923056	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
2344	15097	27805	1.17	1.0E-126	8923056	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
2605	15318	28059	1.49	1.0E-126	6382078	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3089	15635	28479	0.72	1.0E-126	4604116	NT	257203.11 Stragapene pancreas (8537208) Homo sapiens cDNA clone IMAGE:592420 5'
3070	15636	28480	7.54	1.0E-126	AA160709.1	EST_HUMAN	257203.11 Stragapene pancreas (8537208) Homo sapiens cDNA clone IMAGE:592420 5'
3620	16373	29014	1.09	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3647	18400	28040	1.8	1.0E-126	X63941.1	NT	H. sapiens death receptor 6 (DR6), mRNA
4783	17515	30137	1.74	1.0E-126	N34078.1	EST_HUMAN	W87808.11 Soares melanocyte 2NDRM Homo sapiens cDNA clone IMAGE:3926885 5'
5078	17707	30413	0.81	1.0E-126	BE743922.1	EST_HUMAN	60157708.11 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3926885 5'
5816	18412	31328	0.68	1.0E-126	T66998.1	EST_HUMAN	Y832512.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:3926885 5'
6139	18917	31887	3.22	1.0E-126	AA490075.1	EST_HUMAN	z66603.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:798444 5' similar to
6197	18973	31949	4.2	1.0E-126	AB040958.1	NT	TR-G1145880 G1145880 TITIN
6197	18973	31950	4.2	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7399	20077	33157	1.02	1.0E-126	AF257737.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7399	20077	33158	1.02	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7602	20269	33375	0.82	1.0E-126	AF257737.1	EST_HUMAN	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7655	20319	33428	0.99	1.0E-126	AI806483.1	EST_HUMAN	AU135483 PLACET Homo sapiens cDNA clone PLACE1004325 5'
7778	20473	33596	0.76	1.0E-126	AB037715.1	NT	W80801.11 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to
7778	20473	33597	0.76	1.0E-126	AB037715.1	NT	SV-MPP2_HUMAN Q14168 MAGUK P55 SUBFAMILY MEMBER 2
7837	20662	33711	2.55	1.0E-126	X16809.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
8083	20777	33907	0.99	1.0E-126	AA483388.1	EST_HUMAN	Homo sapiens mRNA for KIAA1284 protein, partial cds
9695	22346	35539	0.87	1.0E-126	4505424	NT	Human mRNA for ankyrin (variant 2.1)
							ne74512.11 NCL CGAP_Ewt Homo sapiens cDNA clone IMAGE:909983 similar to SW:TS66_HUMAN
							P80088 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR
							Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10693	23394	36624	1.27	1.0E-126	M83186.1	NT	Human macrophage mannose receptor (MRC1) gene, exon 5
10766	23450	36692	2.36	1.0E-126	BF683176.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288240 5'
11501	24102	37414	6.47	1.0E-126	BE261660.1	EST_HUMAN	601144045F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502126 5'
12460	17787	30413	7.17	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3326885 5'
168	12682	25622	4.63	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
169	12682	25623	4.63	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
169	12682	25623	4.71	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
287	13078	25716	3.54	1.0E-127	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
287	13078	25717	3.54	1.0E-127	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
891	13630	26301	2.03	1.0E-127	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
898	13684	26330	1.37	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1686	14430	27126	1.08	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2059	14790	27515	2.44	1.0E-127	5903065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2059	14790	27516	2.44	1.0E-127	5903065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2197	14926	27681	6.02	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2341	16064	27801	2.73	1.0E-127	AF246506.1	NT	Homo sapiens adiclin mRNA, complete cds
2814	15326	28008	3.04	1.0E-127	X12881.1	NT	Human mRNA for cyclokeratin 18
2826	15338	28031	1.1	1.0E-127	AA460131.1	EST_HUMAN	zx42a02.r1 Soares_tetis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:780088 5'
2826	15338	28032	1.1	1.0E-127	AA460131.1	EST_HUMAN	zx42a02.r1 Soares_tetis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:780088 5'
3791	16543	29178	1.21	1.0E-127	AW161297.1	EST_HUMAN	TR:Q16170 Q16170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4086	16838	29495	0.7	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4227	16958	29592	23.74	1.0E-127	7709239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594) mRNA
4227	16958	29593	23.74	1.0E-127	7709239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594) mRNA
4462	17168	29824	0.94	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinol metabolizing protein P450RAI-2 mRNA, complete cds
4894	17299	29926	4.35	1.0E-127	4505384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4890	17325		1.92	1.0E-127	AL163269.2	NT	Homo sapiens chromosome 21 segment H321C068
4823	17360	29993	1.26	1.0E-127	6812639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5620	18416	31329	1.37	1.0E-127	W03547.1	EST_HUMAN	z001a10.1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE 291268 5' similar to SW-PIP ₂ RAT P10698 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5650	18445	31359	2.4	1.0E-127	4826963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5713	18505	31428	4.25	1.0E-127	X85764.1	NT	H sapiens NOS2 gene, exon 8
6070	18849	31813	2.17	1.0E-127	X84060.1	NT	H sapiens TCF11 gene, exon 3-6
6229	19003	31978	5.28	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6550	19325	32332	0.69	1.0E-127	11421595	NT	Homo sapiens Immunoglobulin superfamily, member 3 (IGSF3), mRNA
6852	19444	32461	0.81	1.0E-127	4826977	NT	Homo sapiens resilin (RELN) mRNA
7684	20348	33461	1.65	1.0E-127	11421814	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7694	20348	33462	1.65	1.0E-127	11421814	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7691	20365	33470	0.64	1.0E-127	AW98292.1	EST_HUMAN	QV5-BN0046-150300-121-111 BN0046 Homo sapiens cDNA
8765	21477	34625	0.8	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8785	21477	34626	0.8	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9540	22183	35377	4.17	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9540	22193	35378	4.17	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9773	22424	36531	1	1.0E-127	A129832.1	EST_HUMAN	qim5h09.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1806449 3'
10241	22889	36101	1.34	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11107	23777	37050	7.88	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11107	23777	37051	7.88	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11627	24224	37546	3.25	1.0E-127	BE895415.1	EST_HUMAN	801434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919517 5'
11627	24224	37547	3.25	1.0E-127	BE895415.1	EST_HUMAN	801434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919517 5'
11927	24524	38622	2.25	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12244	12982	29523	2.25	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12444	24614	31048	2.88	1.0E-127	AB011359.1	NT	Homo sapiens gene for AF-6, complete cds
447	13233	28573	3.04	1.0E-128	BE895617.1	EST_HUMAN	801278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3918822 5'
2058	14795	27520	5.5	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2058	14795	27521	5.5	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2205	14834	27672	8.76	1.0E-128	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2446	15185		1.1	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3389	16148	28802	1.08	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	17351	28985	6.14	1.0E-128	11428673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5458	18257	31147	0.7	1.0E-128	X89539.1	NT	H sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
5883	18672	31613	0.65	1.0E-128	BE747861.1	EST_HUMAN	601580465F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929057 5'
5883	18672	31614	0.65	1.0E-128	BE747861.1	EST_HUMAN	601580465F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929057 5'
6324	19064	32082	2.58	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (PDE1C), mRNA
6831	19493	32516	0.9	1.0E-128	BE224345.1	EST_HUMAN	7889510.X1 NCI CGAP L1242 Homo sapiens cDNA clone IMAGE:3905764 5'
7327	20010	33089	0.62	1.0E-128	BE5614105.1	EST_HUMAN	601503846F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905764 5'
7692	20356	33471	0.67	1.0E-128	11646923	NT	Homo sapiens putative ABC transporter (WHITE2), mRNA
8446	21138	34276	0.73	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8446	21138	34277	0.73	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10037	22685	35503	1.63	1.0E-128	AAC9198.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
10608	23502	36541	3.52	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
10618	23311	36550	3.21	1.0E-128	AA926959.1	EST_HUMAN	Homo sapiens mRNA for TRABID protein (TRABID gene)
10699	23390	36525	1.35	1.0E-128	AI252080.1	NT	601277825F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5'
10761	23445	36689	1.4	1.0E-128	BE384475.1	EST_HUMAN	EST_367360 MAGC resequences, MAGC Homo sapiens cDNA
12177	24610	28539	7.02	1.0E-128	AW955280.1	EST_HUMAN	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
118	13189	26339	1.33	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
404	13189	26339	1.19	1.0E-128	S37722.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1713	14456	27154	2.73	1.0E-128	AL086860.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1717	14460	27158	1.57	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1717	14460	27159	1.57	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1838	14578	27289	2.78	1.0E-128	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3125	15890	28531	1.21	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3125	15890	28532	1.21	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3125	15890	28533	1.21	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3125	15890	28533	1.21	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
4143	16895	29516	1.94	1.0E-128	AB040802.1	NT	Homo sapiens mRNA for KIAA1458 protein, partial cds
4247	16998	29611	2.26	1.0E-128	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYAS
4247	16998	29612	2.26	1.0E-128	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
4247	16998	29612	2.26	1.0E-128	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYAS

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	18781	31742	3.73	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQ1 gene
6818	19477	32499	0.99	1.0E-129	BE899993.1	EST_HUMAN	601449740F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853688 5'
6818	19477	32500	0.99	1.0E-129	BE899993.1	EST_HUMAN	601449740F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853688 5'
7027	19719	32776	4.15	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQ1 gene
7027	19719	32776	4.15	1.0E-129	AJ006345.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
7090	19779	32844	3.93	1.0E-129	AF041059.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7090	19779	32844	3.93	1.0E-129	AF041059.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7428	20105	33181	2.49	1.0E-129	AF041059.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
7428	20105	33182	2.49	1.0E-129	AF041059.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
8217	20921	33635	3.94	1.0E-129	AB014534.1	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
8979	22627	35635	0.97	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
8979	22627	35636	0.97	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10523	23159	36398	0.57	1.0E-129	AA682200.1	EST_HUMAN	aa91207.1, S. Scars, NIHMPu, S1 Homo sapiens cDNA clone IMAGE:1047889 5'
11186	23851	37137	4	1.0E-129	AA682200.1	EST_HUMAN	aa91207.1, S. Scars, NIHMPu, S1 Homo sapiens cDNA clone IMAGE:1047889 5'
11299	19778	32844	6.57	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
11615	24213	37537	1.38	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
11615	24213	37538	1.38	1.0E-129	AU143115.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
12104	24601		1.79	1.0E-129	H83155.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
12483	24842		2.66	1.0E-129	AL120739.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63864], mRNA
74	12501	25538	1.3	1.0E-130	7705530	NT	Homo sapiens hypochlorite protein (HSPC242), mRNA
1147	13502	26564	0.99	1.0E-130	AB037895.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1681	14407	27098	11.38	1.0E-130	BE275192.1	EST_HUMAN	601121695F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3349366 5'
1681	14407	27099	11.38	1.0E-130	BE275192.1	EST_HUMAN	601121695F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3349366 5'
1681	14407	27099	11.38	1.0E-130	X04092.1	NT	Human gene for caldesmon (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13
1976	14712		3.08	1.0E-130	X04092.1	NT	Human gene for caldesmon (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13
2773	15478		5.37	1.0E-130	AJ010230.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2881	15648	28290	1.17	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
2881	15648	28291	1.17	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3565	16320	29290	1.09	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3750	16648	29291	5.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3750	16648	29291	5.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
39715	16668	29305	1.92	1.0E-130	AW603960.1	EST_HUMAN	UHF-ENO-alkyl-o6-U1T1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4053	17237	29428	1.6	1.0E-130	M97710.1	EST_HUMAN	Human 1-cell receptor (V alpha 22.1, J alpha 22.1, J alpha 22.1) mRNA
4501	17237	29428	6.78	1.0E-130	AW603960.1	EST_HUMAN	UHF-ENO-alkyl-o6-U1T1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
5038	17757	30371	1.07	1.0E-130	AW363269.1	EST_HUMAN	RCO-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA
5038	17757	30372	1.07	1.0E-130	AW363269.1	EST_HUMAN	RCO-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA

Page 468 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6629	18391	32405	0.95	1.0E-130	X57825.1	NT	Human germline immunoglobulin lambda light chain pseudogene (VII.1)
6723	19557	32587	0.81	1.0E-130	AW843875.1	EST_HUMAN	OMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6723	19557	32588	0.81	1.0E-130	AW843875.1	EST_HUMAN	OMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6735	18570	32502	0.76	1.0E-130	11425448	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7154	10841	32610	2.62	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC9A7), mRNA
8592	12174	34593	0.46	1.0E-130	AF08551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8718	21410	34593	2.38	1.0E-130	AW958242.1	EST_HUMAN	EST398312 IMAGE, resequences, MAGD Homo sapiens cDNA
8718	21410	34597	1.84	1.0E-130	AB037768.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
9833	22484	36540	1.25	1.0E-130	AW103454.1	EST_HUMAN	zB5605.X1 NCL_GGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
10483	23109	36540	0.81	1.0E-130	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10483	23109	36541	0.81	1.0E-130	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
11242	23904	37164	1.72	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11242	23904	37165	1.72	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11703	24208	37624	2.87	1.0E-130	4504142	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA
12759	15478		1.56	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
4	12832	25448	1.9	0.0E+00	AA228128.1	EST_HUMAN	zF5804.1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	12832	25448	1.9	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
7	12834	25449	1.02	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
14	12841	25454	0.72	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
14	12841	25455	0.72	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
20	12848	25402	6.7	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
20	12848	25463	6.7	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
25	12853	25468	17.04	0.0E+00	AF114348.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	12861	25478	1.19	0.0E+00	M58000.1	NT	Homo sapiens Cdc-2 effector protein 2 (CEP2), mRNA
35	12863	25481	0.82	0.0E+00	6657828	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
39	12867	25486	4.22	0.0E+00	Y17161.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
55	12884	25512	0.76	0.0E+00	Y17161.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
55	12884	25513	0.76	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	12885	25514	3.04	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens human placenta polyA+ (TF-ijwera) Homo sapiens cDNA clone GEN:516H08 5'
59	12885	25515	3.04	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens human placenta polyA+ (TF-ijwera) Homo sapiens cDNA clone GEN:516H08 5'
67	12886	25516	5.76	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
68	12688	25519	12.55	0.0E+00	AW089534.1	EST_HUMAN	cr4807.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_c4807 3'
69	12689	25520	12.65	0.0E+00	AW089534.1	EST_HUMAN	cr4807.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_c4807 3'
83	12691	25524	1.5	0.0E+00	M60376.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
85	12693		0.91	0.0E+00	M60376.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
73	12690	25536	10.36	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
73	12690	25537	10.36	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	12690	25536	10.18	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	12690	25537	10.18	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	12696	25544	0.78	0.0E+00	4501860	NT	Homo sapiens anion channel binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
81	12697		15.25	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
90	12816	25553	17.68	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
83	12819	25558	23.28	0.0E+00	U69277.1	NT	Human polyoma virus 1 homolog (HPV1) mRNA, partial cds
89	12825	25562	3.51	0.0E+00	A114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
100	12828	25563	1.72	0.0E+00	A903784.1	NT	Homo sapiens mRNA for KIAA1353 protein, partial cds
105	12828	25566	1.33	0.0E+00	X91213.1	NT	H sapiens next gene (exon 2)
113	12855	25572	0.89	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCL CGAP U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q98551 Q98551
114	12855	25572	1.47	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCL CGAP U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q98551 Q98551
115	12855	25573	1.48	0.0E+00	N36040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
115	12853	25574	1.48	0.0E+00	N36040.1	EST_HUMAN	y01109.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
128	12943	25588	4.38	0.0E+00	4505938	NT	y01109.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
128	12943	25587	4.38	0.0E+00	4505938	NT	Homo sapiens polynucleotide (RNA) II (DNA directed) polypeptide A (220Kd) (POLR2A) mRNA
136	12950	25593	1.29	0.0E+00	T66945.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220Kd) (POLR2A) mRNA
136	12950	25594	1.29	0.0E+00	T66945.1	EST_HUMAN	y01109.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
149	12964		8.89	0.0E+00	4504444	NT	y01109.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
153	12968	25609	2.1	0.0E+00	BF036981.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
155	12970		25.83	0.0E+00	4504444	NT	6014603.76F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663803 5'
158	12973	25612	1	0.0E+00	AF111168.2	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
160	12975	25613	1.15	0.0E+00	BE295973.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
161	12975	25613	0.83	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
162	12976	25614	5.4	0.0E+00	W73973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
163	12977	25615	0.81	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
163	12977	25616	0.81	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
164	12978	25617	1.42	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
167	12981	25620	25.73	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
167	12981	25621	25.73	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
176	12988	25627	5.95	0.0E+00	BE018970.1	EST_HUMAN	b624e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
176	12988	25628	5.95	0.0E+00	BE018970.1	EST_HUMAN	b624e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
181	12993	25631	3.05	0.0E+00	AB018327.1	NT	CE22631.1
181	12993	25632	3.05	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	13002	25643	67.77	0.0E+00	D50859.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
194	13007	25648	3.74	0.0E+00	AF273045.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
194	13007	25649	3.74	0.0E+00	AF273045.1	NT	Homo sapiens GTC4 tumor antigen se14-3 mRNA, complete cds
198	13009	25651	4.81	0.0E+00	AF167174.1	NT	Homo sapiens GTC4 tumor antigen se14-3 mRNA, complete cds
198	13009	25652	4.81	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
205	15537	25658	9.26	0.0E+00	AI587308.1	EST_HUMAN	tcq4f08.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN)
205	15537	25659	9.26	0.0E+00	AI587308.1	EST_HUMAN	tcq4f08.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN)
207	13018	25661	3.08	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
210	13021	25662	23.37	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
210	13022	25664	4.72	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
214	13026	25664	9.19	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
215	13026	25664	8.34	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
216	13027	25665	3.6	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
229	13041	25678	1.23	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
229	13041	25679	1.23	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
231	13042	25682	3.97	0.0E+00	5459008	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
233	13044	25684	6.94	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
240	13049	25688	3.85	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
242	13051	25691	1.71	0.0E+00	X69772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
250	13059	25700	8.14	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
263	13071	25710	1.68	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
263	13071	25711	1.68	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
265	13073	25713	3.07	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
276	13083		1.19	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
277	13084	25726	3.28	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
277	13084	25727	3.28	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
278	13085		0.78	0.0E+00	AW845283.1	EST_HUMAN	IL2-CT10031-181789-020-B03 CT0031 Homo sapiens cDNA
287	13093	25734	6.95	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
287	13093	25735	6.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
287	13103	25744	4.97	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
288	13104	25745	4.93	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
299	15540		4.23	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
300	13105		3.76	0.0E+00	AA480002.1	EST_HUMAN	zyl8c06.r1 Soares NIH/HPu, S1 Homo sapiens cDNA clone IMAGE:763964 5'
301	13106	25746	18.83	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
302	13108	25748	10.53	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
306	13110	25750	2.33	0.0E+00	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
319	13122	25759	4.97	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
320	13122	25769	6.23	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
335	13136	25771	2.68	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) translocation), translocated to, 4 (MLL14) mRNA
338	13139	25776	1.71	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
341	13142	25780	1.45	0.0E+00	U71600.1	NT	Human zinc finger protein Zfp31 (Zf31) mRNA, partial cds
346	13146	25784	2.42	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
346	13146	25785	2.42	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
347	15541	25786	3.84	0.0E+00	AF231919.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
349	13148	25788	2.33	0.0E+00	4507500	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
352	13161	25792	0.94	0.0E+00	4503854	NT	Human mRNA for KIAA0184 gene, partial cds
353	13162	25793	4.1	0.0E+00	D86008.1	NT	Human mRNA for KIAA0184 gene, partial cds
354	13162	25793	1.9	0.0E+00	D86008.1	NT	Human mRNA for KIAA0184 gene, partial cds
355	13164	25795	1.89	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
367	13163	25806	1.07	0.0E+00	ALU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
378	13203	25849	8.31	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
379	13204	25860	1.54	0.0E+00	A1363014.1	EST_HUMAN	q9b1005.x1 NCL CGAP Brn25 Homo sapiens cDNA clone IMAGE:2018467 3' similar to db:U34199
383	13170	25873	1.83	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN); RC2-CT0320-300100-016-508 CT0320 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain								
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
396	13172	25816		1.58	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
397	13173	25817		2.49	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
387	13173	25818		2.49	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
388	13174	25819		1.17	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
389	13175	25820		1.39	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
389	13175	25821		1.39	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
390	13176	25822		2.77	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
391	13177	25823		0.84	4503680	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29	
392	13178	25824		1.35	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
392	13178	25825		1.35	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
393	13178	25824		1.07	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
393	13178	25825		1.07	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
397	13182	25835		28.13	0.0E+00	4503608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
411	12922	25435		1.5	0.0E+00	R17795.1	EST_HUMAN	Y09022.1 Soares infant brain T1B18 Homo sapiens cDNA clone IMAGE:31652 5'
419	13205	25851		1.31	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, (GART) mRNA
420	13206			3.18	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
421	13207	25852		3.93	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein (SON), partial cds
422	13208	25853		5.45	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
422	13208	25854		5.45	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
423	13209	25855		4.02	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
433	13219	25865		1.99	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
438	13224			2.01	0.0E+00	AA324292.1	EST_HUMAN	EST27054 Carabellum II Homo sapiens cDNA 5' end
439	13226			0.97	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3562348 5'
455	13241	25879		3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
455	13241	25880		3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
461	13246	25888		1.23	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
461	13246	25889		1.23	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
471	13257	25895		2.84	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
472	13258	25896		9.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
472	13258	25897		9.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
481	13266	25902		3.46	0.0E+00	AB033036.1	EST_HUMAN	Homo sapiens mRNA for KIAA1209 protein, partial cds
481	13266	25902		3.46	0.0E+00	AB033036.1	EST_HUMAN	Homo sapiens mRNA for KIAA1209 protein, partial cds
483	13268	25904		1.97	0.0E+00	AL132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
481	13276	25910		2.88	0.0E+00	BE395144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615766 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
492	15543	25911	1.11	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT10065-130400-002-cd9 DT10065 Homo sapiens cDNA
494	13278	25913	1.33	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
495	13279	25914	1.21	0.0E+00	6023955	EST_HUMAN	Homo sapiens PCS28 protein (PCS28), mRNA
499	13283		0.77	0.0E+00	BF379403.1	EST_HUMAN	IL2-FT0150-070800-120-F07 FT0159 Homo sapiens cDNA
508	13290	25924	5.37	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C910
513	16544	25928	1.29	0.0E+00	BE081527.1	EST_HUMAN	QV2-B10635-160400-142-N65 B10635 Homo sapiens cDNA
518	13302	25934	1.14	0.0E+00	BF028005.1	EST_HUMAN	801764555F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:396698 5'
624	13308	25941	1.68	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
627	13311	25944	27.88	0.0E+00	6006030	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
628	13312	25945	4.33	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
628	13312	25946	4.33	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	13314	25948	0.97	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
530	13314	25948	0.97	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
530	13314	25948	0.97	0.0E+00	8923831	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
535	13318		5.82	0.0E+00	AF003528.1	NT	U1H-BH1-acb-H-04-0-JL1.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
543	13326	25958	1.86	0.0E+00	AW135324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
553	13336		8	0.0E+00	D10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
572	13353	25982	2.63	0.0E+00	5174742	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
585	13365		7	0.0E+00	J04056.1	NT	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
585	13368	25988	1.83	0.0E+00	BF104598.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
590	13370	25989	0.98	0.0E+00	6023831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
590	13370	25989	0.98	0.0E+00	6023831	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
595	13373	26002	0.76	0.0E+00	4501854	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
595	13373	26002	1.15	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
600	13378	26009	1.15	0.0E+00	AF221712.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
600	13378	26018	3.18	0.0E+00	AF149773.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
609	13387		1.2	0.0E+00		NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	13390	26021	3.83	0.0E+00	6006918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
613	13391	26022	3.83	0.0E+00	6006918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
613	13391	26023	3.83	0.0E+00	6006918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
614	13392	26024	0.82	0.0E+00	6006918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
614	13392	26025	0.82	0.0E+00	6006918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
620	13396	26034	1.35	0.0E+00	AA399486.1	EST_HUMAN	26000711 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:728732 5'
624	13403	26038	10.1	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
628	13407	28041	0.76	0.0E+00	W78811.1	EST_HUMAN	z551b04.r1 Soares, fetal liver, spleen, 1NfLS, S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
629	13407	28042	0.78	0.0E+00	W78811.1	EST_HUMAN	z551b04.r1 Soares, fetal liver, spleen, 1NfLS, S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
631	13410		4.89	0.0E+00	485528	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
638	13417	28054	2.88	0.0E+00	600603	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
640	13418	28057	1.17	0.0E+00	6031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
643	13422	28061	2.53	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
647	13426	28064	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
647	13426	28065	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
653	13431	28070	4.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
653	13431	28071	4.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
659	15647		1.15	0.0E+00	X67147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
687	13443	28084	10.4	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 1 (HMG1) mRNA
672	13448	28088	4.49	0.0E+00	AB026012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
681	13456	28101	2.43	0.0E+00	7657469	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
693	13468	28115	9.24	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI CGAP Br.1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
698	13471	28119	4.34	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
698	13471	28120	4.34	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
705	13481	28128	1.71	0.0E+00	6032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	13486	28135	4.95	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	13486	28136	4.95	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
714	13488	28138	12.29	0.0E+00	11545900	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
719	13493	28146	2.12	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCOA Homo sapiens cDNA clone TCAAP0779
739	13512	28170	1.07	0.0E+00	AF226960.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
739	13512	28171	1.07	0.0E+00	AF226960.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	13513	28172	2.41	0.0E+00	AF170462.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
743	13516	28175	1.07	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
743	13516	28176	1.07	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
746	13519	28177	1.38	0.0E+00	8912749	NT	Homo sapiens zinc finger protein 212 (ZNF212) mRNA
748	15551	28179	1.88	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
749	13521	28180	3.01	0.0E+00	BE869735.1	EST_HUMAN	B01445647.F1 NIH IMGC_65 Homo sapiens cDNA clone IMAGE:3949803 5'

Page 475 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
752	13524	25183	3.51	0.0E+00	R48915.1	EST HUMAN	Y6908.1 Soares breast 2N4H8st Homo sapiens cDNA clone IMAGE:154046 5'
753	13525	25184	2.07	0.0E+00	6032085	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
761	13533	25192	2.07	0.0E+00	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
764	13537	25180	2.34	0.0E+00	7681965	NT	Homo sapiens KIAA0770 gene product (KIAA0770), mRNA
775	13547	26208	1.18	0.0E+00	D80006.1	NT	Human mRNA for KIAA0784 gene, partial cds
775	13547	26209	1.18	0.0E+00	D80006.1	NT	Human mRNA for KIAA0784 gene, partial cds
780	13552	26213	2.13	0.0E+00	X86772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
784	13556	26217	5.97	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	13556	26218	5.97	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
788	13560	26222	9.88	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
789	13561		11.63	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
805	13577	26242	1.96	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
805	13578	26243	4.28	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
808	13580	26245	2.51	0.0E+00	4557688	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNK1) mRNA
814	13585	26251	1.39	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBR) mRNA, complete cds
819	13590	26257	1.39	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBR) mRNA, complete cds
823	13593	26262	2.09	0.0E+00	4507500	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
823	13593	26263	2.09	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
830	13600		1.32	0.0E+00	AF027153.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
834	13604	26274	4.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
834	13604	26276	4.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
835	13605	26276	9.56	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
838	13606	26277	4.34	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	13607	26278	0.8	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
841	13611	26281	2.2	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
841	13611	26282	2.2	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
842	13612	26283	2.46	0.0E+00	AA633272.1	EST HUMAN	U86407.s1 NCI CGAP P10 Homo sapiens cDNA clone IMAGE:997453
842	13612	26284	2.46	0.0E+00	AA633272.1	EST HUMAN	U86407.s1 NCI CGAP P10 Homo sapiens cDNA clone IMAGE:997453
843	13613		9.44	0.0E+00	BF677694.1	EST HUMAN	602089579F1 NIH JMG_33 Homo sapiens cDNA clone IMAGE:4246915 5'
847	13617	26285	1.94	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
847	13617	26286	1.94	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	13618	26287	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	13618	26288	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
871	13840	26311	0.91	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
878	13847	26316	2.57	0.0E+00	BE08592.1	EST_HUMAN	QV0-B10703-280400-211-g11 B10703 Homo sapiens cDNA
878	13847	26317	2.57	0.0E+00	BE08592.1	EST_HUMAN	QV0-B10703-280400-211-g11 B10703 Homo sapiens cDNA
888	13857	26328	0.48	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
888	13866		4.96	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (LR1, ribosomal protein SA) (LAMR1), mRNA
900	13866		8.49	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (LR1, ribosomal protein SA) (LAMR1), mRNA
901	13868	26332	1.21	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-methylcysteine precursor, mRNA, partial cds
902	13869	26333	1.78	0.0E+00	Z2101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
905	13872	26336	1.05	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
905	13872	26337	1.05	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
926	13663	26356	2.98	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0384 protein, partial cds
926	13663	26357	2.98	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0384 protein, partial cds
931	13668	26382	1.19	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
932	13668	26383	9.95	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
933	13700	26384	0.9	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
934	13701	26395	2.18	0.0E+00	4507430	NT	Homo sapiens thymidine phosphorylase factor (TEF), mRNA
934	13701	26396	2.18	0.0E+00	4507430	NT	Homo sapiens thymidine phosphorylase factor (TEF), mRNA
942	15568	26373	3.38	0.0E+00	AB011948.1	EST_HUMAN	os98603.t1 NC1 CGAP_GC3 Homo sapiens cDNA clone IMAGE1613404 3'
942	15568	26374	3.38	0.0E+00	AB011948.1	EST_HUMAN	os98603.t1 NC1 CGAP_GC3 Homo sapiens cDNA clone IMAGE1613404 3'
943	13709	26375	9.49	-0.0E+00	7657266	NT	Homo sapiens KIAA0029 protein Mac2 interacting nuclear target (MINT), mRNA
954	13716	26395	3.16	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
982	13727	26391	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
982	13727	26392	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
982	13727	26393	1.11	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
983	13728	26394	1.69	0.0E+00	X62207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
983	13728	26395	1.69	0.0E+00	X62207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
972	13737	26402	2.03	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
984	13748	26410	1.66	0.0E+00	U83698.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
985	13749	26411	50.9	0.0E+00	U83698.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
985	13749	26411	25.17	0.0E+00	U83698.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
989	13762		5.52	0.0E+00	AF198460.1	NT	Homo sapiens Bg22.1 region and MTG8 (CBFA2T1) gene, partial cds
990	13762		8.84	0.0E+00	AF198460.1	NT	Homo sapiens Bg22.1 region and MTG8 (CBFA2T1) gene, partial cds
993	13755	26416	1.17	0.0E+00	AF11170.3	NT	Homo sapiens 14q32, legged2 gene, complete cds, and unknown gene

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
994	13755	28416	1.83	0.0E+00	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
995	13755	28416	2.3	0.0E+00	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
996	13756	28417	3.76	0.0E+00	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
998	13759	28420	3.06	0.0E+00	7651685	NT	Homo sapiens DKFZ568M0722 protein (DKFZ568M0722), mRNA
999	13759	28420	2.5	0.0E+00	5903114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (TIMM), mRNA
1003	13763	28424	1.43	0.0E+00	AA458680.1	EST_HUMAN	Homo sapiens fetal retina 837202 Homo sapiens cDNA clone IMAGE:538286 3' similar to SW:PR59_HUMAN P47210 28S PROTEASE REGULATORY SUBUNIT 8;
1004	13764		1.9	0.0E+00	N43182.1	EST_HUMAN	EST15124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1007	13767	28428	1.9	0.0E+00	N43182.1	EST_HUMAN	EST15124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1007	13767	28429	1.9	0.0E+00	N43182.1	EST_HUMAN	EST15124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1010	13770		3.95	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11108 (FLJ11108), mRNA
1025	13785	28445	2.49	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 98 (hsc70-2) (HSP98B), mRNA
1025	13785	28445	1.89	0.0E+00	4829872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1043	13802	28460	1.89	0.0E+00	4829872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1043	13802	28461	1.89	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1047	13806	28465	3.63	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1047	13806	28466	3.63	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1048	13807	28467	119.02	0.0E+00	AJ245622.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1048	13807	28467	1.19	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20680 (FLJ20680), mRNA
1050	13809		3.52	0.0E+00	5174394	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1052	13811	28471	2.3	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1052	13811	28471	2.2	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1074	13832	28490	6.04	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1097	13855	28514	6.04	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1097	13855	28515	6.04	0.0E+00	4825047	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1107	13867	28526	0.9	0.0E+00	4825047	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1110	13867	28526	0.9	0.0E+00	4825047	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1110	13867	28526	4.27	0.0E+00	4825047	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1111	13868	28527	0.96	0.0E+00	8923280	NT	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
1113	13870	28528	23.77	0.0E+00	AB002059.1	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1113	13870	28528	23.77	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2X4, complete cds
1116	13873	28532	44.3	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2X4, complete cds
1118	13875	28533	5.51	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
1119	13876	28534	5.51	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
1119	13876	28535	5.51	0.0E+00	7706500	NT	Homo sapiens Npy3B-binding protein Npy3B (LOC51729), mRNA
1122	13878	28537	1.1	0.0E+00	7706500	NT	Homo sapiens Npy3B-binding protein Npy3B (LOC51729), mRNA
1123	13878	28538	0.87	0.0E+00	X58826.1	NT	H.sapiens ART14 gene

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No:	Top Hit Database Source	Top Hit Descriptor
1123	13878	28539	0.87	0.0E+00	X96828.1	NT	H sapiens ART14 gene
1124	13880	28540	0.92	0.0E+00	AI147850.1	EST HUMAN	q22d10.x1 Soares_prenatal_oligos_N84PU Homo sapiens cDNA clone IMAGE:1897011 3'
1126	13882	28542	1.36	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1133	13889	28548	0.71	0.0E+00	4758081	NT	Homo sapiens chondrotin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1133	13889	28548	0.71	0.0E+00	4758081	NT	Homo sapiens chondrotin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1134	13890	28550	1.39	0.0E+00	6968844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3) mRNA
1145	13900	28581	6.83	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1145	13900	28582	6.83	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1148	13903	28585	1.85	0.0E+00	AB037855.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1155	13910	28574	0.76	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1167	13921	28583	4.64	0.0E+00	AF034986.1	NT	Homo sapiens amphipysin 1 mRNA, alternative splice isoform, complete cds
1187	13939	28617	1.7	0.0E+00	8627336	NT	Homo sapiens multi (E. coli) homolog 3 (MLH3), mRNA
1201	13953	28617	1.7	0.0E+00	8627336	NT	Homo sapiens multi (E. coli) homolog 3 (MLH3), mRNA
1204	13956	28620	1.53	0.0E+00	AF264750.1	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
1204	13956	28621	1.53	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1204	13957	28622	1.71	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1205	15592	28623	1.53	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1206	15592	28646	9.12	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1224	13974	28647	1.71	0.0E+00	4503086	NT	Homo sapiens chondrotin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1225	13975	28647	2.33	0.0E+00	Y182000.1	NT	Homo sapiens NF2 gene
1243	13982	28687	23.59	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1251	14000	28678	3.07	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1258	14007	28678	3.07	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1265	14014	28681	2.07	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1265	14014	28682	2.07	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1268	14014	28682	2.04	0.0E+00	5174748	NT	Homo sapiens Wilfram syndrome (WFS) mRNA
1277	14027	28685	2.04	0.0E+00	5174748	NT	Homo sapiens Wilfram syndrome (WFS) mRNA
1277	14027	28686	2.04	0.0E+00	5174748	NT	Homo sapiens Wilfram syndrome (WFS) mRNA
1277	14027	28687	2.04	0.0E+00	5174748	NT	Homo sapiens Wilfram syndrome (WFS) mRNA
1278	14028	28709	3.78	0.0E+00	AF096166.1	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1288	15594	28709	1.63	0.0E+00	7657629	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1288	15594	28710	1.63	0.0E+00	7657629	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1293	14042	28715	2.03	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1294	14043	28716	0.89	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1296	14045	28717	1.12	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1297	14046	28718	0.72	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14048	28720	4.71	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1300	14049	28721	2.04	0.0E+00	7681065	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1301	14050	28722	6.88	0.0E+00	7681065	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1302	14051	28723	3.01	0.0E+00	8687387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1302	14051	28724	3.01	0.0E+00	8687387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1314	14052	28737	1.82	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1387	14134	28909	1.38	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1388	14140	28817	3.39	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1388	14143	28821	1.59	0.0E+00	AJ208758.1	EST_HUMAN	qg3806.ct Source_testis_NHT Homo sapiens cDNA IMAGE:1837427 3' similar to WP:127A1.5 CE14213;
1397	14153	28822	13.21	0.0E+00	6042205	NT	RAN, member RAS oncogene family-homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1406	14153	28833	5	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1408	14153	28834	5	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1408	14155	28837	4.08	0.0E+00	7705865	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1408	14156	28838	4.08	0.0E+00	7705865	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1410	14157	28939	4.59	0.0E+00	AJ230093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1420	14168	28852	3.02	0.0E+00	AF038260.1	NT	Homo sapiens alpha1-fucosyltransferase (alpha1-6fucT) gene, exon 7
1431	14178	28863	6.39	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1431	14178	28864	6.39	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1436	14183	28859	17.93	0.0E+00	U35837.1	NT	Human nebulin mRNA, partial cds
1436	14183	28859	17.93	0.0E+00	U35837.1	NT	Human nebulin mRNA, partial cds
1448	14193	28876	2.59	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1447	14194	28877	1.82	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1451	14198	28882	1.73	0.0E+00	DB0707.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	14201	28885	4.53	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1456	14203	28887	1.55	0.0E+00	7681065	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	14203	28888	1.55	0.0E+00	7681065	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1460	14207	28893	0.97	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1460	14207	28894	0.97	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1500	14246	28932	1.37	0.0E+00	7706434	NT	Homo sapiens PHDC for homolog of Drosophila headcase (LOC51696), mRNA
1516	14283	28949	1.21	0.0E+00	AW95687.1	EST_HUMAN	EST131167 IMAGE resequences, MAGF Homo sapiens cDNA
1517	14294	28960	1.76	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCI CGAP GGB1 Homo sapiens cDNA clone IMAGE:815118 5'
1522	14298	28953	49.82	0.0E+00	AF023860.1	NT	Carcinopithecus aethiops cytoophillin A mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1522	14269	26954	49.82	0.0E+00	AF023860.1	NT	Ceroid lipofuscinosis aethiops cyclophilin A mRNA, complete cds
1524	14271	26957	1.24	0.0E+00	AW976097.1	EST_HUMAN	EST389206 MAGE sequences, MAGN Homo sapiens cDNA
1524	14271	26958	1.24	0.0E+00	AW976097.1	EST_HUMAN	EST389206 MAGE sequences, MAGN Homo sapiens cDNA
1525	14272	26959	5.48	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalin
1527	14274		2.07	0.0E+00	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
1528	14275	26962	2.1	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1528	14275	26963	2.1	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1530	14277	26965	3.3	0.0E+00	7682408	NT	Homo sapiens KIAA0987 protein (KIAA0987), mRNA
1531	14278		7.28	0.0E+00	7655872	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1537	14284	26971	1.84	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1540	14287	26973	3.72	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
1540	14287	26974	3.72	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
1541	15572		11.72	0.0E+00	4505654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1542	14288	26976	11.72	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1553	14300	26988	2.86	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
1553	14300	26989	2.86	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
1555	14302	26990	11.7	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1555	14302	26990	11.7	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1558	14310		1.21	0.0E+00	D06333.1	NT	Human c-yes-2 gene
1574	14321	27007	1.65	0.0E+00	Z63739.1	NT	H. sapiens H12B16 gene
1575	14322	27008	1.59	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1575	14322	27009	1.59	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1576	14326	27010	11.18	0.0E+00	AV690831	EST_HUMAN	AV690831 GRG Homo sapiens cDNA clone GKCBOR92.5
1576	14326	27011	11.18	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GRG Homo sapiens cDNA clone GKCBOR92.5
1579	15573	27014	9.85	0.0E+00	AB040906.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1583	14329	27015	1.63	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1585	14331	27016	9.78	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1585	14331	27019	9.78	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1587	14333	27020	42.76	0.0E+00	5728978	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1587	14333	27021	42.76	0.0E+00	5728978	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1589	14335	27023	7.94	0.0E+00	M91903.1	NT	Homo sapiens sodium channel mRNA
1604	14360	27039	5.85	0.0E+00	H26973.1	EST_HUMAN	y976c05.s1 Soares adult brain N26-H1B5Y Homo sapiens cDNA clone IMAGE183848.3
1614	14361	27051	2	0.0E+00	AB046929.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1614	14361	27052	2	0.0E+00	AB046929.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1659	14405	27095	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0106-191199-004-511 HT0106 Homo sapiens cDNA
1659	14405	27096	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0106-191199-004-511 HT0106 Homo sapiens cDNA
1663	14409	27100	1.68	0.0E+00	AJ768104.1	EST_HUMAN	wg1507.x1 Soares NSF F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2HIS2 ZINC FINGER PROTEIN ;
1664	14410	27101	1.2	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1665	14411	27102	2.81	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1669	14414	27106	1.76	0.0E+00	M29590.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1669	14414	27107	1.76	0.0E+00	M29590.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1671	14416	27109	1.35	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1672	14417	27110	1.6	0.0E+00	7657085	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG) mRNA
1675	14420	27113	1.12	0.0E+00	BE222374.1	EST_HUMAN	h11d05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O85147 O85147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1675	14420	27114	1.12	0.0E+00	BE222374.1	EST_HUMAN	h11d05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O85147 O85147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1677	14421	27116	3.24	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1680	14424	27119	3.18	0.0E+00	H30132.1	EST_HUMAN	y659408.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1680	14424	27120	3.18	0.0E+00	H30132.1	EST_HUMAN	y659408.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1682	14426	27122	1.32	0.0E+00	Z80780.1	NT	H. sapiens h25h gene
1685	14429	27123	1.32	0.0E+00	Z80780.1	NT	H. sapiens h25h gene
1685	14429	27123	13.71	0.0E+00	5031748	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1693	14437	27133	1.11	0.0E+00	AF163663.1	NT	Homo sapiens FOXJ2 forkhead factor (FOXJ2) mRNA
1695	14438	27136	3.93	0.0E+00	8523841	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1702	14445	27145	1.11	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1708	14451	27152	4.08	0.0E+00	AB028542.1	NT	TCR zeta [human, GenomE/mRNA, 365 nt, segment 1 of 8]
1710	14453	27157	2.19	0.0E+00	S84400.1	NT	Homo sapiens NOD2 protein (NOD2) mRNA
1725	15577	27187	1.16	0.0E+00	11545811	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1739	14481	27181	1.93	0.0E+00	AF273841.1	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1778	15578	27228	0.96	0.0E+00	4306718	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1782	14523	27228	3.37	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1782	14523	27229	3.37	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1784	14525	27232	1.42	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1787	14528		1.2	0.0E+00	W76571.1	EST_HUMAN	z66509.r1 Soares fetal_haer_NBH19W Homo sapiens cDNA clone IMAGE:345684 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1788	16579	27236	2.74	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1800	14540	27251	5.68	0.0E+00	U114987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1802	14542	27254	2.78	0.0E+00	AB023331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1803	14543	27255	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1803	14543	27256	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1803	14543	27257	4.07	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1812	14552	27268	1.93	0.0E+00	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
1826	14565	27276	5.82	0.0E+00	6003855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1826	14565	27277	5.82	0.0E+00	6003855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1836	14575	27287	1.12	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1836	14575	27288	1.12	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1840	14578	27290	4.35	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1840	14578	27291	4.35	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1841	14578	27292	5.47	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1841	14578	27293	5.47	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1844	14582	27296	1.46	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-4in-F07-Q-U1st NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1844	14582	27297	1.46	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-4in-F07-Q-U1st NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1868	14606	27316	3.49	0.0E+00	BE277465.1	EST_HUMAN	60117816AF1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5'
1868	14606	27317	3.49	0.0E+00	BE277465.1	EST_HUMAN	60117816AF1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5'
1868	14606	27317	3.49	0.0E+00	BE277465.1	EST_HUMAN	60117816AF1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5'
1887	14624	27334	0.83	0.0E+00	BE006262.1	EST_HUMAN	RC2-BN0128-200300-012-04 BN0128 Homo sapiens cDNA
1916	14653	27362	2.18	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1916	14653	27362	2.18	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1916	14653	27363	2.18	0.0E+00	4506384	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1924	14661	27372	1.22	0.0E+00	AF157476.1	NT	Human transglutaminase mRNA, complete cds
1925	15582	27372	1.19	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1925	15582	27373	1.19	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1930	14666	27380	1.93	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1930	14666	27381	1.93	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1933	14668	27393	1.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1935	14870		4.27	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1940	14876		1.35	0.0E+00	M55932.1	NT	Human topoisomerase I pseudogene 1
1949	14884	27398	1.94	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1949	14884	27397	1.94	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1959	14895		1.15	0.0E+00	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C032
1981	14697	27410	1.09	0.0E+00	8400718	NT	Homo sapiens nebulin (NEB) mRNA
1981	14697	27411	1.09	0.0E+00	8400718	NT	Homo sapiens nebulin (NEB) mRNA
1982	14698	27412	2.49	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1982	14698	27413	2.49	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1973	14709	27427	1.38	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1973	14709	27428	1.38	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1878	14715	27432	1.69	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1878	14715	27433	1.69	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1979	14715	27433	1.57	0.0E+00	AW193024.1	EST_HUMAN	X08801.x1 NCI CGAP_Pon1 Homo sapiens cDNA clone IMAGE:2679913 3'
1981	14717	27434	1.57	0.0E+00	AW193024.1	EST_HUMAN	X08801.x1 NCI CGAP_Pon1 Homo sapiens cDNA clone IMAGE:2679913 3'
1981	14717	27435	1.57	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1982	14718	27436	5.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1982	14718	27437	5.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1884	14720	27439	2	0.0E+00	7682066	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1885	14721	27440	1.19	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1988	14722	27441	1.58	0.0E+00	Z47558.1	NT	H sapiens genes for semenogelin I and semenogelin II
1988	14722	27442	1.58	0.0E+00	Z47558.1	NT	H sapiens genes for semenogelin I and semenogelin II
1993	14729	27451	3.75	0.0E+00	AB040460.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2014	14749	27476	1.02	0.0E+00	AF273941.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2014	14749	27477	1.02	0.0E+00	AF273941.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2049	14779	27507	1.84	0.0E+00	7709742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2052	14785	27511	4.13	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE2 Homo sapiens cDNA clone PLACE4000321 5'
2053	14155	26837	1.55	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2053	14155	26838	1.55	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2055	14787	27513	2.04	0.0E+00	AA077889.1	EST_HUMAN	7B22E10 Chromosome 7 fetal brain cDNA library Homo sapiens cDNA clone 7B22E10
2055	14787	27514	2.04	0.0E+00	AA077889.1	EST_HUMAN	7B22E10 Chromosome 7 fetal brain cDNA library Homo sapiens cDNA clone 7B22E10
2057	14789		2.41	0.0E+00		NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
2059	14791		1.91	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, cod. alpha (PDE8A), mRNA
2060	14792	27517	0.97	0.0E+00	Z42359.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2082	14784	27528	1.78	0.0E+00	AI242427.1	EST_HUMAN	q90108.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2087	14789	27528	3.46	0.0E+00	BE877225.1	EST_HUMAN	6014851466 F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 6'
2089	14801	27528	1.48	0.0E+00	BF315325.1	EST_HUMAN	601902604 F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 6'
2089	14801	27529	1.48	0.0E+00	BF315325.1	EST_HUMAN	601902604 F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2092	14804	27532	3.07	0.0E+00	BE689725.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2092	14804	27533	3.07	0.0E+00	BE689725.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2080	14812	27544	3.71	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2080	14812	27545	3.71	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2086	14817	27549	1.98	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2107	14838		2.08	0.0E+00	BE767964.1	EST_HUMAN	QV1-0N0005-140900-378-G10 GN0005 Homo sapiens cDNA
2108	14839		1.59	0.0E+00	AF018933.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2110	14841	27572	3.78	0.0E+00	BF027652.1	EST_HUMAN	601672065 F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 6'
2111	14842	27573	1.03	0.0E+00	BE072824.1	EST_HUMAN	PMA-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2113	14844	27574	1.06	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2116	14847	27576	1.3	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271059-022-G10 CT0219 Homo sapiens cDNA
2117	14848	27577	1.47	0.0E+00	L76527.1	NT	Homo sapiens metabotropic glutamate receptor 1 alpha (mGluR1alpha) mRNA, complete cds
2119	14850	27579	6.39	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2119	14850	27580	6.39	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2153	14853		1.05	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNNM3L), mRNA
2179	14908		1.22	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2183	14912	27644	1.05	0.0E+00	BE274698.1	EST_HUMAN	601122339 F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2185	14914	27647	7.59	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNDDE08 5'
2185	14914	27648	7.59	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNDDE08 6'
2187	14916	27650	1.4	0.0E+00	AA931091.1	EST_HUMAN	oa32a01.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2191	14920	27654	5.68	0.0E+00	BF344434.1	EST_HUMAN	602014828 F1 NCL CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2192	14921	27655	12.14	0.0E+00	BE746890.1	EST_HUMAN	601572185 F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3836012 3'
2196	14925	27659	3.55	0.0E+00	BF377897.1	EST_HUMAN	CMT-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2196	14925	27660	3.55	0.0E+00	BF377897.1	EST_HUMAN	CMT-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2200	15588	27665	2.04	0.0E+00	BF313617.1	EST_HUMAN	601902031 F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2203	14931	27668	1.93	0.0E+00	BE018750.1	EST_HUMAN	0884602.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TRQ15170 Q15170 TRANSCRIPTION FACTOR S-H-RELATED PROTEIN;

Page 486 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2204	14932	27669	1.55	0.0E+00	AA042813.1	EST_HUMAN	345307.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN);
2204	14932	27670	1.55	0.0E+00	AA042813.1	EST_HUMAN	345307.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN);
2212	14940	27678	3.37	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2212	14940	27678	3.37	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2213	14941	27680	2.3	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2213	14941	27681	2.3	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2218	14946	27704	1.37	0.0E+00	U36264.1	NT	Homo beta-prime-adaptin (BAM22) gene, exon 18
2238	14984	27704	6.71	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2243	14971	27709	2.03	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2250	14978	27717	1.71	0.0E+00	BE985281.1	EST_HUMAN	601435255F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818607 5'
2253	14981	27720	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2253	14981	27721	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2256	14983	27723	2.35	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2259	15024	27750	4.02	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2269	15024	27760	4.02	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2300	15025	27761	1.87	0.0E+00	AA078404.1	EST_HUMAN	3478a1.1.1 Soares_fetal_liver_spleen_INF15_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2302	15027	27763	2.33	0.0E+00	AA428001.1	EST_HUMAN	3478a1.1.1 Soares_fetal_liver_spleen_INF15_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2302	15027	27764	2.33	0.0E+00	BF347039.1	EST_HUMAN	3478a1.1.1 Soares_fetal_liver_spleen_INF15_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2304	15029	27765	1.75	0.0E+00	U2840.1	NT	602021846F1 NCI CGAP Bms77 Homo sapiens cDNA clone IMAGE:4157339 5'
2309	15034	27772	1.52	0.0E+00	AB020717.1	NT	Homo sapiens potassium channel K2.1 mRNA, complete cds
2310	15035	27773	1.61	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2310	15035	27774	1.61	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2311	15036	27775	1.59	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2317	15042	27780	1.17	0.0E+00	BE676095.1	EST_HUMAN	722a02.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:O94939 O94939 KIAA0857 PROTEIN
2320	15045	27782	4.73	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHK42) gene, exon 32
2321	15046	27783	1.9	0.0E+00	AB25542.1	EST_HUMAN	3478a08.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2238182 3'
2325	15050	27785	1.88	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2325	15050	27785	1.88	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2326	15053	27789	1.95	0.0E+00	5603178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2328	15053	27790	1.95	0.0E+00	5603178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2334	15058	27793	1.24	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2334	15058	27784	1.24	0.0E+00	7692007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2348	15071	27807	3.2	0.0E+00	5174878	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2352	15074	27811	2.39	0.0E+00	AU131142.1	EST_HUMAN	AU131142.1 NT2P3 Homo sapiens cDNA clone NT2P30202084 5'
2353	15075		4.31	0.0E+00	BE794028.1	EST_HUMAN	011586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2354	15076	27812	1.51	0.0E+00	AW687076.1	EST_HUMAN	MRI-5N0033-120400-002-ad4 SN0033 Homo sapiens cDNA
2355	15077	27813	2.99	0.0E+00	7692017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2356	15078	27814	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2356	15078	27815	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2357	15079		5.25	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2359	15081	27817	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2359	15081	27818	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2359	15081	27819	7.98	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2360	15082	27820	0.98	0.0E+00	8823089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2377	15099		0.91	0.0E+00	BE814424.1	EST_HUMAN	MRC-SN0070-080600-028-d12 BN0070 Homo sapiens cDNA
2415	15135	27872	1.05	0.0E+00	AU118562.1	EST_HUMAN	AU118562 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2416	15137		3.74	0.0E+00	AU42035.1	EST_HUMAN	060502.x1 Source: NIHMPUL_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR-006662
2417	15138	27873	0.98	0.0E+00	8823620	NT	008662 230K04 PHOSPHATIDYLINOSITOL 4-KINASE
2420	15141		4.44	0.0E+00	BE895005.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2424	15145	27878		0.0E+00	BE837632.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2433	15154		0.98	0.0E+00	AB005822.1	EST_HUMAN	MRI-TN0021-280900-001-h06 TN0021 Homo sapiens cDNA
2437	15157	27892	4.5	0.0E+00	6066002	NT	AB005822 HaLa cDNA (T.Nam) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2441	15160	27899	2.09	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
2441	15160	27899	2.09	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
2449	15169	27908	1.91	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 10 variant 4 (LIT4) gene, exon 6
2454	15172	27911	1.22	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NC1 CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2461	15179	27919	4.45	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2465	15183	27922	1.24	0.0E+00	BE831003.1	EST_HUMAN	GMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2465	15183	27923	1.24	0.0E+00	BE831003.1	EST_HUMAN	GMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2470	15188	27927	0.93	0.0E+00	U13968.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2470	15188	27928	0.93	0.0E+00	U13968.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2471	15189	27929	2.08	0.0E+00	BF580144.1	EST_HUMAN	602184658T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2482	15200	27940	3.34	0.0E+00	AW469222.1	EST_HUMAN	h04M4A.x1 NCL CGAP Kid12 Homo sapiens cDNA clone IMAGE:2872789 3'
2484	15202	27941	2.89	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BPp-as-c07-Q-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2488	15215	27938	0.91	0.0E+00	5453985	NT	U1-HF-BPp-as-c07-Q-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2498	15215	27958	0.91	0.0E+00	5453985	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2509	16228	27971	1.66	0.0E+00	AW813853.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2514	16231	27971	5.22	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0187-303030-016-c04 S10197 Homo sapiens cDNA
2515	16058	27983	1.4	0.0E+00	BE706542.1	EST_HUMAN	RC3-ST0187-303030-016-c04 S10197 Homo sapiens cDNA
2516	16232	27972	1.48	0.0E+00	BE706542.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2518	15234	27974	1.83	0.0E+00	232884.2	NT	U1-HF-BPp-as-c07-Q-U1.1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2520	16236	27977	3.28	0.0E+00	5453871	EST_HUMAN	U1-HF-BPp-as-c07-Q-U1.1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2522	15238	27977	1.3	0.0E+00	BE910378.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2523	15239	27978	1.96	0.0E+00	7657468	NT	U1-HF-BPp-as-c07-Q-U1.1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2524	15240	27979	2.01	0.0E+00	8923340	NT	Homo sapiens death receptor 8 (DR8), mRNA
2525	15241	27980	2.21	0.0E+00	U63239.1	NT	Homo sapiens death receptor 8 (DR8), mRNA
2530	15246	27984	1.44	0.0E+00	BE886490.1	EST_HUMAN	U1-HF-BPp-as-c07-Q-U1.1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2534	15249	27989	6.16	0.0E+00	BE875511.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2534	15249	27990	6.16	0.0E+00	BE875511.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2538	15251	27993	1.19	0.0E+00	AF245905.1	NT	Homo sapiens death receptor 8 (DR8), mRNA
2554	15258	28002	1.2	0.0E+00	BE536921.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2561	15275	28012	2.97	0.0E+00	AU143277.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2561	15275	28013	2.97	0.0E+00	AU143277.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2562	15276	28014	1.8	0.0E+00	BE292898.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2562	15276	28015	1.8	0.0E+00	BE292898.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2563	15277	28016	1.07	0.0E+00	BF23041.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28018	7.84	0.0E+00	AF245905.1	NT	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28019	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28020	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28021	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28022	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28023	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28024	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28025	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28026	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28027	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28028	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28029	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28030	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28031	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28032	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28033	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28034	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28035	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28036	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28037	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28038	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28039	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28040	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28041	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28042	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28043	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28044	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28045	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28046	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28047	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28048	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28049	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28050	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28051	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28052	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28053	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28054	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28055	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28056	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28057	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28058	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28059	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28060	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28061	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28062	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28063	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28064	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28065	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28066	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28067	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28068	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28069	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2569	15280	28070	2.22	0.0E+00	BE286513.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2618	15328	28072	2.08	0.0E+00	AI571737.1	EST_HUMAN	In18608.x1 NCI CGAP Br25 Homo sapiens cDNA clone IMAGE:218055 3' similar to hL20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF2)
2619	15330	28073	2.19	0.0E+00	5032150	NT	mRNA
2621	15333	28077	4.85	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
2622	15334	28078	1.02	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2623	15337	28079	1.02	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2625	15337	28080	2.56	0.0E+00	BE596328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3061398 5'
2632	15344	28098	4.92	0.0E+00	BE782472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2641	15352	28098	1.61	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2651	15361	28103	1.27	0.0E+00	U78027.1	NT	Homo sapiens Brudin's tyrosine kinase (BTK), alpha-D galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2652	15362	28103	6.55	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2658	15368	28106	1.22	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 5
2659	15369	28107	1.08	0.0E+00	U59225.1	NT	Human bullock parathyroid antigen (BPAG1) mRNA, complete cds
2661	15371	28108	2.22	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 5'
2663	15373	28110	2.22	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 5'
2666	15376	28115	1.71	0.0E+00	AF1887016.1	EST_HUMAN	RG1-OT0086-223300-011-407 OT0088 Homo sapiens cDNA
2667	15377	28116	1.26	0.0E+00	BF000018.1	EST_HUMAN	7h1505.x1 NCI CGAP Cor16 Homo sapiens cDNA clone IMAGE:3318089 3'
2668	15378	28116	4.97	0.0E+00	BE333165.1	EST_HUMAN	601286714F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3629923 5'
2668	15378	28116	2.57	0.0E+00	BE531263.1	EST_HUMAN	601286714F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2725	15432		4.21	0.0E+00	AA316728.1	EST_HUMAN	EST18414 HCC cell line (malaestasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2726	15433	28169	5.57	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943561 5'
2732	15439	28177	3.83	0.0E+00	U36253.1	NT	Human beta-pine-adenin (BAM22) gene, exon 5
2733	15440	28178	1.33	0.0E+00	7699517	NT	Homo sapiens neurogranin 1 (NRG1) transcript variant SMDP, mRNA
2734	15441	28179	1.78	0.0E+00	AF107653.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2736	15443	28181	1.27	0.0E+00	AB051626.1	EST_HUMAN	Homo sapiens h22K mRNA for GTP-binding protein like 1, complete cds
2742	15448	28187	2.77	0.0E+00	BE796378.1	EST_HUMAN	601581981F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3845983 5'
2745	15454	28191	3.48	0.0E+00	BE663433.1	EST_HUMAN	601336465F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2746	15451		1.18	0.0E+00	AU721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTB5VE09 5'
2748	15453	28194	2.25	0.0E+00	5174483	NT	Homo sapiens spermatogenesis associated PDI (KIAA0787) mRNA
2748	15453	28195	2.25	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PDI (KIAA0787) mRNA
2748	15453	28196	1.21	0.0E+00	8623441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2749	15454	28196					

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2749	15454	28107	1.21	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2750	15455	28198	2.6	0.0E+00	AF280185.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2751	15456	28199	13.89	0.0E+00	AV851068.1	EST_HUMAN	AV851068 GLC Homo sapiens cDNA clone GLCOLD07.3
2752	15457	28199	3.13	0.0E+00	BF377697.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2753	15457	28200	3.13	0.0E+00	BF377697.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2754	15461	28203	33.8	0.0E+00	4757663	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2756	15461	28204	33.8	0.0E+00	4757663	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2758	15461	28204	33.8	0.0E+00	4757663	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2760	15465	28209	2.88	0.0E+00	BE747193.1	EST_HUMAN	601560503F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472.5
2771	15476	28219	1.15	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2772	15477	28219	3.38	0.0E+00	BF514110.1	EST_HUMAN	UHLBW1-annw-07-0-LJ1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340.3
2778	15483	28227	0.99	0.0E+00	4933068	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2784	15489	28228	2.1	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2785	15489	28228	2.1	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2785	15489	28228	4.67	0.0E+00	BF677694.1	EST_HUMAN	602085570F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4246915.5
2791	15498	28237	1.78	0.0E+00	7427822	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2794	15499	28240	13.56	0.0E+00	AV726534.1	EST_HUMAN	AV726534 HTC Homo sapiens cDNA clone HTCCCA03.5
2794	15499	28240	13.56	0.0E+00	AV726534.1	EST_HUMAN	AV726534 HTC Homo sapiens cDNA clone HTCCCA03.5
2798	15501	28246	7.61	0.0E+00	AI879163.1	EST_HUMAN	ai85404.V1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663.5 similar to
2799	15504	28246	5.41	0.0E+00	BF630691.1	EST_HUMAN	SW-R13A_HUMAN P40429 BGS RIBOSOMAL PROTEIN L13A ;
2800	15505	28246	5.55	0.0E+00	BE672768.1	EST_HUMAN	602071667F1 NCI CGAP_Bim7 Homo sapiens cDNA clone IMAGE:4214679.5
2802	15507	28247	1.6	0.0E+00	AU131484.1	EST_HUMAN	601460912F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3864642.5
2802	15507	28247	1.6	0.0E+00	AU131484.1	EST_HUMAN	AU131484 NT2RP3 Homo sapiens cDNA clone NT2RP302672.5
2803	15508	28249	20.28	0.0E+00	BE300344.1	EST_HUMAN	AU131484 NT2RP3 Homo sapiens cDNA clone NT2RP302672.5
2803	15508	28250	20.28	0.0E+00	BE300344.1	EST_HUMAN	60094794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980806.5
2809	12895	25634	4.22	0.0E+00	S76830.1	NT	60094794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980806.5
2812	15515	28144	4.35	0.0E+00	AB033281.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2818	13491	28145	8.39	0.0E+00	AF284750.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2818	13491	28145	8.39	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2822	13776	28436	3.52	0.0E+00	4503202	NT	Homo sapiens cyclochrome P450, subfamily1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2822	13776	28437	3.52	0.0E+00	4503202	NT	Homo sapiens cyclochrome P450, subfamily1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2840	15508	28258	3.52	0.0E+00	X85980.1	NT	H sapiens urate hydroxymethyltransferase pseudogene

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2841	15609		1.34	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2843	15611		1.22	0.0E+00	AB040860.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2849	15617	28263	2.61	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2852	15620	28266	2.63	0.0E+00	M91803.1	NT	Human sodium channel mRNA
2854	15622	28267	1.94	0.0E+00	M80602.1	NT	Human ADHNAK nucleoprotein mRNA, 5' end
2857	15625	28268	1.26	0.0E+00	BE164504.1	EST_HUMAN	PMA-HIT0343-281289-003-002 HT0343 Homo sapiens cDNA
2857	15625	28270	1.20	0.0E+00	BE164504.1	EST_HUMAN	PMA-HIT0343-281289-003-002 HT0343 Homo sapiens cDNA
2859	15627		1.18	0.0E+00	X73426.1	NT	H sapiens lds gene for HLH type transcription factor
2860	15628		2.59	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2861	15629	28272	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2861	15629	28273	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2861	15629	28274	1.03	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2866	15633	28277	18.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3) pseudogene
2866	15633	28278	18.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3) pseudogene
2869	15635	28281	1.69	0.0E+00	AL096957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2870	15637		7.2	0.0E+00	Y10658.1	NT	H sapiens mRNA for nuclear DNA helicase II
2871	15638		1.42	0.0E+00	AF16203.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2872	15639	28282	47.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2872	15639	28283	47.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2882	15649	28292	2.35	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 8 (STK8) mRNA
2885	15652	28296	1.05	0.0E+00	AL047599.1	EST_HUMAN	DKFZ5656G0821.1 5861 (synonym: hule1) Homo sapiens cDNA clone DKFZ5656G0821
2888	15653	28297	0.97	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2888	15653	28298	0.97	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2887	15654		2.66	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2890	15657	28300	5.46	0.0E+00	BE081893.1	EST_HUMAN	QV2-BT0638-130400-139-103 BT0638 Homo sapiens cDNA
2890	15657	28301	5.46	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0638-130400-139-103 BT0638 Homo sapiens cDNA
2897	15664	28312	2.08	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C068
2897	15664	28313	2.08	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C068
2905	15671		4.18	0.0E+00	Y18210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
2907	15673	28321	1.33	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2908	15674	28322	20.94	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2909	15676	28323	1.91	0.0E+00	AL681002.1	EST_HUMAN	U18607.X1 NC1 CGAP Brn25 Homo sapiens cDNA clone IMAGE2167981 3' similar to TR:O18247 O18247 F44E7.2 PROTEIN. ;

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2909	15975	28324	1.91	0.0E+00	AI581002.1	EST_HUMAN	In18d07.x1 NCI CGAP Brn28 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2911	15977	28326	1.63	0.0E+00	F62740	SW/SSPROT	O16247 F44E7.2 PROTEIN 132
2912	15978	28327	2.01	0.0E+00	AF162388.1	NT	Homo sapiens procathepsin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2928	15984	28339	1.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2928	15984	28340	1.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2929	15995	28341	4.58	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2929	15995	28342	4.58	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2932	15998	28345	3.58	0.0E+00	AB040941.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2932	15998	28346	3.58	0.0E+00	7691903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2933	15999	28347	3.21	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2933	15999	28348	3.21	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2938	15703	28352	1.16	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2938	15703	28353	1.16	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17293 PROTEIN ;
2948	15712	28364	2.15	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2948	15712	28365	2.15	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2953	15719	28370	1.99	0.0E+00	4759827	NT	Homo sapiens neurxin III (NRXN3) mRNA
2954	15720		0.98	0.0E+00	X08494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2957	15723	28373	2.38	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2958	15724	28374	5.98	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2958	15724	28375	5.98	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2959	15726	28376	7.64	0.0E+00	AF106276.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2973	15739		1.13	0.0E+00	AI146880.1	EST_HUMAN	q143106.x1 Soares, beta, NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2980	15746	28354	1.12	0.0E+00	4506118	NT	H. sapiens NF-H gene, exon 4
2981	15747	28355	2.85	0.0E+00	AB044684.1	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2991	15757	28404	1.92	0.0E+00	7692273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2993	15759	28405	3.75	0.0E+00	5729765	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2993	15759	28407	3.75	0.0E+00	5729765	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2997	15763	28412	1.1	0.0E+00	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
3025	15791	28439	1.17	0.0E+00	M74069.1	NT	Human displacement protein (OC4A1) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3033	15799	28445	0.71	0.0E+00	4505882	NT	Homo sapiens semaphorin 1 (SEMP1) mRNA
3039	15905		4.82	0.0E+00	AF186953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3042	15909	28454	3.74	0.0E+00	5879469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3042	15908	28453	3.74	0.0E+00	5879469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3044	15810		5.68	0.0E+00	AL359403.1	NT	Isolom 2 of a novel human mRNA from chromosome 22
3049	15815	28460	1.6	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CRE5 (CRE5) mRNA, partial cds
							Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM4 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3052	15818		1.08	0.0E+00	AF198779.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3056	16832	28475	1.19	0.0E+00	AF170492.1	NT	Human germline gene 16.1 for Ig lambda6 L-chain C region (lgL-C16.1)
3074	15840	28483	2.8	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL6 (FBL5) mRNA, complete cds
3080	15845		1.54	0.0E+00	AF196355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3084	15849	28490	1.72	0.0E+00	AF064399.1	NT	Homo sapiens SWI/SNF complex protein p270 mRNA, partial cds
3104	15869	28509	3.2	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3105	15870	28510	7.83	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469) mRNA
3110	15875	28514	3.42	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469) mRNA
3111	15876	28515	1.21	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
							Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3138	15902	28547	3.74	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3149	15911	28555	25.81	0.0E+00	L20541.1	NT	Human Tenth heavy chain mRNA, complete cds
3151	15914	28559	1.32	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3151	15914	28560	1.32	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
							Homo sapiens mRNA for KIAA0549 protein, partial cds
3158	15921	28567	8.63	0.0E+00	T94970.1	EST_HUMAN	h32703.1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP-S26539
3172	15935	28584	0.98	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K -1
3178	15941	28591	4.39	0.0E+00	X68922.1	NT	601876507F1 NIH MSG_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3178	15941	28592	4.39	0.0E+00	X68922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3187	15950	28601	1.31	0.0E+00	4759827	NT	H. sapiens mRNA for gamma-glutamyltransferase
3187	15950	28602	1.31	0.0E+00	4759827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3187	15950	28602	1.31	0.0E+00	4759827	NT	Homo sapiens neurexin I receptor, type 1 (IL-IR1) mRNA
3195	15958	28610	8.46	0.0E+00	4504658	NT	Homo sapiens nucleolar phosphoprotein B23 (NP41) mRNA, complete cds
3211	15974	28625	3.25	0.0E+00	M28659.1	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
							Homo sapiens CREB binding protein (Rubshtan-Taybi syndrome) (CREBBP) mRNA
3214	15977	28628	1.96	0.0E+00	4502008	NT	
3220	15983	28636	0.85	0.0E+00	4759055	NT	

Table 4

Single EYon Probes Expressed in Brain

[illegible]

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16156	28807	0.95	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3398	16166	28808	0.95	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3401	16169	28810	1.36	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC61594), mRNA
3402	16160	28811	1.42	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds
3406	16164		0.99	0.0E+00	AW867015.1	EST_HUMAN	MR1-3N0033-100-001-001-008 3N0033 Homo sapiens cDNA
3418	16175	28824	1.69	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3418	16175	28826	1.66	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3419	16176	28828	1.34	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filenah (BFSP1) mRNA
3421	16178	28827	5.37	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3430	15441	28179	1.75	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3435	16191	28840	2.4	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3438	16194	28844	5.47	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and hcaA, hcaB, and hcaC incompatibility determinants
3440	16198	28846	1.5	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3448	16204	28853	3.54	0.0E+00	A1935159.1	EST_HUMAN	wp14410.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819.3 similar to TR:O739334 O739334 NEURAL CELL ADHESION MOLECULE.1
3448	16204	28854	3.54	0.0E+00	A1935159.1	EST_HUMAN	wp14410.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819.3 similar to TR:O739334 O739334 NEURAL CELL ADHESION MOLECULE.1
3452	16208	28859	2.48	0.0E+00	AJ276120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3459	16215	28868	1.82	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3459	16215	28869	1.82	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3484	16220	28874	1.31	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3470	16226	28880	5.4	0.0E+00	U43283.1	NT	Human MIDSTA (AML1/MDS1 fusion) mRNA, partial cds
3475	16231	28884	1.18	0.0E+00	9589718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3475	16231	28885	1.18	0.0E+00	9589718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3479	16235	28890	1.84	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KGI transcriptional regulatory protein p54 mRNA, complete cds
3479	16235	28891	1.84	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KGI transcriptional regulatory protein p54 mRNA, complete cds
3484	16241	28898	1.12	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3486	16252	28905	2.21	0.0E+00	BE304791.1	EST_HUMAN	601143853FT.NH_MGC.15 Homo sapiens cDNA clone IMAGE:3051373.5
3488	16252	28909	2.21	0.0E+00	BE304791.1	EST_HUMAN	601143853FT.NH_MGC.15 Homo sapiens cDNA clone IMAGE:3051373.5
3489	16255	28908	0.92	0.0E+00	4828795	NT	Homo sapiens potassium voltage-gated channel, task-related family, member 2 (KCNK2) mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3504	16280	28914	0.89	0.0E+00	AI384007.1	EST_HUMAN	1635g12.x1 Scores_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:2085742 3' similar to TR:000498
3507	16283	28917	1.11	0.0E+00	M10976.1	NT	000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN :
3529	16285	28940	1.29	0.0E+00	AF701869.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
3530	16286	28941	0.95	0.0E+00	450884	NT	AV701869 ADB Homo sapiens cDNA clone ADBDA06 5'
3531	16287	28945	1.74	0.0E+00	AF078688.1	NT	Homo sapiens semaphorin II (SEM2) mRNA
3539	16295	28946	1.49	0.0E+00	AF193204.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3542	16297	28948	1.21	0.0E+00	AB040909.1	NT	Novel human gene mapping to chromosome X
3551	16316	28963	1.37	0.0E+00	6597248	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3551	16316	28964	1.37	0.0E+00	6597248	NT	Homo sapiens sat (Drosophila)-like 1 (SALL1), mRNA
3562	16317	28987	1.04	0.0E+00	AI081907.1	EST_HUMAN	Homo sapiens sat (Drosophila)-like 1 (SALL1), mRNA
3564	16319	28987	1.04	0.0E+00	6325463	NT	CE13742 :
3569	16324	28987	4.17	0.0E+00	AW852217.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 3, member A3 (BTNA3), mRNA
3578	16331	28976	0.78	0.0E+00	AF18846.1	NT	QV6-CT0225-230300-169-601 C70225 Homo sapiens cDNA
3577	16332	28976	8.46	0.0E+00	BF676393.1	EST_HUMAN	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3599	16356	28988	0.9	0.0E+00	AW837677.1	EST_HUMAN	602084683F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248666 5'
3603	16356	28988	0.74	0.0E+00	BF672054.1	EST_HUMAN	QV6-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3603	16356	28997	0.74	0.0E+00	BF672054.1	EST_HUMAN	602152495F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4253645 5'
3604	16357	28997	0.95	0.0E+00	4826967	NT	602152495F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4253645 5'
3606	16359	28999	1.08	0.0E+00	AW654693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3606	16359	29000	1.08	0.0E+00	AW654693.1	EST_HUMAN	h184g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3609	16362	29004	1.42	0.0E+00	4826763	NT	h184g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3611	16364	29007	0.93	0.0E+00	7682319	NT	Homo sapiens heparan sulfate (glycosaminoglycan) 3-O-sulfatase 1 (H3SST1) mRNA
3621	16374	29016	0.92	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
3621	16374	29016	0.92	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
3638	16391	29030	2.67	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3642	16393	29049	3.32	0.0E+00	7686491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3658	16411	29049	2.6	0.0E+00	AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3660	16413	29051	3.38	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3660	16413	29052	3.38	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3668	16421	29061	1.65	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3668	16421	29062	1.65	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3671	16424	29065	1.52	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-605 CT0222 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3673	16426	29087	1.53	0.0E+00	S728028	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3675	16428	29089	1.81	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0766 protein, partial cds
3676	16430	29090	1.1	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3677	16430	29071	1.1	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3677	16430	29072	22.21	0.0E+00	7682237	NT	Homo sapiens KIAA0670 protein/echinus (KIAA0670), mRNA
3679	16432	29074	22.21	0.0E+00	7682237	NT	Homo sapiens KIAA0670 protein/echinus (KIAA0670), mRNA
3679	16432	29075	22.21	0.0E+00	AW298134.1	EST_HUMAN	U1-H-BW0-ajc-e-12-U1st NC1 CGAP. Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3682	16445	29084	4.35	0.0E+00	AW298134.1	EST_HUMAN	U1-H-BW0-ajc-e-12-U1st NC1 CGAP. Sub6 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3682	16445	29085	4.35	0.0E+00	AW298134.1	EST_HUMAN	sa0601.r1 Soares NIHMPU.S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3714	16467	29105	1.08	0.0E+00	AA463659.1	EST_HUMAN	SW/KR84_SHEEP P24445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1]:
3718	16471	29109	1.14	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3721	16474	29111	3.31	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3730	16482	29120	0.82	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3742	16489	29130	4.9	0.0E+00	7662183	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3746	16498	29133	4.29	0.0E+00	4506716	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3751	16503	29138	1.06	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3751	16503	29139	1.09	0.0E+00	7657065	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3800	16552	29139	0.71	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3802	16564	29185	2.88	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3804	16566	29187	2.3	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3804	16566	29188	2.3	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3804	16566	29189	1.24	0.0E+00	4759011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3808	16560	29183	1.24	0.0E+00	10181139	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3808	16561	29184	1.01	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3809	16571	29197	1.01	0.0E+00	AF137699.1	EST_HUMAN	ta6210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3812	16584	29197	1.01	0.0E+00	AF137699.1	EST_HUMAN	ta6210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3813	16585	29198	1.97	0.0E+00	AF152468.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3814	16586	29198	1.14	0.0E+00	4758169	NT	Homo sapiens desmoglein (DPI, DPL1) (DSP) mRNA
3818	16570	29202	10.39	0.0E+00	S76885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ9BIR1) gene, complete cds
3819	16571	29203	2.22	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3820	16572	29204	6.03	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3824	16576	29207	1.23	0.0E+00	AF089601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3824	16576	29208	1.23	0.0E+00	AF089601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3825	16578	29213	0.97	0.0E+00	AB001523.1	NT	Homo sapiens gene for TNFEM1 and PWP2, complete and partial cds
3825	16580	29214	0.97	0.0E+00	AB001523.1	NT	Homo sapiens gene for TNFEM1 and PWP2, complete and partial cds
3826	16580	29214	0.97	0.0E+00	AB001523.1	NT	Homo sapiens gene for TNFEM1 and PWP2, complete and partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
38331	16582	282216	1.12	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
38335	16586	292222	6.18	0.0E+00	4603178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
38336	16588	292223	6.18	0.0E+00	4603178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
38337	16588	292226	4.04	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
38338	16588	292227	0.89	0.0E+00	AF174488.1	NT	Homo sapiens interseccion short isoform (ITSN) mRNA, complete cds
38441	16592	292229	2.96	0.0E+00	4829783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
38445	16595	292232	1.05	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
38455	16598	292233	1.43	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
38477	16598	292235	0.74	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
38559	16609	292244	2.16	0.0E+00	AB884727.1	EST_HUMAN	wk01f01.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411066 3' similar to TR:O43340
38562	16612	292248	4.24	0.0E+00	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
38572	16617	292251	1.35	0.0E+00	AL040338.1	EST_HUMAN	DKFZB434N0413.71 434 (synonym: Hs3) Homo sapiens cDNA clone DKFZB434N0413 5'
38577	16617	292256	1.28	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
38577	16617	292257	1.28	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
38569	16619	292259	3.22	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
38711	16621	292259	1.82	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
38715	16625	292263	1.18	0.0E+00	AF149412.1	NT	Homo sapiens HBP1/ hepatin-binding and FGF-binding protein gene, complete cds
3884	16634	292273	1.2	0.0E+00	4509758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
38883	16638	292277	1.47	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KJAA0412) mRNA
38995	16646	292286	1.18	0.0E+00	BF355295.1	EST_HUMAN	RC3-H10860-170800-01-1-12 H10860 Homo sapiens cDNA
38998	16648	292288	1.06	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986726 similar to MXRA5
38998	16648	292289	1.05	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
38998	16648	292289	1.05	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
39004	16654	292295	1.82	0.0E+00	AF129533.1	NT	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986726 similar to MXRA5
39017	16657	292298	1	0.0E+00	AF451306.1	EST_HUMAN	Matrix remodeling associated gene 5
3912	16662	292303	2.81	0.0E+00	BE376002.1	EST_HUMAN	U1-HB3-alk-g-07-0-1 NCL CGAP_S145 Homo sapiens cDNA clone IMAGE:2756943 3'
3920	16670	29312	0.92	0.0E+00	AF490740.1	EST_HUMAN	601239866-1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606800 5'
3922	16673	29312	2.49	0.0E+00	5360215	NT	PM5-L10031-100100-003-109 L10031 Homo sapiens cDNA
3923	16673	29313	0.98	0.0E+00	BE284998.1	EST_HUMAN	Homo sapiens idiuronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
3923	16673	29314	0.98	0.0E+00	BE294998.1	EST_HUMAN	601193827-1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3952	16702	29339	1.42	0.0E+00	U10991.1	NT	601165827-1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
							Human G2 protein mRNA, partial cds

Page 498 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3952	16702	28340	1.42	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
3952	16702	28341	1.42	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
3952	16706	28344	4.69	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3957	16706	28345	0.69	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3957	16706	28345	0.69	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3966	16715	28351	4.39	0.0E+00	M23910.1	NT	Human KIFC class II lymphocyte antigen DPW4-beta-2 pseudogene, exon 2
3966	16715	28351	4.39	0.0E+00	M23910.1	NT	Human KIFC class II lymphocyte antigen DPW4-beta-2 pseudogene, exon 2
3966	16717	28359	5.74	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3975	16724	28359	1.35	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
3975	16724	28361	3.22	0.0E+00	AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C084
3975	16724	28361	3.22	0.0E+00	AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C084
3987	16735	28369	1.71	0.0E+00	AL163293.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3987	16735	28369	1.71	0.0E+00	AL163293.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3989	16747		27.98	0.0E+00	4503470	NT	Homo sapiens KIAA0563 protein, cDNA clone IMAGE:2247334 3' similar to TR:090309 O60309
4003	16750		1.15	0.0E+00	A057076.1	EST_HUMAN	KIAA0563 PROTEIN ;
4003	16751	28382	2.97	0.0E+00	7682183	NT	Homo sapiens KIAA0563 gene product (KIAA0569), mRNA
4005	16761	28382	2.97	0.0E+00	7682183	NT	Homo sapiens KIAA0563 gene product (KIAA0569), mRNA
4005	16762	28383	2.65	0.0E+00	U09368.1	EST_HUMAN	Human zinc finger protein ZNF133
4013	16769	28387	0.95	0.0E+00	AW339490.1	NT	Chlorococcus ethiops mRNA for UGA suppressor RNA-associated antigenic protein (RNA48 gene)
4024	16769	28401	0.33	0.0E+00	AB015610.1	NT	Homo sapiens mRNA for KIAA0316 protein, partial cds
4033	16776		3.72	0.0E+00	AJ238817.1	NT	Homo sapiens chromosome 21 segment HS21C003
4045	16790	28418	1.32	0.0E+00	AB002314.2	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4045	16791	28419	1.04	0.0E+00	AL163203.2	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4047	16792	28420	1.18	0.0E+00	AFQ36943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4047	16793	28421	2.65	0.0E+00	AJ277276.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4048	16793	28422	2.65	0.0E+00	AJ277276.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4054	16799	28426	6.29	0.0E+00	5032028	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4054	16799	28430	6.29	0.0E+00	5032028	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4059	16813	28442	5.98	0.0E+00	4885306	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4070	16814	28443	4.7	0.0E+00	AB006625.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4073	16817	28444	1.11	0.0E+00	4759807	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4074	16818	28445	5.87	0.0E+00	11419287	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4075	16819	28446	1.94	0.0E+00	AL049857.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4082	16826	28453	2.71	0.0E+00	AF165527.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4091	13857	28453	0.82	0.0E+00	4828947	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4091	13857	28453	0.82	0.0E+00	4828947	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4091	13857	28453	0.82	0.0E+00	4828947	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4097	16840	28468	1.09	0.0E+00	5901805	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
4098	16842	28469	1.08	0.0E+00	4503854	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds

Page 499 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4099	16842	29470	1.08	0.0E+00	4903854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4107	16850	29478	0.89	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0885 protein, partial cds
4112	16855	29482	0.93	0.0E+00	AB02597.1	EST_HUMAN	Homo sapiens mRNA for KIAA0885 protein, partial cds IMAGE:25169753
4121	16863	29483	4.93	0.0E+00	AB02597.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:25169753
4116	16857	29485	0.82	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4115	16857	29486	0.82	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4120	16862		2.34	0.0E+00	BE274217.1	EST_HUMAN	6011207767 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:26876803
4128	16868	29495	0.99	0.0E+00	AB032851.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4126	16866	29498	0.99	0.0E+00	AB032851.1	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4128	16870	29498	2.24	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4135	16877		5.52	0.0E+00	AW675569.1	EST_HUMAN	ba5704.x1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:26000853 similar to SW:TH2_BOVIN
4140	16882	29511	1.14	0.0E+00	AW408788.1	EST_HUMAN	Q85108 MITOCHONDRIAL THIOREDOXIN PRECURSOR
4142	16884	29514	1.28	0.0E+00	8922468	NT	UHF-BMO-sdx-c2-c2-U1.T NIH_MGC 38 Homo sapiens cDNA clone IMAGE:30631475
4142	16884	29515	1.28	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4151	16893		2.8	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REL (sperm receptor for egg jelly sea urchin homolog)-like (PKDREL) mRNA
4169	16908	29537	8.97	0.0E+00	AA401438.1	EST_HUMAN	zu69h07.s1 Soares, testis, NIH-T Homo sapiens cDNA clone IMAGE:7431973 similar to contains Alu repetitive element/contains element MER35 repetitive element
4169	16909	29538	8.97	0.0E+00	AA401438.1	EST_HUMAN	zu69h07.s1 Soares, testis, NIH-T Homo sapiens cDNA clone IMAGE:7431973 similar to contains Alu repetitive element/contains element MER35 repetitive element
4203	16946		1.01	0.0E+00	AL163303.2	NT	repetitive element/contains element MER35 repetitive element
4240	16951	29606	4.08	0.0E+00	J02610.1	NT	Homo sapiens chromosome 21 segment HS21G103
4255	16996	29625	0.93	0.0E+00	AW936889.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G103
4261	17002	29633	0.74	0.0E+00	4826827	NT	PM2-DT0023-480300-004-a08 DT0023 Homo sapiens cDNA
4261	17002	29634	0.74	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4281	17004	29636	4.71	0.0E+00	AF174500.1	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4283	17004	29636	4.71	0.0E+00	AF174500.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4270	17010		2.52	0.0E+00	AI189944.1	EST_HUMAN	ga23906.x1 Soares, placenta, 8weeks, ZN0HP865W Homo sapiens cDNA clone IMAGE:17245793 similar to contains MER20 b2 MER20 repetitive element
4273	17012		4.32	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4285	17024	29650	1.35	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4291	17030	29657	0.76	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4291	17030	29658	0.76	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4291	17036	29664	1.58	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds

Table 4

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4297	17036	29695	1.58	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4307	17046	29671	8.31	0.0E+00	6012281	NT	Human sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4327	17069		1.16	0.0E+00	AF163047.2	NT	Human sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4337							Human sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4337	17076	29704	4.17	0.0E+00	L14551.1	NT	H sapiens H2BfH gene
4341	17080	29709	2.88	0.0E+00	Z00780.1	NT	H sapiens H2BfH gene
4341	17080	29710	2.88	0.0E+00	Z00780.1	EST	XP_694104.1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:583351.4 3' similar to TR:P97365 P97365
4342	17081	29711	0.94	0.0E+00	AW169933.1	EST_HUMAN	ZINC FINGER PROTEIN 64:
4348	17087	29717	1.42	0.0E+00	XG0483.1	NT	H sapiens H4d gene for H4 histone
4348	17087	29718	1.42	0.0E+00	XG0483.1	NT	H sapiens H4d gene for H4 histone
4353	17091	29724	8.62	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4353	17091	29725	8.62	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4356	17104	29740	12.59	0.0E+00	4895126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4367	17105	29741	1.14	0.0E+00	AJ271739.1	NT	Homo sapiens Xa pseudocatalase region; segment 2/2
4400	17137	29766	0.98	0.0E+00	T0194556	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4408	17145	29778	1.25	0.0E+00	AJ249765.1	NT	Homo sapiens myosin bound arthropod-specific P (XAPBP2) gene, complete cds
4414	17161	29779	1.25	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4436	17172		1.81	0.0E+00	AF200629.1	NT	Homo sapiens HPS-1 gene, intron 5
4453	17169	29814	1.43	0.0E+00	T010233.1	EST_HUMAN	seq1329 b4HB3MA C08b-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C08b-HAP-F1025 5'
4453	17169	29815	1.43	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA C08b-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C08b-HAP-F1025 5'
4456	17192		0.73	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4465	17202	29828	5.68	0.0E+00	AW084064.1	EST_HUMAN	xc68048.x1 NCL CGAP_E602 Homo sapiens cDNA clone IMAGE:2596446 3' similar to SW_AHNN_HUMAN
4468	17202		1.57	0.0E+00	8031619	NT	Q09499 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK:
4468	17202		1.57	0.0E+00	8031619	NT	Q09499 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK:
4470	17205	29831	0.93	0.0E+00	AJ966933.1	EST_HUMAN	PT33 repetitive element:
4473	17208		8.82	0.0E+00	AL163207.2	NT	Human sapiens chromosome 21 segment HS21C007
4475	17210	29835	3.17	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101189-002-003 HT0305 Homo sapiens cDNA
4481	17216	29842	1.99	0.0E+00	AJ276120.1	NT	Homo sapiens mRNA for putative enkyrin-repeat containing protein (ORF1)
4481	17216	29843	1.99	0.0E+00	AJ276120.1	NT	Homo sapiens mRNA for putative enkyrin-repeat containing protein (ORF1)
4481	17216	29845	1.99	0.0E+00	AJ276120.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4483	17218	29846	2.88	0.0E+00	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4484	17219	29846	2.88	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (NNB1) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483	17229	29898	1.26	0.0E+00	S76984.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ5BIR1) gene, exon
4484	17230	29899	1.06	0.0E+00	AF111163.1	NT	Homo sapiens p70 (MEFV) gene, complete cds
4494	17230	29880	1.06	0.0E+00	AF111163.1	NT	Homo sapiens p70 (MEFV) gene, complete cds
4502	17882	29870	2.56	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 193 (ZNF193) mRNA
4507	17242	29875	6.16	0.0E+00	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4512	17247	29882	4.31	0.0E+00	AF16237.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4515	17250	29886	1.32	0.0E+00	5434175	NT	Homo sapiens zinc finger protein 211 (ZNF211) mRNA
4525	17250	29894	15.47	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4532	17267	29900	0.79	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4536	17271	29903	1.61	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4540	17275	29908	2.03	0.0E+00	4502656	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4544	17279		2.38	0.0E+00	L35485.1	NT	Homo sapiens lauroyl sulphate sulphatase (LSS) gene, complete cds
4546	17281	29910	12.72	0.0E+00	7682091	NT	Homo sapiens KIA03590 gene product (KIA03590), mRNA
4546	17281	29911	12.72	0.0E+00	7682091	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4563	17298	29925	0.96	0.0E+00	AF143314.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4568	17301	29928	10.33	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4568	17301	29929	10.33	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4581	17316		1.68	0.0E+00	AA174072.1	EST HUMAN	zfp1808.s1 Stragene (cds) ratina 937202 Homo sapiens cDNA clone IMAGE:509854 3'
4583	17318		1.46	0.0E+00	7657410	NT	Homo sapiens odc (Odc) gene, complete cds
4585	17320		3.16	0.0E+00	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4588	17321	29947	1.04	0.0E+00	H82741.1	EST HUMAN	y82b01.s1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4588	17321	29948	1.04	0.0E+00	H82741.1	EST HUMAN	y82b01.s1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4597	17322	29949	2.8	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKR) gene, complete cds
4598	17323	29950	4.04	0.0E+00	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4599	17324		1.66	0.0E+00	AB037621.1	NT	Homo sapiens gene for nucleotide protein, partial cds
4598	17331	29958	1.53	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4598	17331	29959	1.53	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4597	17332	29960	1.52	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4597	17332	29961	1.52	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds

Page 502 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4598	17333	29992	1.5	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4605	17340	29970	1.22	0.0E+00	AB029970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4605	17340	29970	1.22	0.0E+00	AB029970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4611	17346	29978	5.25	0.0E+00	U18800.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4617	17352	29987	1.08	0.0E+00	AA418246.1	EST_HUMAN	2x86507.s1 Screez_NH/MPU_S1 Homo sapiens cDNA clone IMAGE:767605.3
4624	17358		2.27	0.0E+00	AF089541.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4629	17364	29998	1.06	0.0E+00	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4629	17364	29999	1.06	0.0E+00	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17365	30000	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4630	17365	30001	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4631	17366	30002	2.67	0.0E+00	AB74095.1	NT	Human displacement protein (GCAAT) mRNA
4635	17370	30005	1.84	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4635	17370	30006	1.84	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4636	17370	25593	0.82	0.0E+00	T56945.1	EST_HUMAN	y83p04.2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
4636	17370	25594	0.82	0.0E+00	T56945.1	EST_HUMAN	y83p04.2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
4639	17373		1.31	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:350521.5'
4660	17394	30028	1.33	0.0E+00	U56551.1	NT	Mus musculus neuroexophilin 1 (Nuph1) gene, large exon and 3' end of the intron, and partial cds
4665	17399	30033	6.97	0.0E+00	M804021.1	NT	Human AHNK nucleoporin mRNA, 5' end
4668	17402	30036	2.23	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4668	17402	30037	2.23	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4668	17402	30037	2.23	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (NKTR) gene, complete cds
4671	17405	30040	1.9	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4673	17407	30042	2.02	0.0E+00	7682181	NT	Homo sapiens KIAA0363 gene product (KIAA0363), mRNA
4680	17414	30049	0.95	0.0E+00	U07593.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4681	17415	30050	0.97	0.0E+00	S71448.1	NT	SCN1A-brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1598 nt]
4681	17415	30051	0.97	0.0E+00	S71448.1	NT	SCN1A-brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1596 nt]
4682	17426	30051	1.45	0.0E+00	X58497.1	NT	Human CYP2D7A2 pseudogene for cytochrome P450 2D6
4682	17426	30055	1.06	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4701	17435	30068	1.05	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4709	17441	30073	1.4	0.0E+00	AF028801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4712	17444	30076	0.84	0.0E+00	7016320	NT	Homo sapiens protein p008 (AD013), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4712	17444	30077	0.84	0.0E+00	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4735	17467	30103	1.88	0.0E+00	AW444637.1	EST_HUMAN	U-H-913-qw-c4-q-01.51 NC1 CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4740	17472		1.82	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4750	17482		2.28	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4790	17521		2.79	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4794	17525	30147	2.02	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4796	17527	30149	1.11	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSGR9) mRNA, complete cds
4797	17528	30150	1.98	0.0E+00	AF007416.1	NT	Homo sapiens zinc finger transcription factor Kairo mRNA, complete cds
4798	17529	30161	3.07	0.0E+00	4503766	NT	Mus musculus fragile X mental retardation 2 (FMR2) mRNA
4800	17531	30153	13.57	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4801	17532	30154	1.04	0.0E+00	P82740	SWISSPROT	ZINC FINGER PROTEIN 132
4803	17536	30159	5.7	0.0E+00	8623080	NT	Homo sapiens hypocalcemic protein FLJ20073 (FLJ20073), mRNA
4809	17540	30163	0.97	0.0E+00	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4810	17541	30164	1.84	0.0E+00	M64081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4810	17541	30165	1.84	0.0E+00	M94081.1	NT	J61 segments; and Tcr-C-alpha gene, exons 1-4
4812	17543	30167	1.44	0.0E+00	X94928.1	NT	J61 segments; and Tcr-C-alpha gene, exons 1-4
4812	17543	30168	1.44	0.0E+00	X94928.1	NT	J61 segments; and Tcr-C-alpha gene, exons 1-4
4815	17546	30171	2.86	0.0E+00	AL163280.2	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4823	17564	30176	1.17	0.0E+00	6032160	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4830	17591	30183	1.09	0.0E+00	X92841.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4832	17593	30185	1.91	0.0E+00	4585842	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4833	17594	30186	1.81	0.0E+00	AB014533.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4834	17595	30187	2.24	0.0E+00	6677848	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4836	17598	30188	0.95	0.0E+00	5174580	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4836	17597	30189	1.19	0.0E+00	4758199	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4838	17599	30191	1.81	0.0E+00	7705546	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4842	17572	30198	12.82	0.0E+00	AF055068.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4844	17574		3.47	0.0E+00	4505508	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4845	17575	30199	2.39	0.0E+00	AF091711.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4858	17587	30210	1.07	0.0E+00	D63562.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4860	17589	30212	1.68	0.0E+00	4503984	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4865	17624	30252	1.03	0.0E+00	4506952	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4875	17602	30224	3.09	0.0E+00	AB006825.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4876	17602	30225	3.09	0.0E+00	AB006825.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4885	17612	30232	0.95	0.0E+00	AB026898.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4889	17626	30243	1.45	0.0E+00	AL163284.2	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4908	17633	30248	1.02	0.0E+00	AW452728.1	EST_HUMAN	U1H-B15-414-02-0-U1.1 NCL CGAP, Sub5 Homo sapiens cDNA clone IMAGE:3068591 3'
4909	17637	30251	1.61	0.0E+00	8922928	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4912	17640	30235	1.09	0.0E+00	4502398	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4915	17643		4.68	0.0E+00	U14067.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4924	17652		2.95	0.0E+00	BE408653.1	EST_HUMAN	601303720F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3538118 5'
4928	17658	30286	3.18	0.0E+00	4759189	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4933	17661	30271	1.16	0.0E+00	7662401	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4938	17666	30274	1.01	0.0E+00	AB026898.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4947	17674	30283	2.34	0.0E+00	8923441	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4947	17674	30284	2.34	0.0E+00	8923441	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4958	17683	30291	0.81	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCL CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
4958	17683	30292	0.81	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCL CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
4988	17683	30293	0.81	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCL CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
4991	17688	30295	1.11	0.0E+00	AF161463.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4991	17688	30296	1.11	0.0E+00	AF161463.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4973	13019	25661	0.71	0.0E+00	AF165658.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4976	17699		0.84	0.0E+00	AL050253.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4985	17708	30312	1.63	0.0E+00	AF016705.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4986	17709	30313	1.5	0.0E+00	Y18186.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4986	17709	30314	1.5	0.0E+00	Y18186.1	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA
4984	17717		1.26	0.0E+00	AL163289.2	NT	Homo sapiens fatty acyl CoA synthetase (fatty acyl CoA synthetase, dimethylallyltransferase, geranyltransferase) (FAPS) mRNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4987	17720		25.03	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3) pseudogene
5001	17724	30326	0.97	0.0E+00	AA084272.1	EST_HUMAN	zr03g10.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546402 5'
5001	17724	30327	0.97	0.0E+00	AA084272.1	EST_HUMAN	zr03g10.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546402 5'
5012	16924	29563	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5012	16924	29564	0.95	0.0E+00	4307720	NT	Homo sapiens titin (TTN) mRNA
5028	17727	30350	3	0.0E+00	X52988.1	NT	Bacillus amyloquelicifaciens sacB gene for levanucrase (EC 2.4.1.10)
5042	17761	30376	1.04	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5042	17761	30376	1.04	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5045	17764	30380	1.95	0.0E+00	7657074	NT	Homo sapiens ecotropic viral integration site 2A (EV2A) mRNA
5045	17764	30381	1.95	0.0E+00	7657074	NT	Homo sapiens ecotropic viral integration site 2A (EV2A) mRNA
5049	17768	30387	1.11	0.0E+00	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21O081
5050	17769	30388	1.03	0.0E+00	1142100.1	NT	Homo sapiens HEF like Protein (HEFL) mRNA
5052	17771	30389	1.05	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5058	17775	30391	2.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5058	17775	30392	2.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5058	17775	30394	1.07	0.0E+00	Y06032.1	NT	Human endogenous retrovirus-K, LTR US and gag gene
5079	17798	30414	1.01	0.0E+00	8923922	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5079	17798	30415	1.01	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5081	17800	30417	0.76	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597) mRNA
5081	17800	30418	0.76	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597) mRNA
5088	17807	30423	2.59	0.0E+00	7657008	NT	Homo sapiens deleted in bladder cancer chromosome region candidate 1 (DBCCR1), mRNA
5097	17816	30433	2.05	0.0E+00	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
5109	17827	30444	1.23	0.0E+00	D46802.1	NT	Mus musculus mRNA for leucine-rich repeat protein, partial cds
5110	17828	30446	1.14	0.0E+00	AF227534.1	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice variant
5111	17829	30446	1.88	0.0E+00	AF227534.1	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice variant
5112	17830	30447	0.98	0.0E+00	AF245702.1	NT	Homo sapiens toll-like receptor 7 (TLR7) mRNA, complete cds
5115	17833	30449	6.83	0.0E+00	4958966	NT	Homo sapiens microtubule-associated protein 2 (MAP2) mRNA
5116	17834	30450	1.5	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5116	17834	30451	1.5	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5117	17835	30452	1.6	0.0E+00	AW05819.1	EST_HUMAN	EST337880 IMAGE resequencing, MAGO Homo sapiens cDNA
5119	17837		1.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
5128	17844		1.72	0.0E+00	AJ010179.1	NT	Homo sapiens gabar1 receptor gene, exon 6

Page 506 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	17857	30473	5.57	0.0E+00	AB027013.1	NT	Homo sapiens mRNA for Nucleosome Assembly Protein 1-like 2, complete cds
5150	17861	30477	1.19	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for neuroxin-1 alpha protein, complete cds
5151	17868	30481	1.18	0.0E+00	AB029040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
5154	17871		1.08	0.0E+00	M91803.1	NT	Human sodium channel mRNA
5155	17872	30484	1.37	0.0E+00	5454073	NT	Homo sapiens ring finger protein 16 (RNF16), mRNA
5162	17893		3.44	0.0E+00	AF063093.1	NT	Homo sapiens acylase (AC02) gene, nuclear gene encoding mitochondrial protein, exon 15
5172	17981	30495	2.82	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5172	17981	30496	2.82	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5192	18000	30523	1.29	0.0E+00	AB044954.1	EST_HUMAN	Homo sapiens keratin 12 (KRT12) gene, complete cds
5195	18003	30528	1.77	0.0E+00	AB044954.1	EST_HUMAN	Homo sapiens keratin 12 (KRT12) gene, complete cds
5209	18017	30539	3.81	0.0E+00	BE931030.1	EST_HUMAN	Human sodium channel mRNA
5213	18021	30543	3	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2), mRNA, complete cds
5213	18021	30544	3	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2), mRNA, complete cds
5220	18027	30552	1.69	0.0E+00	X59163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5220	18027	30553	1.69	0.0E+00	X59163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5289	18104	30763	6.56	0.0E+00	BE67498.1	EST_HUMAN	7110c05.x1 NCI CGAP GLT1 Homo sapiens cDNA clone IMAGE:3294250 3'
5300	18105	30764	1.75	0.0E+00	BE220763.1	EST_HUMAN	H89a02.x1 NCI CGAP LUG2 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5301	18108	30766	1.93	0.0E+00	BE784412.1	EST_HUMAN	P42894 HYPOTHETICAL PROTEIN KIAA0064.1
5301	18108	30766	1.93	0.0E+00	BE784412.1	EST_HUMAN	601589422F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943804 5'
5301	18108	30766	1.93	0.0E+00	BE784412.1	EST_HUMAN	601589422F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943804 5'
5302	18107	30767	0.81	0.0E+00	AI189142.1	EST_HUMAN	qp04a04.x1 Soares_placenta_8108weeks_2N6P180c9W Homo sapiens cDNA clone IMAGE:1722702 3'
5308	18111	30770	6.17	0.0E+00	M29908.1	NT	similar to SW:17203_ORFOME P45946 TRANSCRIPTION INITIATION FACTOR TF1D 85 KD SUBUNIT ;
5319	25068	30780	4.68	0.0E+00	11421038	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5329	18132	30791	7.18	0.0E+00	BF965962.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5330	18133	30791	0.73	0.0E+00	AF134408.1	EST_HUMAN	602118028F1 NIH_MGC.65 Homo sapiens cDNA clone IMAGE:4276254 5'
5330	18133	30792	0.73	0.0E+00	AF134408.1	EST_HUMAN	AUI34408 OVARC1 Homo sapiens cDNA clone OVARC1001884 5'
5335	18138	30799	1	0.0E+00	BE538657.1	EST_HUMAN	AUI34408 OVARC1 Homo sapiens cDNA clone OVARC1001884 5'
5344	18147	30826	1.07	0.0E+00	BE202784.1	EST_HUMAN	601081489F1 NIH_MGC.10 Homo sapiens cDNA clone OVARC1001884 5'
5348	18151	30831	1.69	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5348	18151	30832	1.69	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5367	18491	32513	1.82	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5370	18171	30958	0.81	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds

Page 507 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5370	18171	30859	0.91	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5374	18174	30863	4.85	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5374	18174	30864	4.85	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5387	18187	30878	1.08	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5387	18187	30878	1.08	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5401	18201	30906	1.88	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5407	18206	30912	0.81	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5428	18225	30936	0.78	0.0E+00	D61664.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5428	18225	30937	0.78	0.0E+00	D61664.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5429	18228	30941	2.65	0.0E+00	BF529931.1	EST_HUMAN	802043232F1 NCI CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4179988 5'
5429	18228	30942	2.55	0.0E+00	BF529931.1	EST_HUMAN	802043232F1 NCI CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4179988 5'
5434	18233	30946	2.92	0.0E+00	BF313139.1	EST_HUMAN	801897558F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5445	18244	31132	4.37	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5477	18276	31171	1.15	0.0E+00	BE260777.1	EST_HUMAN	801160252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5488	18285	31166	3.51	0.0E+00	AV1887316.1	EST_HUMAN	MRO-SN0037-030400-001-107 SN0037 Homo sapiens cDNA
5500	18298	31197	2.33	0.0E+00	BE292899.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5500	18298	31197	2.33	0.0E+00	BE292899.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5521	18318	31219	1.51	0.0E+00	11420818	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5521	18319	31220	1.51	0.0E+00	11420818	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5528	18326	31229	4.35	0.0E+00	AF064264.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5528	18326	31229	4.35	0.0E+00	AF064264.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5535	18333	31239	2.94	0.0E+00	AJ224539.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5535	18333	31240	2.95	0.0E+00	AJ224539.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5566	18363	31271	0.91	0.0E+00	AI198515.1	EST_HUMAN	qfag1 0.21 Soares, placenta, 2NBHP816GW Homo sapiens cDNA clone IMAGE:1757730 3'
5570	18367	31277	6.98	0.0E+00	MB5719.1	EST_HUMAN	similar to SW-CADC, HUMAN P45268 BRAIN-CAOHERIN PRECURSOR,
5577	18374	31286	4.83	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Stragene (cat#93206) Homo sapiens cDNA clone IMAGE:3087658 5'
5590	18398	31298	1.25	0.0E+00	Z26269.1	NT	UHRF-BL0-auth-4Q2-4-UL17 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3087658 5'
5591	18398	31306	1.94	0.0E+00	AW361877.1	EST_HUMAN	H.sapiens isoform 1 gene for L-type calcium channel, exon 14, seq 15
5601	18398	31307	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM5-CT0283-091299-007-105 CT0283 Homo sapiens cDNA
5601	18398	31307	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM5-CT0283-091299-007-105 CT0283 Homo sapiens cDNA
5601	18398	31307	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM5-CT0283-091299-007-105 CT0283 Homo sapiens cDNA
5601	18398	31307	1.94	0.0E+00	AW361877.1	EST_HUMAN	PM5-CT0283-091299-007-105 CT0283 Homo sapiens cDNA
5605	18401	31315	2.55	0.0E+00	U39281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13

Page 508 of 536
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5638	18431	31344	1.03	0.0E+00	AB046891.1	NT	Homo sapiens mRNA for KIA11641 protein, partial cds
5639	18432	31345	1.56	0.0E+00	AJ003435.1	NT	Homo sapiens KVLQ11 gene
5640	18433	31346	1.56	0.0E+00	AJ003435.1	NT	Homo sapiens KVLQ11 gene
5641	18434	31347	1.56	0.0E+00	AJ003435.1	NT	Homo sapiens KVLQ11 gene
5642	18435	31348	1.19	0.0E+00	A02076.1	EST_HUMAN	HAC2981 Human fetal liver cDNA library Homo sapiens cDNA
5643	18436	31349	1.19	0.0E+00	A02076.1	EST_HUMAN	HAC2981 Human fetal liver cDNA library Homo sapiens cDNA
5644	18437	31350	1.19	0.0E+00	A02076.1	EST_HUMAN	HAC2981 Human fetal liver cDNA library Homo sapiens cDNA
5645	18438	31351	1.19	0.0E+00	A02076.1	EST_HUMAN	HAC2981 Human fetal liver cDNA library Homo sapiens cDNA
5646	18439	31352	1.19	0.0E+00	A02076.1	EST_HUMAN	HAC2981 Human fetal liver cDNA library Homo sapiens cDNA
5647	18440	31353	1.21	0.0E+00	BE71173.1	EST_HUMAN	Homo sapiens prolactin beta-2 (PDB-H2) mRNA
5648	18441	31354	1.21	0.0E+00	BE71173.1	EST_HUMAN	Homo sapiens prolactin beta-2 (PDB-H2) mRNA
5649	18442	31355	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5650	18443	31356	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5651	18444	31357	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5652	18445	31358	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5653	18446	31359	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5654	18447	31360	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5655	18448	31361	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5656	18449	31362	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5657	18450	31363	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5658	18451	31364	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5659	18452	31365	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5660	18453	31366	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5661	18454	31367	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5662	18455	31368	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5663	18456	31369	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5664	18457	31370	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5665	18458	31371	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5666	18459	31372	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5667	18460	31373	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5668	18461	31374	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5669	18462	31375	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5670	18463	31376	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5671	18464	31377	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5672	18465	31378	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior-sensitive calton channel 1, nuclear (dogenein) (ACGN1), mRNA
5673	18466	31379	1.13	0.0E+00	9989843	EST_HUMAN	Homo sapiens amelior

Page 509 of 536
Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5872	18659	31600	0.77	0.0E+00	BF155870.1	EST_HUMAN	QV44-UT0894-200900-399-a10 HT0594 Homo sapiens cDNA
5878	18684	31604	3.22	0.0E+00	W33069.1	EST_HUMAN	z08h06r1 Soares_pituitary_tumor_NHMPA Homo sapiens cDNA clone IMAGE:321755 5'
5878	18684	31605	3.22	0.0E+00	W33069.1	EST_HUMAN	z08h06r1 Soares_pituitary_tumor_NHMPA Homo sapiens cDNA clone IMAGE:321755 5'
5879	18685		2.51	0.0E+00	AF012818.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
5882	18686	31609	3.33	0.0E+00	BE280197.1	EST_HUMAN	60118515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
5900	18676	31620	2.8	0.0E+00	BE888670.1	EST_HUMAN	601512630F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3914238 5'
5905	18690	31639	0.8	0.0E+00	AW752848.1	EST_HUMAN	IL3-CT0220-111789-028-E04 CT0220 Homo sapiens cDNA
5908	18692	31641	1.1	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5908	18692	31642	1.1	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5908	18693	31643	0.88	0.0E+00	BE801608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5909	18693	31644	0.88	0.0E+00	BE801608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5909	18693	31645	0.88	0.0E+00	BE801608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
5923	25081	31691	10.65	0.0E+00	9789866	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCNQ2), mRNA
5928	18710	31694	1.2	0.0E+00	AA169508.1	EST_HUMAN	z40h01r1 Soares_NHMPcL_S1 Homo sapiens cDNA clone IMAGE:665005 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 6. ;
5928	18710	31695	1.2	0.0E+00	AA169508.1	EST_HUMAN	z40h01r1 Soares_NHMPcL_S1 Homo sapiens cDNA clone IMAGE:665005 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
5948	18730	31699	18.77	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
5948	18730	31699	18.77	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
5987	18768	31732	0.99	0.0E+00	BE255330.1	EST_HUMAN	60114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
5997	18778	31740	1.2	0.0E+00	BE166591.1	EST_HUMAN	QVQ-HT0368-090200-099-a09 HT0368 Homo sapiens cDNA
6007	18789	31750	0.85	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6040	18820	31781	1.32	0.0E+00	BE379007.1	EST_HUMAN	601234276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6048	18826	31787	1.39	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone IMAGE:1007201 5'
6086	18845	31809	3.76	0.0E+00	U45692.1	NT	Human G protein-coupled receptor GPR-8-8 gene, complete cds
6094	18872	31839	4.52	0.0E+00	AA204740.1	EST_HUMAN	TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6095	18873	31840	3.97	0.0E+00	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6098	18873	31841	3.97	0.0E+00	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6129	18907	31875	1.14	0.0E+00	11426387	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6133	18911	31880	2.87	0.0E+00	BE251773.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6147	18924		0.85	0.0E+00	A1686048.1	EST_HUMAN	607110x1 NCL_GAP_P128 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:O14839 C14839 MI-2 PROTEIN. ;

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6151	18928	31897	1.53	0.0E+00	35630.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6159	18938	31903	1.22	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6159	18936	31904	1.22	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6170	18947	31919	0.57	0.0E+00	A1198025.1	EST_HUMAN	q150511.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR-Q12838 Q12838
6170	18947	31920	0.57	0.0E+00	A1198025.1	EST_HUMAN	q150511.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR-Q12838 Q12838
6172	18949	31921	0.85	0.0E+00	BF357123.1	EST_HUMAN	TFIIC ALPHA SUBUNIT ;
6180	18957	31931	1.08	0.0E+00	11435830	NT	MRQ-HT0923-220800-102-505 HT0923 Homo sapiens cDNA
6189	18968	31939	0.95	0.0E+00	D55849.1	NT	Homo sapiens peptide transporter 3 (LOC61296), mRNA
6207	18982	31981	1.03	0.0E+00	AW178142.1	EST_HUMAN	Human mRNA for alpha mannosidase II isozyme, complete cds
6228	19002	31978	0.66	0.0E+00	BE874544.1	EST_HUMAN	IL3-HT0062-010899-014-A04 HT0062 Homo sapiens cDNA
6232	19006	31983	1.33	0.0E+00	7682039	NT	7e2c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN
6248	19020	32003	8.59	0.0E+00	AV950020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6254	19028	32003	3.13	0.0E+00	AW675598.1	EST_HUMAN	AV550020 GLC Homo sapiens cDNA clone GI CGA009 3'
6257	19031	32006	6.26	0.0E+00	H01255.1	EST_HUMAN	UHF-BLQ-acc-g-12-d-J1.x1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6259	19042	32019	1.6	0.0E+00	X16377.1	NT	y27503.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:149833 5'
6271	19044	32021	0.65	0.0E+00	AA456375.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6272	19045	32022	1.3	0.0E+00	A161284.1	EST_HUMAN	act4e07.r1 Scores_NHIMPUL S1 Homo sapiens cDNA clone IMAGE:813252 5'
6278	19051	32028	4.71	0.0E+00	BE735989.1	EST_HUMAN	act4e07.r1 Scores_NHIMPUL S1 Homo sapiens cDNA clone IMAGE:813252 5'
6278	19051	32029	4.71	0.0E+00	BE735989.1	EST_HUMAN	act4e07.r1 Scores_NHIMPUL S1 Homo sapiens cDNA clone IMAGE:813252 5'
6282	19055	32035	0.86	0.0E+00	AW746596.1	EST_HUMAN	P57789 SODIUM- AND CHLORIDE-DEPENDENT OCREATINE TRANSPORTER 2 ;
6282	19055	32036	0.86	0.0E+00	AW746596.1	EST_HUMAN	601305369F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639618 5'
6283	19056	32036	0.86	0.0E+00	AW746596.1	EST_HUMAN	601305369F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639618 5'
6283	19056	32036	0.86	0.0E+00	U77629.1	NT	MRQ-BT0284-221189-002-411 BT0284 Homo sapiens cDNA
6285	19058	32039	15.59	0.0E+00	AU119245.1	EST_HUMAN	MRQ-BT0284-221189-002-411 BT0284 Homo sapiens cDNA
6285	19058	32039	15.59	0.0E+00	AU119245.1	EST_HUMAN	MRQ-BT0284-221189-002-411 BT0284 Homo sapiens cDNA
6285	19058	32039	15.59	0.0E+00	AU119245.1	EST_HUMAN	MRQ-BT0284-221189-002-411 BT0284 Homo sapiens cDNA
6288	19062	32044	0.8	0.0E+00	BE780453.1	EST_HUMAN	MRQ-BT0284-221189-002-411 BT0284 Homo sapiens cDNA
6290	19076	32045	1.12	0.0E+00	X82217.1	NT	Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6304	19083	32062	1.52	0.0E+00	A1898483.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1003560 5'
6317	19088	32072	6.91	0.0E+00	BE203153.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1003560 5'
6317	19088	32073	6.91	0.0E+00	BE203153.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1003560 5'

Page 511 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6355	19125	32119		0.58	BF057438.1	EST_HUMAN	7k34h05.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3478468 3' similar to TR:O14553 O14553 R31240.1
6358	19167	32157	1.89	0.0E+00	AW406348.1	EST_HUMAN	UHF1-BL0-coch-02-Q-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3056631 5'
6358	19167	32158	1.89	0.0E+00	AW406348.1	EST_HUMAN	UHF1-BL0-coch-02-Q-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3056631 5'
6418	19165	32184	0.79	0.0E+00	AV718444.1	EST_HUMAN	AV718444 GLC-Homo sapiens cDNA clone GLCEHC05 5'
6427	19165	32191	0.99	0.0E+00	BE589340.1	EST_HUMAN	601881160F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6427	19165	32192	0.98	0.0E+00	BE589340.1	EST_HUMAN	601881150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6430	19198	32195	2.24	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1e (CACNA1G) mRNA, complete cds
6433	19201	32197	1.17	0.0E+00	11420668	NT	Homo sapiens transcription/transcription domain-associated protein (TRRAP), mRNA
8440	19208	32204	7.5	0.0E+00	AW163840.1	EST_HUMAN	al69h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O16390 O15390 GT24. [3] TR:O43840 TR:O43206
8440	19208	32205	7.5	0.0E+00	AW163840.1	EST_HUMAN	al69h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O16390 O15390 GT24. [3] TR:O43840 TR:O43206
8444	19212	32208	0.97	0.0E+00	W37163.1	EST_HUMAN	z22a08.r1 Soares fetal lung, NBL10W Homo sapiens cDNA clone IMAGE:3026228 5' similar to z22a06.r1 Soares fetal lung, NBL10W Homo sapiens cDNA clone IMAGE:3026228 5' similar to SW:ZN46_HUMAN_Q02988 ZINC FINGER PROTEIN 45
8444	19212	32209	0.97	0.0E+00	W37163.1	EST_HUMAN	z22a08.r1 Soares fetal lung, NBL10W Homo sapiens cDNA clone IMAGE:3026228 5' similar to SW:ZN46_HUMAN_Q02988 ZINC FINGER PROTEIN 45
8459	19228	32226	1.08	0.0E+00	BE704853.1	EST_HUMAN	60159371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
8459	19233	32233	6.81	0.0E+00	BE706873.1	EST_HUMAN	60159371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
8467	19234	32234	0.56	0.0E+00	BE707955.1	EST_HUMAN	QV1-GN0065-140800-318-H02 GN0065 Homo sapiens cDNA
8467	19234	32235	0.56	0.0E+00	BE707955.1	EST_HUMAN	QV1-GN0065-140800-318-H02 GN0065 Homo sapiens cDNA
8471	19238	32238	6.95	0.0E+00	BE689813.1	EST_HUMAN	601512039F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
8471	19238	32239	6.95	0.0E+00	BE689813.1	EST_HUMAN	601512039F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
8480	19247	32247	5.92	0.0E+00	L24485.1	NT	Human antigen GD27 gene, exons 1-2
8485	19252	32251	1.98	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8485	19252	32252	1.98	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8491	19258	32258	4.05	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (epimer receptor) (ZP3A), mRNA
8494	19260	32261	4.76	0.0E+00	AL638412.1	EST_HUMAN	h31111.x1 NCI_CGAP_G038 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR
8495	19261	32262	1.39	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
8507	19272	32273	4.12	0.0E+00	AA434584.1	EST_HUMAN	zms20303.r1 Soares fetal, NBL2HFB_9w Homo sapiens cDNA clone IMAGE:773668 5'
8520	19285	32281	0.98	0.0E+00	BE721200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103683 5'
8523	19289	32283	1.82	0.0E+00	BE228975.1	EST_HUMAN	QV2-BN0047-300800-278-c05 BN0047 Homo sapiens cDNA

Page 512 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6554	19319	32325	1.11	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 8 (SLC1A8), mRNA
6554	19319	32325	1.11	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6554	19319	32326	1.11	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6571	19337	32346	1.86	0.0E+00	AU125928.1	EST_HUMAN	PM2-28928 NT28M4 Homo sapiens cDNA, clone NT28M4-002430.5'
6573	19337	32348	1.86	0.0E+00	BE701434.1	EST_HUMAN	PM2-289174-260700-007-H10 NN0174 Homo sapiens cDNA
6573	19337	32349	1.86	0.0E+00	BE701434.1	EST_HUMAN	PM2-289174-260700-007-H10 NN0174 Homo sapiens cDNA
6584	19357	32371	1.87	0.0E+00	BE142263.1	EST_HUMAN	GMA-H10143-270569-062-008 HT0143 Homo sapiens cDNA
6614	19377	32391	1.44	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-260300-032-004 BN0121 Homo sapiens cDNA
6614	19377	32392	1.44	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-260300-032-004 BN0121 Homo sapiens cDNA
6638	19400	32415	8.38	0.0E+00	BF035687.1	EST_HUMAN	PM3-H10520-230200-002-008 HT0520 Homo sapiens cDNA
6640	19402	32417	1.93	0.0E+00	BF035687.1	EST_HUMAN	PM3-H10520-230200-002-008 HT0520 Homo sapiens cDNA
6678	19595	32683	3.49	0.0E+00	AA1190765.1	EST_HUMAN	IL5-GN0032-180900-145-007 GN0032 Homo sapiens cDNA
6690	19607	32647	0.94	0.0E+00	U39573.1	NT	zfp96b03.1 Striatagene Hda cell s3 837216 Homo sapiens cDNA, clone IMAGE:627282.5'
6693	19610	32649	0.91	0.0E+00	BE671987.1	EST_HUMAN	Homo salivary peroxidase mRNA, complete cds
6703	19618	32660	6.68	0.0E+00	AI60821.1	EST_HUMAN	7649607.x1 NC1 CGAP_G06 Homo sapiens cDNA, clone IMAGE:3222037.3' similar to TR:Q9Z285 Q9Z285 TEKTN1.
6714	19629	32681	6.89	0.0E+00	AI604621.1	EST_HUMAN	IL3-ST0024-230769-001-B01 S10024 Homo sapiens cDNA
6714	19629	32681	1.91	0.0E+00	AI604621.1	EST_HUMAN	IL3-ST0024-230769-001-B01 S10024 Homo sapiens cDNA
6726	19660	32592	0.99	0.0E+00	AL042443.1	EST_HUMAN	Homo sapiens CD8 antigen (CD8), mRNA
6729	19693	32595	0.9	0.0E+00	AI169270.1	EST_HUMAN	cdk1d01.x1 Soares NSF F8 SW OT_PA_S1 Homo sapiens cDNA, clone DKFZp434D2021.5'
6734	19598	32600	0.83	0.0E+00	BE734087.1	EST_HUMAN	TRC-26823 Q26823 TEKTN1 C1.
6752	17621	30565	1.68	0.0E+00	BE568381.1	EST_HUMAN	601597370.F1 NIH_MGC_21 Homo sapiens cDNA, clone IMAGE:3842080.5'
6761	17630	30565	11.84	0.0E+00	BE687899.1	EST_HUMAN	601339977.F1 NIH_MGC_53 Homo sapiens cDNA, clone IMAGE:3982287.5'
6761	17630	30566	11.84	0.0E+00	BE687899.1	EST_HUMAN	601443657.F1 NIH_MGC_65 Homo sapiens cDNA, clone IMAGE:3847697.5'
6761	17630	30566	11.84	0.0E+00	BE687899.1	EST_HUMAN	601443657.F1 NIH_MGC_65 Homo sapiens cDNA, clone IMAGE:3847697.5'
6766	19510	32535	2.2	0.0E+00	BE550162.1	EST_HUMAN	7649603.x1 NC1 CGAP_L024 Homo sapiens cDNA, clone IMAGE:3231581.3' similar to SW:GG95_HUMAN Q08378 GOLGN-95.
6766	19510	32536	2.2	0.0E+00	BE550162.1	EST_HUMAN	7649603.x1 NC1 CGAP_L024 Homo sapiens cDNA, clone IMAGE:3231581.3' similar to SW:GG95_HUMAN Q08379 GOLGN-95.
6780	18634	32562	1.28	0.0E+00	BF088376.1	EST_HUMAN	CM4-H10877-080900-397-g11 HT0877 Homo sapiens cDNA
6786	19540	32588	2.45	0.0E+00	AA1195106.1	EST_HUMAN	3734g03.1 Soares NHHMPu_S1 Homo sapiens cDNA, clone IMAGE:655332.5'
6803	19464		12.37	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6805	19466	32487	1.08	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
6807	19468	32490	0.6	0.0E+00	BE313076.1	EST_HUMAN	601150662F1 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3503391 5'
6807	19468	32491	0.6	0.0E+00	BE313076.1	EST_HUMAN	601150662F1 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3503391 5'
6822	19483	32655	2.69	0.0E+00	BF569005.1	EST_HUMAN	60218582F1 NIH_MGC, 45 Homo sapiens cDNA clone IMAGE:4310076 5'
6837	19465		2.32	0.0E+00	U03098.1	NT	Human MYO2.2 gene, complete cds
6845	19445	32573	3.52	0.0E+00	AF217268.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6845	19445	32574	3.52	0.0E+00	AF217268.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6848	19446	32575	1.18	0.0E+00	M83113.1	NT	Human neurofibromin type 1 gene, exon x5
6868	17935	30571	3.2	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
6859	17936	30572	0.74	0.0E+00	AI419089.1	EST_HUMAN	Ig53c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW_OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN ;
6859	17936	30573	0.74	0.0E+00	AI419089.1	EST_HUMAN	Ig53c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW_OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN ;
6863	17940	30576	0.78	0.0E+00	BE256708.1	EST_HUMAN	60115516F1 NIH_MGC, 18 Homo sapiens cDNA clone IMAGE:3503391 5'
6874	17950	30546	0.58	0.0E+00	BE904655.1	EST_HUMAN	60146873F1 NIH_MGC, 70 Homo sapiens cDNA clone IMAGE:3503391 5'
6884	17960	30514	1.05	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBAT Homo sapiens cDNA clone HEMBA1003679 5'
6887	17963	30518	8.08	0.0E+00	BE262941.1	EST_HUMAN	601148954F1 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3501829 5'
6888	17984	30516	2.28	0.0E+00	Z37976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6888	17984	30520	2.28	0.0E+00	Z37976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6889	17965	30521	3.28	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6889	17965	30522	3.28	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6894	17970	30527	1.06	0.0E+00	AF310103.1	NT	Homo sapiens NALP1 mRNA, complete cds
6899	19037	32681	1.03	0.0E+00	BE782770.1	EST_HUMAN	QV3-NT0022-140600-223-01 NT0022 Homo sapiens cDNA
6904	19042	32687	2.37	0.0E+00	BF569005.1	EST_HUMAN	60218582F1 NIH_MGC, 45 Homo sapiens cDNA clone IMAGE:4310076 5'
6908	19046	32692	4.53	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
6913	19050	32696	0.79	0.0E+00	AW502362.1	EST_HUMAN	U1-HF-BR0p-aka-d-10-Q-U1r1 NIH_MGC, 52 Homo sapiens cDNA clone IMAGE:3076290 5'
6913	19050	32697	0.79	0.0E+00	AW502362.1	EST_HUMAN	U1-HF-BR0p-aka-d-10-Q-U1r1 NIH_MGC, 52 Homo sapiens cDNA clone IMAGE:3076290 5'
6922	19058	32704	0.7	0.0E+00	AL039561.1	EST_HUMAN	DKFZp43D221.1 L1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43D221 5'
6922	19058	32705	0.7	0.0E+00	AL039561.1	EST_HUMAN	DKFZp43D221.1 L1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43D221 5'
6929	19065	32711	6.87	0.0E+00	BF306968.1	EST_HUMAN	60158082F1 NIH_MGC, 17 Homo sapiens cDNA clone IMAGE:4123948 5'
6934	19069	32715	2.33	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6972	19454	32474	1.18	0.0E+00	AL049764.1	NT	Novel human gene mapping to chromosome 13
7008	19700	32764	0.85	0.0E+00	AB026990.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds

Page 514 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7008	19700	32755	0.65	0.0E+00	AB026933.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7013	19705	32761	1.07	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7013	19705	32762	1.07	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7019	19711	32768	1.2	0.0E+00	AI954806.1	EST_HUMAN	EST368978 IMAGE sequences, MAGC Homo sapiens cDNA
7020	19712	32769	0.9	0.0E+00	BE254103.1	EST_HUMAN	60113658F1 NIP_MGC, 18 Homo sapiens cDNA clone IMAGE:3354668 5'
7033	19726	32781	0.98	0.0E+00	U19173.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7041	19732	32791	0.64	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
7041	19732	32792	0.64	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
7047	19736	32799	2.73	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2R94 Homo sapiens cDNA clone NT2R94001556 5'
7062	19753	32818	0.95	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7064	19755	32820	0.56	0.0E+00	AA312125.1	EST_HUMAN	EST182818 Jurkat T-cells VI Homo sapiens cDNA 5' and
7069	19760		2.57	0.0E+00	AU143708.1	EST_HUMAN	AU143708 Y76AA1 Homo sapiens cDNA clone Y76AA1002365 5'
7070	19761	32825	0.94	0.0E+00	4758539	NT	Homo sapiens netrin 1 (NTN1), mRNA
7079	19770	32834	1.32	0.0E+00	BE591286.1	EST_HUMAN	60143181F1 NIH_MGC, 72 Homo sapiens cDNA clone IMAGE:3917164 5'
7079	19770	32836	1.32	0.0E+00	BE591286.1	EST_HUMAN	60143181F1 NIH_MGC, 72 Homo sapiens cDNA clone IMAGE:3917164 5'
7100	17691	30495	2.54	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7100	17691	30495	2.54	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7122	19810	32876	5.01	0.0E+00	11435592	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7122	19810	32877	5.01	0.0E+00	11435592	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7137	19824	32891	0.55	0.0E+00	AF22744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds
7156	19843	32911	37.67	0.0E+00	AI128344.1	EST_HUMAN	q637a07.x1 Soares, placenta, 8d6weeks 2NbpHP8169W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P81689 ARYL SULFATASE D PRECURSOR, contains element HGR repetitive element:
7156	19843	32912	37.67	0.0E+00	AI128344.1	EST_HUMAN	q637a07.x1 Soares, placenta, 8d6weeks 2NbpHP8169W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P81689 ARYL SULFATASE D PRECURSOR, contains element HGR repetitive element:
7158	19845	32914	0.66	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor, T2R9 gene, complete cds
7158	19845	32915	0.86	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor, T2R9 gene, complete cds
7161	19848	32918	4.85	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7161	19848	32918	4.85	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7163	19850		15.23	0.0E+00	BF337375.1	EST_HUMAN	60203509F1 NC1 CGAP Brn64 Homo sapiens cDNA clone IMAGE:4192839 5'
7165	19852	32921	2.85	0.0E+00	AA128453.1	EST_HUMAN	z6d0709.1 Straatene muscle 837209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 G806562 NEBULIN;

Page 515 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7170	19859	32927	0.7	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0228_t1.434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B0228.5'
7170	19859	32928	0.7	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0228_t1.434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B0228.5'
7208	19893	32959	1.09	0.0E+00	BE29506.1	EST_HUMAN	801174767F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3529794.5'
7210	19895	32970	1	0.0E+00	11427365	NT	Homo sapiens hypothetical protein [FLJ20281]. mRNA
7213	19898		1.42	0.0E+00	AL118607.1	EST_HUMAN	AL118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003569.5'
7214	19899	32973	1.96	0.0E+00	AF005273.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7214	19899	32974	1.99	0.0E+00	AF005273.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7226	19911	32984	0.87	0.0E+00	AF245905.1	NT	Homo sapiens sulfacin mRNA, complete cds
7232	19917	32989	8.04	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7234	19919	32991	8.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7234	19919	32992	8.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7247	19932	33007	0.86	0.0E+00	AW956903.1	EST_HUMAN	EST1989573 IMAGE resequences, IMAGE Homo sapiens cDNA
7249	19934	33009	0.56	0.0E+00	BE872445.1	EST_HUMAN	7a60h08.x1 NC1_QGAP_G08 Homo sapiens cDNA clone IMAGE:3223167.3' similar to gb:IM54911_mn1 IG
7250	19935	33010	2.52	0.0E+00	AW950516.1	EST_HUMAN	HEAVY CHAIN PRECURSOR Y-II REGION (HUMAN);
7273	19957	33033	0.57	0.0E+00	AF001543.1	EST_HUMAN	EST392566 IMAGE resequences, MAGA Homo sapiens cDNA
7273	19957	33034	0.57	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa.S.C.) Homo sapiens cDNA clone kappa_200
7273	19957	33035	0.57	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa.S.C.) Homo sapiens cDNA clone kappa_200
7292	19975		0.56	0.0E+00	M90354.1	NT	Human BTf3 protein homologue gene, complete cds
7293	19976	33053	0.98	0.0E+00	BE408293.1	EST_HUMAN	601302670F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3637434.5'
7305	19988	33064	0.6	0.0E+00	AW402542.1	EST_HUMAN	U1HF-BKO-acc-p-07-UJL1 NIH_MGC.38 Homo sapiens cDNA clone IMAGE:3054924.5'
7322	20005		1.43	0.0E+00	R87430.1	EST_HUMAN	YMR8H010.1 Scores adult brain N24H55Y Homo sapiens cDNA clone IMAGE:166051.5'
7323	20006	33063	1.88	0.0E+00	AW236326.1	EST_HUMAN	x39a05.y1 NC1_QGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640.5' similar to TR:Q08050 Q08050
7342	20023		1.31	0.0E+00	AW117553.1	EST_HUMAN	HNF3FH TRANSCRIPTION FACTOR GENESIS ;
7344	20025	33101	3.97	0.0E+00	11427138	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R). mRNA
7366	20046	33125	0.58	0.0E+00	BF229235.1	EST_HUMAN	MRO-AN0083-270600-004-007 AN0083 Homo sapiens cDNA
7372	20052	33133	0.67	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7397	20075	33154	1.18	0.0E+00	BF306966.1	EST_HUMAN	601898923F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4123948.5'
7397	20075	33155	1.18	0.0E+00	BF306966.1	EST_HUMAN	601898923F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4123948.5'
7408	20083	33166	0.92	0.0E+00	AW118767.1	EST_HUMAN	AL118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314.5'
7460	20133	33223	4.16	0.0E+00	A1752561.1	EST_HUMAN	cm17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnt17d05 random

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7460	20139	33224	4.16	0.0E+00	A1762681.1	EST_HUMAN	cn17405.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17405 random
7635	20208	33301	1.83	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7635	20205	33302	1.83	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7643	20213	33313	1.14	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7657	20227	33330	1.1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7570	20239	33343	2.28	0.0E+00	AW672785.1	EST_HUMAN	ba01e08.x1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02608
7570	20238	33344	2.28	0.0E+00	AW672785.1	EST_HUMAN	ba01e08.x1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02608
7588	20264	33360	1.97	0.0E+00	A1825904.1	EST_HUMAN	phosphatidylinositol 3-KINASE REGULATORY SUBUNIT 1; PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT 1; wh17G05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR-O75363 O75363
7588	20254	33361	1.97	0.0E+00	A1825904.1	EST_HUMAN	wh17G05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR-O75363 O75363
7594	20262	33370	1.51	0.0E+00	6912735	NT	ABIC1 ; Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7599	20265	33373	1.09	0.0E+00	N76128.1	EST_HUMAN	zab6e05.x1 Soares_fetal_lung NIH_MGC_67 Homo sapiens cDNA clone IMAGE:299456 3'
7604	20270	33377	5.87	0.0E+00	BF217905.1	EST_HUMAN	601083465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4103729 5'
7613	20278	33387	5.41	0.0E+00	AU128622.1	EST_HUMAN	AU128622 NT2P22 Homo sapiens cDNA clone NT2P2005913 5'
7633	25117	33407	0.97	0.0E+00	AW069274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7638	20301	33409	6.26	0.0E+00	4501848	NT	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7643	20308	33416	1.73	0.0E+00	A1758487.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7645	20309	33417	6.31	0.0E+00	BE736870.1	EST_HUMAN	A1758487 BM Homo sapiens cDNA clone BMERGG05 5'
7645	20300	33418	6.31	0.0E+00	BE736870.1	EST_HUMAN	AU1593166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7645	20310	33419	1.18	0.0E+00	6912461	NT	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7646	20310	33420	1.18	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; actinW receptor interacting protein 1 (KIAA0705), mRNA
7647	20311	33421	0.71	0.0E+00	AU120424.1	EST_HUMAN	Homo sapiens atrophin-1 interacting protein 1; actinW receptor interacting protein 1 (KIAA0705), mRNA
7647	20311	33422	0.71	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBBT1 Homo sapiens cDNA clone HEMBB1000685 5'
7650	20344	33456	1.81	0.0E+00	BE787610.1	EST_HUMAN	AU120424 HEMBBT1 Homo sapiens cDNA clone HEMBB1000685 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7680	20344	33457	1.81	0.0E+00	BE787010.1	EST_HUMAN	60148173F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884259 5'
7720	20384	33488	0.63	0.0E+00	W62673.1	EST_HUMAN	z89010.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5'
7734	20398	33513	0.56	0.0E+00	AW402332.1	EST_HUMAN	UJHF-SK02-06-00.U1.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053915 5'
7735	20400	33516	0.76	0.0E+00	AA760692.1	EST_HUMAN	nz13a08.r1 NCI CGAP_CGB1 Homo sapiens cDNA clone IMAGE:1287698 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);
7735	20400	33516	0.76	0.0E+00	AA760692.1	EST_HUMAN	nz13a08.r1 NCI CGAP_CGB1 Homo sapiens cDNA clone IMAGE:1287698 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);
7735	20400	33516	0.76	0.0E+00	AA760692.1	EST_HUMAN	nz13a08.r1 NCI CGAP_CGB1 Homo sapiens cDNA clone IMAGE:1287698 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);
7752	20448	33572	0.82	0.0E+00	BE133013.1	EST_HUMAN	AJ133187.NT2R94 Homo sapiens cDNA clone IMAGE:3503050 5'
7812	20519	33645	1.13	0.0E+00	AA149781.1	EST_HUMAN	60116034.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:568410 5'
7824	20519	33645	1.13	0.0E+00	AA149781.1	EST_HUMAN	z201c08.r1 Striatum cDNA (883724) Homo sapiens cDNA clone IMAGE:568410 5'
7837	20532	33659	0.84	0.0E+00	BF026628.1	EST_HUMAN	z833108.r1 Scars retina N2b4HR Homo sapiens cDNA clone IMAGE:3555131 5'
7849	20544	33672	0.45	0.0E+00	AA017021.1	EST_HUMAN	60130565.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
7853	20561	33698	2.31	0.0E+00	BE735046.1	EST_HUMAN	Human amyloid-beta protein (APP) gene, exon 11
7881	20576	33703	10.46	0.0E+00	M34972.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7881	20576	33704	10.46	0.0E+00	M34972.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7909	20604	33734	0.74	0.0E+00	AW674581.1	EST_HUMAN	FB34402.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652
7909	20604	33735	0.74	0.0E+00	AW674581.1	EST_HUMAN	FB34402.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652
7916	20611	33741	3.91	0.0E+00	AA397651.1	EST_HUMAN	F17K2.26 PROTEIN;
7818	20613	33742	1.43	0.0E+00	AW387191.1	EST_HUMAN	z81804.r1 Striatum scilicet brain S11 Homo sapiens cDNA clone IMAGE:728718 5' similar to TR:G300482
7921	20616	33742	0.73	0.0E+00	AB020951.1	NT	G300482 POLYMERASE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
7922	20617	33744	7.02	0.0E+00	AJ142402.1	EST_HUMAN	MRO-ST0031-061099-003-411 ST0031 Homo sapiens cDNA
7928	20621	33748	1.63	0.0E+00	BE398421.1	EST_HUMAN	Human sapiens mRNA for KIAA0684 protein, partial cds
7926	20621	33749	1.63	0.0E+00	BE398421.1	EST_HUMAN	Human sapiens cDNA clone Y78AA1000277 5'
7942	20637	33764	1.09	0.0E+00	W95278.1	EST_HUMAN	60128550.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7942	20637	33765	1.09	0.0E+00	W95278.1	EST_HUMAN	z805001.r1 Scars fetal heart NBH191W Homo sapiens cDNA clone IMAGE:358081 5'
7944	20639	33765	6.59	0.0E+00	BF673098.1	EST_HUMAN	z805001.r1 Scars fetal heart NBH191W Homo sapiens cDNA clone IMAGE:358081 5'
7948	20643	33782	0.97	0.0E+00	AJ134114.1	EST_HUMAN	60133008.F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
7962	20657	33782	0.96	0.0E+00	BF525534.1	EST_HUMAN	AJ134114.OVARC1 Homo sapiens cDNA clone OVARC1001268 5'
7962	20657	33783	0.96	0.0E+00	BF525534.1	EST_HUMAN	60206663.F1 NCI CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4212727 5'
7962	20687	33813	1.59	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.r1 NC1 CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4212727 5'
7962	20687	33814	1.59	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.r1 NC1 CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4212727 5'

Page 518 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8035	20730		1.32	0.0E+00	BE877693.1	EST_HUMAN	601486254F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:368773 5'
8057	20751	33982	2.48	0.0E+00	AW600549.1	EST_HUMAN	UHF-3NC-aq-f01-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077498 5'
8065	20759	33988	18.05	0.0E+00	AW157233.1	EST_HUMAN	ku36b08.x1 Schneider fetal brain 03004 Homo sapiens cDNA clone IMAGE:2783769 3' similar to TR:060463 OB0463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. (1):
8082	20776	33906	0.68	0.0E+00	AW072985.1	EST_HUMAN	xa07412.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2857639 3' similar to contains element ORF repetitive element;
8099	20783	33924	1.09	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8102	20786	33927	1.07	0.0E+00	W01816.1	EST_HUMAN	xa36d05.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:294633 5'
8104	20788	33929	1.22	0.0E+00	BE746597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926988 5'
8104	20788	33930	1.22	0.0E+00	BE746597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926988 5'
8115	20809	33943	1.46	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8154	20848	33980	0.85	0.0E+00	AB97350.1	EST_HUMAN	q08b12.x1 NCL CGAP_LU2 Homo sapiens cDNA clone IMAGE:1889334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
8165	20859	33991	2.93	0.0E+00	BE974157.1	EST_HUMAN	7a76ad4.x1 NCL CGAP_LU24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O85763 O85763 STAUFEN PROTEIN. ;
8167	20861	33983	1.19	0.0E+00	AB85671.1	EST_HUMAN	w60b10.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRX METALLOPROTEINASE-14 PRECURSOR ;
8180	20874	34009	1.07	0.0E+00	BE563950.1	EST_HUMAN	601334750F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8180	20874	34010	1.07	0.0E+00	BE563950.1	EST_HUMAN	601334750F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8189	20883	34020	1.83	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8189	20883	34021	1.83	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8191	20885	34023	3.2	0.0E+00	AA403192.1	EST_HUMAN	z66f02.r1 Soares_tetis_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8191	20885	34024	3.2	0.0E+00	AA403192.1	EST_HUMAN	TR:G1304132 G1304132 TPRD. ;
8231	20925		4.83	0.0E+00	AA39851.1	EST_HUMAN	z773406.x1 Soares_tetis_NHT Homo sapiens cDNA clone IMAGE:727068 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8240	20934	34071	0.95	0.0E+00	BE837693.1	EST_HUMAN	RC2-FN0894-120600-013-107 FN0894 Homo sapiens cDNA
8241	20935	34072	1.17	0.0E+00	AW384874.1	EST_HUMAN	QV3-D1T0045-221-289-048-407 DT0045 Homo sapiens cDNA
8241	20935	34073	1.17	0.0E+00	AW384874.1	EST_HUMAN	QV3-D1T0045-221-289-048-407 DT0045 Homo sapiens cDNA
8280	20954	34092	1.88	0.0E+00	BE612386.1	EST_HUMAN	601452412F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3656179 5'
8280	20954	34093	1.88	0.0E+00	BE612386.1	EST_HUMAN	601452412F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3656179 5'
8275	20969	34110	1.82	0.0E+00	AL193209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8275	20969	34111	1.82	0.0E+00	AL193209.2	NT	Homo sapiens chromosome 21 segment HS21C009

Page 519 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8289	20980	34120	1.3	0.0E+00	A1884477.1	EST_HUMAN	wn33a11.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR.O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
8293	20987	34126	1.27	0.0E+00	AA502294.1	EST_HUMAN	ne25d10.x1 NCL CGAP_C63 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR.G1136434
8298	20992		0.59	0.0E+00	11476799	NT	G1136434 KIAA0187 PROTEIN.
8305	20999	34137	1.02	0.0E+00	A1980780.1	EST_HUMAN	Homo sapiens proteodherin beta 3 (PCDH3). mRNA
8308	21002		1.84	0.0E+00	BE890787.1	EST_HUMAN	ta04711.x1 Sceres pregnant uterus NHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8334	21027	34163	0.72	0.0E+00	AW245765.1	EST_HUMAN	60143123BT NIH_MGC 72 Homo sapiens cDNA clone IMAGE:391659 5'
8334	21027	34164	0.72	0.0E+00	AW245765.1	EST_HUMAN	2822701.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822701 5'
8335	21028	34165	2.24	0.0E+00	4759093	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13). mRNA
8335	21028	34166	2.24	0.0E+00	4759095	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13). mRNA
8339	21032	34170	0.59	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165). gene, exons 2 and 3
8339	21032	34170	0.59	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165). gene, exons 2 and 3
8404	21097	34233	0.68	0.0E+00	AJ251760.1	NT	Homo sapiens NESP55. GNA31 antisense (partial) and XLa1phas (partial) genes
8409	21102	34239	2.63	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8409	21102	34240	2.63	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8409	21102	34241	2.63	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8424	21117	34255	0.68	0.0E+00	U82078.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8465	21157	34300	0.88	0.0E+00	AF022855.1	NT	Homo sapiens cap260 centrosome associated protein mRNA, complete cds
8466	21157	34301	0.88	0.0E+00	AF022855.1	NT	Homo sapiens cap260 centrosome associated protein mRNA, complete cds
8468	21160	34303	2.28	0.0E+00	AU131871.1	EST_HUMAN	AU131871 NT2RP3 Homo sapiens cDNA clone NT2RP3003018 5'
8463	21175	34320	0.65	0.0E+00	11425572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2). mRNA
8467	21176		1.92	0.0E+00	AW519513.1	EST_HUMAN	xc46a01.x1 NCL CGAP_U17 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb.M14123_cds4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN).
8489	21181	34323	14.55	0.0E+00	D52850.1	EST_HUMAN	HLU084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8520	21212	34356	4.04	0.0E+00	BE378495.1	EST_HUMAN	60123848BF1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3008709 5'
8528	21218	34360	2.58	0.0E+00	AA410545.1	EST_HUMAN	2832604.T Sceres ovary tumor NHOT Homo sapiens cDNA clone IMAGE:724062 5'
8528	21220		2.91	0.0E+00	BF313948.1	EST_HUMAN	60190051F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4126744 5'
8535	21227	34366	0.52	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3). mRNA
8540	21232	34374	1.46	0.0E+00	AW139873.1	EST_HUMAN	UH-H-B11-adv-e-12-o-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8540	21232	34376	1.46	0.0E+00	AW139873.1	EST_HUMAN	UH-H-B11-adv-e-12-o-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8545	21237		0.49	0.0E+00	AI640190.1	EST_HUMAN	w8905.0.x1 NCL CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2289578 3' similar to TR.O15044
8564	21259	34393	0.78	0.0E+00	BF377897.1	EST_HUMAN	O15044 KIAA0335. ;
8574	21268	34406	0.59	0.0E+00	AI163501.2	NT	CMT1-TN0141-250500-436-b08 TN0141 Homo sapiens cDNA
8580	21272	34410	5.89	0.0E+00	BE260272.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
8585	21277	34414	2.51	0.0E+00	BF700165.1	EST_HUMAN	60115050.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3502835 5'
8595	21277	34415	2.51	0.0E+00	BF700165.1	EST_HUMAN	60212766.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8595	21277	34416	2.51	0.0E+00	BF700165.1	EST_HUMAN	60212766.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8600	21292	34434	0.53	0.0E+00	AI469722.1	EST_HUMAN	60212766.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8628	21318	34460	0.88	0.0E+00	AL449770.1	EST_HUMAN	IK13111.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
8631	21329	34494	7.75	0.0E+00	AA862527.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stanley GS) Homo sapiens cDNA
8637	21329	34472	3.09	0.0E+00	10947037	NT	ribosomal protein L7A (HUMAN);
8637	21329	34473	3.09	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8660	21352	34469	1.3	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exon 3-41
8662	21354	34601	1.92	0.0E+00	BE278917.1	EST_HUMAN	601156330.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8672	21364		1.91	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
8678	21371	34616	3.33	0.0E+00	AW337277.1	EST_HUMAN	AV72907.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb-X63587
8685	21377	34621	1.12	0.0E+00	AU124051	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8761	21453	34601	1.05	0.0E+00	AU14704	EST_HUMAN	AU124051 NT2B22 Homo sapiens cDNA clone NT2B22001875 5'
8771	21463	34610	0.96	0.0E+00	AB007923.1	NT	AU14704 PLACE2 Homo sapiens cDNA clone PLACE400088 5'
8776	21468	34614	0.54	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8776	21468	34615	0.54	0.0E+00	R17132.1	EST_HUMAN	XP09609.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:31674 5'
8780	21472	34617	4.43	0.0E+00	AW692233.1	EST_HUMAN	XP09609.1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:31674 5'
8815	21507	34662	1.04	0.0E+00	AW692233.1	EST_HUMAN	XP09609.1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2835068 3'
8827	21519	34684	1.04	0.0E+00	AU128804.1	EST_HUMAN	XP09609.1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2835068 3'
8843	21535	34679	2.79	0.0E+00	AV714764.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone NT2RP2004249 5'
8843	21535	34680	2.78	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone DCBAUA08 5'
8843	21535	34680	2.78	0.0E+00	AL040428.1	EST_HUMAN	DKFZp343C1814.s1_434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp343C1814 3'
8849	21540	34686	1.17	0.0E+00	AF133901.1	NT	DKFZp343C1814.s1_434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp343C1814 3'
8851	21542	34689	2.03	0.0E+00	AB040945.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
8858	21549	34690	0.85	0.0E+00	BF675505.1	EST_HUMAN	602139483.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274708 5'

Page 521 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8860	21551			0.8	BF058289.1	EST_HUMAN	762803.x1 NCL_GCAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR:036448 036448 S GAG :
8868	21560	34720	3.97	0.0E+00	11422867	NT	Homo sapiens tumor protein p73 (TP73), mRNA
8868	21560	34720	3.97	0.0E+00	K01241.1	NT	Human Ig recombined H-chain epsilon-3 pseudogene, constant region
8893	21568	34728	1.19	0.0E+00	K01241.1	NT	Human Ig recombined H-chain epsilon-3 pseudogene, constant region
8905	21596	34737	4.27	0.0E+00	A8020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8905	21596	34738	4.27	0.0E+00	A8020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8910	21601	34744	1.79	0.0E+00	AV660739.1	EST_HUMAN	AV660739 Homo sapiens cDNA clone GLCGRG12 3'
8916	21607	34750	2.89	0.0E+00	7706638	NT	Homo sapiens polyoma-L (PKDL), mRNA
8921	21612	34755	0.5	0.0E+00	BE793328.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
8922	21613	34756	0.73	0.0E+00	A8033077.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
8922	21613	34757	0.73	0.0E+00	A8033077.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
8934	21625		0.91	0.0E+00	H73937.1	EST_HUMAN	Y03108.r1 Scores fetal liver spleen TNF- α Homo sapiens cDNA clone IMAGE:232767 5'
8944	21635	34778	4.57	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8944	21635	34780	4.57	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8954	21645	34795	0.46	0.0E+00	BE512721.1	EST_HUMAN	601452582F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856100 5'
8954	21645	34796	0.46	0.0E+00	BE512721.1	EST_HUMAN	601452582F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856100 5'
8957	21648		0.45	0.0E+00	M89986.1	NT	Human polymorphic loci in Xq28
8959	21650	34800	3.68	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
8960	21670	34820	2.93	0.0E+00	A061395.1	EST_HUMAN	an28e94.x1 Cesario Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
8985	21675	34824	1.95	0.0E+00	A954807.1	EST_HUMAN	w334r12.x1 NCL_GCAP_GG8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MG83_HUMAN
8989	21679	34828	4.65	0.0E+00	9256596	NT	OT5480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9000	21690	34840	1.42	0.0E+00	AW95311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9011	21701	34851	2.48	0.0E+00	8535487	NT	Homo sapiens cDNA
9028	21716	34869	1.63	0.0E+00	AU142662.1	EST_HUMAN	Human endogenous retrovirus, complete genome
9042	21732	34887	1.76	0.0E+00	11436993	NT	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA100678 5'
9043	21733		1.18	0.0E+00	BE410768.1	EST_HUMAN	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9058	21745	34904	1.83	0.0E+00	BF02024.1	EST_HUMAN	Q9UHB2 HYPOTHETICAL 425 KD PROTEIN ;
9071	21758	34920	1.1	0.0E+00	A8011150.1	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
9071	21760	34921	7.72	0.0E+00	BE794823.1	EST_HUMAN	601588294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943453 5'
9075	21764	34926	0.99	0.0E+00	BE810262.1	EST_HUMAN	RC3-PT0161-380600-011-c05 PT0151 Homo sapiens cDNA
9075	21764	34927	0.99	0.0E+00	BE810262.1	EST_HUMAN	RC3-PT0161-380600-011-c05 PT0151 Homo sapiens cDNA
9078	21787	34930	2.93	0.0E+00	AU136229.1	EST_HUMAN	AU136229 PLAGE1 Homo sapiens cDNA clone IMAGE:1003804 5'

Page 522 of 536

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9083	21772	34935	1.27	0.0E+00	BE883943.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9083	21772	34936	1.27	0.0E+00	BE883943.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9102	21780	34933	0.62	0.0E+00	AB011165.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9108	21794	34937	1.4	0.0E+00	AA344801.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9108	21794	34938	1.4	0.0E+00	AA344801.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9184	21834	34938	1.13	0.0E+00	AW673469.1	EST_HUMAN	ba9408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
9184	21834	34939	1.13	0.0E+00	AW673469.1	EST_HUMAN	ba9408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
9188	21887	35031	1.62	0.0E+00	BE207063.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gbl:35049 Mus musculus
9188	21887	35032	1.62	0.0E+00	BE207063.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gbl:35049 Mus musculus
9209	22088	35280	1.61	0.0E+00	BF348013.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gbl:35049 Mus musculus
9244	21923	35093	2.77	0.0E+00	BE712513.1	EST_HUMAN	Bd-xL mRNA, complete cds (MOUSE);
9277	22031	35201	0.88	0.0E+00	BF094377.1	EST_HUMAN	602023150F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4195300 5'
9277	22031	35202	0.88	0.0E+00	BF094377.1	EST_HUMAN	602023150F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4195300 5'
9283	22037	35209	0.5	0.0E+00	AI906351.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3459035 5'
9286	22040	35211	0.81	0.0E+00	5803069	NT	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3459035 5'
9286	22040	35212	0.81	0.0E+00	5803069	NT	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3459035 5'
9296	21963	35137	1.5	0.0E+00	AL042278.1	EST_HUMAN	FC-BT108-O40399-032 BT108 Homo sapiens cDNA clone IMAGE:3859035 5'
9331	21998	35171	1.28	0.0E+00	AI088043.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9338	20409	33624	0.72	0.0E+00	BF309862.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9340	20411	33527	2.51	0.0E+00	11560151	NT	DKFP434L0120_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFP434L0120 5'
9340	20411	33528	2.51	0.0E+00	11560151	NT	ow060H01.x1 Soares, NSF_Fg_9W_OT_PA_P_51 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:O14677 Q14677 KIAA0171 PROTEIN, 1
9342	20413	33531	9.88	0.0E+00	AI200909.1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4135068 5'
9342	20413	33532	9.88	0.0E+00	AI200909.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22804 (FLJ22804), mRNA
9343	20414	33533	1.99	0.0E+00	AW959390.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22804 (FLJ22804), mRNA
9370	21945	35117	3.07	0.0E+00	AF153466.1	NT	gmo0905.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
							gmo0905.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
							P28319 GOS RIBOSOMAL PROTEIN L23A.1
							EST366026 MAGE repeats, MAGE Homo sapiens cDNA
							Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8

Page 523 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9373	21948	35121	0.86	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9373	21948	35122	0.86	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9382	22044	35123	7.32	0.0E+00	BE255829.1	EST_HUMAN	601108942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9385	22047	35219	1.09	0.0E+00	BE781382.1	EST_HUMAN	601468829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870007 5'
9385	22047	35220	1.09	0.0E+00	BE781382.1	EST_HUMAN	601468829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870007 5'
9387	22049	35221	12.62	0.0E+00	AW163779.1	EST_HUMAN	au86cd0.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M56072
9409	22071	35243	2.98	0.0E+00	BE283181.1	EST_HUMAN	601540504F1 RIFONAL PROTEIN L7A (HUMAN);
9427	22105	35278	4.29	0.0E+00	C06158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180477 5'
9427	22105	35279	4.29	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9429	22107	35282	2.63	0.0E+00	BE746218.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9439	22117	35293	2.14	0.0E+00	11437282	NT	601578686F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9439	22117	35294	2.14	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9439	22117	35294	2.14	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	22209	35179	1.44	0.0E+00	BE900548.1	EST_HUMAN	601673426F1 NIH_MGC_21 Homo sapiens cDNA clone AD8BYH01 5'
9475	22128	35307	1.01	0.0E+00	AW701829.1	EST_HUMAN	AW701829 ADB Homo sapiens cDNA clone AD8BYH01 5'
9489	22142	35321	2.62	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9489	22142	35322	2.62	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9522	22176	35359	0.94	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
9541	22184	35379	1.74	0.0E+00	AW500283.1	EST_HUMAN	U1HF-BN0-8kb-b-12-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076543 5'
9541	22184	35380	1.74	0.0E+00	AW500283.1	EST_HUMAN	U1HF-BN0-8kb-b-12-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076543 5'
9550	22203	35396	1.45	0.0E+00	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9550	22203	35397	1.45	0.0E+00	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9552	22203	35398	0.89	0.0E+00	BE763272.1	EST_HUMAN	601470824F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874037 5'
9552	22203	35398	0.89	0.0E+00	BE763272.1	EST_HUMAN	601470824F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874037 5'
9561	22214	35400	0.54	0.0E+00	W56629.1	EST_HUMAN	z116a1.1.1 Scores fetal heart NBH19W Homo sapiens cDNA clone IMAGE:340844 5'
9561	22214	35401	0.54	0.0E+00	W56629.1	EST_HUMAN	z116a1.1.1 Scores fetal heart NBH19W Homo sapiens cDNA clone IMAGE:340844 5'
9572	22228	35470	1.83	0.0E+00	AB035358.1	NT	Homo sapiens mRNA for neuridin alpha protein, complete cds
9578	22231	35415	0.8	0.0E+00	AT24780.1	EST_HUMAN	hm59at1.1x1 Johnson frontal cortex Homo sapiens cDNA clone IMAGE:1839548 3'
9578	22231	35415	3.59	0.0E+00	AW500528.1	EST_HUMAN	U1HF-BN0-8kb-c-07-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077384 5'
9624	22277	35496	1.53	0.0E+00	AF006988.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9652	22304	35499	2.23	0.0E+00	S78466.1	NT	ALF=androgen-induced growth factor ALF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9652	22304	35500	2.23	0.0E+00	S78466.1	NT	ALF=androgen-induced growth factor ALF [human, placenta, Genomic/mRNA, 498 nt, segment 6 of 6]
9655	22307	35505	2.63	0.0E+00	BE58320.1	EST_HUMAN	60133403G1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE368880 5'
9674	22326	35521	1.84	0.0E+00	AW363135.1	EST_HUMAN	CH2-C70311-301189-043-H11 C70311 Homo sapiens cDNA
9692	22343	35537	0.46	0.0E+00	11436432	NT	Homo sapiens multidin (MMDN), mRNA
9693	22344	35538	0.51	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITM domains), member 3 (LILRB3), mRNA
9702	22353	35548	0.54	0.0E+00	BE206710.1	EST_HUMAN	bb26d01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE2864000 3'
9719	22370	35568	2.97	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9719	22370	35568	2.97	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9726	22376	35581	0.77	0.0E+00	AW500396.1	EST_HUMAN	U1-HF-BP0-ar-f-06-O-U11 NIH_MGC_51 Homo sapiens cDNA clone IMAGE3072897 5'
9723	22384	35586	0.08	0.0E+00	BE740490.1	EST_HUMAN	601565558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3949383 5'
9733	22384	35587	0.08	0.0E+00	BE740490.1	EST_HUMAN	601565558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3949383 5'
9734	22385	35588	0.48	0.0E+00	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
9747	22388	35593	1.73	0.0E+00	AB033057.1	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9765	22410	35623	1.59	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9770	22421	35629	1.53	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2416 5'
9780	22431	35636	2.54	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9781	22432	35637	2.37	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
9808	22456	35664	2.63	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9808	22458	35665	2.63	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9824	22475	35678	1.81	0.0E+00	BF092896.1	EST_HUMAN	MR-L-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
9824	22504	35704	2.41	0.0E+00	BE280783.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3138708 5'
9854	22514	35710	0.86	0.0E+00	BE388700.1	EST_HUMAN	601286335F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3613043 5'
9864	22514	35711	0.86	0.0E+00	BE388700.1	EST_HUMAN	601286335F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3613043 5'
9873	22523	35717	3.03	0.0E+00	AW236269.1	EST_HUMAN	xn72h01.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE268997 3' similar to gb:X02162_cds1 L
9874	22524	35718	1.06	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN)
9904	22553	35748	0.97	0.0E+00	AW964113.1	EST_HUMAN	EST378166 IMAGE resequences, MAGH Homo sapiens cDNA
9915	22564	35769	7.01	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
9915	22564	35769	7.01	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6918	22667	35763	2.98	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIR3CL gene, exons 2, 3, and 4
6921	22668	35765	2.76	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
6921	22668	35765	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
6958	22604	35609	3	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLAGE1004737 5'
6958	22604	35610	3	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLAGE1004737 5'
6972	22620	35824	2.08	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin 7 and partial ZNF143 gene
6972	22620	35825	2.08	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin 7 and partial ZNF143 gene
6977	22625	35832	1.04	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKX Homo sapiens cDNA clone GKDXA07 5'
6977	22625	35833	1.04	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKX Homo sapiens cDNA clone GKDXA07 5'
6983	22631	35843	0.74	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIR3CL gene, exons 2, 3, and 4
6985	22633	35843	3.11	0.0E+00	AA106387.1	EST_HUMAN	231101.1.r1 Stratiagene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10011	22658	35973	1	0.0E+00	AA131248.1	EST_HUMAN	231101.1.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10011	22658	35974	1	0.0E+00	AA131248.1	EST_HUMAN	231101.1.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10058	22704	35922	1.44	0.0E+00	AF176308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10101	22749	35904	0.92	0.0E+00	BE980658.1	EST_HUMAN	601401566F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863657 5'
10112	22760	35972	6.22	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10112	22760	35973	6.22	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10117	22765	35977	0.97	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10127	22775	35988	0.87	0.0E+00	BE968511.1	EST_HUMAN	601648134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10127	22776	35989	0.87	0.0E+00	BE968511.1	EST_HUMAN	601648134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10144	22792	36007	0.68	0.0E+00	BE987487.1	EST_HUMAN	601432177F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10155	22802	36020	0.67	0.0E+00	AA311824.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10155	22803	36021	1.01	0.0E+00	4758827	NT	Homo sapiens neuron III (NRXN3) mRNA
10168	22814	36032	0.57	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917398 5'
10169	22817	36033	1.13	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10179	22827	36041	1.72	0.0E+00	AB028290.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10180	22829	36042	0.46	0.0E+00	BE304522.1	EST_HUMAN	601105489F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:2887918 5'
10180	22829	36043	0.46	0.0E+00	BE304522.1	EST_HUMAN	601105489F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:2887918 5'
10187	22835	36048	8.02	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22835	36048	8.02	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22835	36049	6.02	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10183	22841	36056	1.06	0.0E+00	AA704457.1	EST_HUMAN	218008.g1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gbm14123 cdsl RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10195	22843	36057	0.74	0.0E+00	MJ22821.1	NT	Human bora 1.4-galactosyl-transferase mRNA, complete cds
10187	22845	36060	5.45	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4184939 5'

Page 526 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10167	22845	36081	5.45	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Brd64 Homo sapiens cDNA clone IMAGE:4184939 5'
10222	22870	36082	0.83	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10222	22870	36083	0.83	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10262	22890	36110	0.85	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DGB Homo sapiens cDNA clone DCBBDC09 5'
10262	22890	36111	0.85	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DGB Homo sapiens cDNA clone DCBBDC09 5'
10282	22930	36143	2.36	0.0E+00	AI631818.1	EST_HUMAN	w63603.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10282	22930	36144	2.36	0.0E+00	AI631818.1	EST_HUMAN	w63603.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10288	22936	36149	0.49	0.0E+00	11545730	NT	Q61204 NOTCH2-LIKE
10288	22945	36150	1.52	0.0E+00	T03078.1	EST_HUMAN	F023A4 Fetal brain, Stralagene Homo sapiens cDNA clone FB23A4 3' end
10323	22970	36190	0.94	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10323	22976	36196	0.46	0.0E+00	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10348	22995	36214	2.5	0.0E+00	BF436218.1	EST_HUMAN	rab45a12.x1 Scarsa, NSE_F8_9W_OI_PA_F1 S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10349	22996		0.87	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLC02C07 3'
10369	23015	36231	2.75	0.0E+00	AW517690.1	EST_HUMAN	xj74601.x1 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:U69068 MOESIN (hU69068)
10374	23020	36236	8.82	0.0E+00	BE446213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10389	23035	36281	0.76	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10414	23060	36279	2.78	0.0E+00	BE781742.1	EST_HUMAN	601467416F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870700 5'
10435	23081	36307	1.9	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10435	23081	36308	1.9	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10442	23088	36316	0.66	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10442	23088	36316	0.66	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10454	23100	36331	1.33	0.0E+00	BE743215.1	EST_HUMAN	601675895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2244612 3'
10454	23100	36332	1.33	0.0E+00	BE743215.1	EST_HUMAN	601675895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2244612 3'
10459	23105	36336	2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3865168 5'
10459	23105	36336	2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3865168 5'
10481	23127	36355	0.87	0.0E+00	133605.1	EST_HUMAN	xp01a10.r1 Scarsa, brest 3NH8at Homo sapiens cDNA clone IMAGE:186138 5'
10508	23164	36380	1.01	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10510	23165	36392	0.46	0.0E+00	AF081364.1	EST_HUMAN	Synthetic construct CD300 ligand-ectonin A fusion protein (CD300-ETA fusion) mRNA, partial cds
10519	23165	36392	1.02	0.0E+00	BE172254.1	EST_HUMAN	MRO-HT0559-270300-006-412 HT0559 Homo sapiens cDNA
10519	23165	36393	1.02	0.0E+00	BE172254.1	EST_HUMAN	MRO-HT0559-270300-006-412 HT0559 Homo sapiens cDNA
10532	23229	36463	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAKG98 5'

Page 527 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10532	23226	36464	2.76	0.0E+00	AV171076.1	EST_HUMAN	AV171076 Ou Homo sapiens cDNA clone CUA/KG05 5'
10534	23231		2.13	0.0E+00	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10542	23238	36472	7.02	0.0E+00	AW963693.1	EST_HUMAN	RC3716633 IMAGE resources, MAGH Homo sapiens cDNA
10565	23251	36487	3.19	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10555	23251	36488	3.19	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10559	23255	36492	2.08	0.0E+00	AW057621.1	EST_HUMAN	wf6109.x1 Soares_NSF_F8_gw_OT_PA_3_51 Homo sapiens cDNA clone IMAGE:2550605 5' similar to TR:060566 Q60566 VDX;
10567	23262	36499	1.6	0.0E+00	BE249270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Bayler-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10568	23263	36500	2.85	0.0E+00	AG65239.1	EST_HUMAN	wb2812.X1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element WS812.MS1 repetitive element;
10568	23263	36501	2.85	0.0E+00	AG65239.1	EST_HUMAN	WS812.MS1 repetitive element;
10573	23268	36506	1.54	0.0E+00	BF306642.1	EST_HUMAN	WS2812.X1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element WS812.MS1 repetitive element;
10580	23275	36513	5.06	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10586	23290	36528	1.98	0.0E+00	AW404705.1	EST_HUMAN	UHFH-BL0-ann-04-04-U17.NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058383 5'
10600	23294	36533	3.17	0.0E+00	11424829	EST_HUMAN	Homo sapiens hypochelated protein FL120078 (FL120078), mRNA
10601	23295	36534	7.47	0.0E+00	4504536	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10602	23298	36538	7.67	0.0E+00	AB01827.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10605	23298	36540	4.48	0.0E+00	BE882109.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10609	23303	36542	8.24	0.0E+00	BE861630.1	EST_HUMAN	UHFH-BL0-ann-04-04-U17.NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3916636 5'
10612	23306	36545	1.68	0.0E+00	8923939	NT	001434522.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916636 5'
10612	23306	36545	1.68	0.0E+00	8923939	NT	001434522.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916636 5'
10616	23312	36551	1.4	0.0E+00	AB014608.1	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10616	23312	36552	1.4	0.0E+00	AB014608.1	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10628	23321	36559	1.31	0.0E+00	BE903304.1	EST_HUMAN	Homo sapiens mRNA for KIAA0708 protein, partial cds
10631	18484	31403	1.65	0.0E+00	AA195905.1	EST_HUMAN	001674332.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10582	23343	36581	5.53	0.0E+00	BE793408.1	EST_HUMAN	z985b11.1 Stragosome muscle 937269 Homo sapiens cDNA clone IMAGE:6271693 5' similar to gb-X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10580	23351	36588	1.79	0.0E+00	BE729706.1	EST_HUMAN	001583825.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10600	23351	36589	1.76	0.0E+00	BE729706.1	EST_HUMAN	001583825.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832576 5'
10601	23352	36590	33.89	0.0E+00	AV1727392.1	EST_HUMAN	001162294.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832576 5'
10601	23352	36590	33.89	0.0E+00	AV1727392.1	EST_HUMAN	AV1727392 HIC Homo sapiens cDNA clone HTCAOH06 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10661	23352	36591	33.99	0.0E+00	AV727362.1	EST_HUMAN	AV727362.1 HTC Homo sapiens cDNA clone HTCAH08 5'
10674	23365	36606	9.59	0.0E+00	AW610055.1	EST_HUMAN	X04910.1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
10680	23371	36613	3.18	0.0E+00	AU135741.1	EST_HUMAN	AU135741.1 PLACE1 Homo sapiens cDNA clone IMAGE:1002764 5'
10686	23377	36617	3.41	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
10688	23377	36616	3.41	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
10688	23377	36618	3.41	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
10688	23379	36620	1.89	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
10689	23380	36621	2.97	0.0E+00	F13069.1	EST_HUMAN	HS0310031 normalized infant brain cDNA Homo sapiens cDNA clone c-3lco3
10700	23391	36628	1.79	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10708	23396	36634	1.33	0.0E+00	4758281	NT	Homo sapiens EPHA7 (EPHA7) mRNA
10709	23396	36635	1.33	0.0E+00	4758281	NT	Homo sapiens EPHA7 (EPHA7) mRNA
10718	23407	36648	2.13	0.0E+00	AW338094.1	EST_HUMAN	xx6801.x1 NCJ CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832885 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
10719	23408	36649	4.62	0.0E+00	AW451230.1	EST_HUMAN	UHH-B13-alt-e-01-0-Ulat NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738649 3'
10719	23408	36650	4.92	0.0E+00	AW451230.1	EST_HUMAN	UHH-B13-alt-e-01-0-Ulat NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738649 3'
10721	13021		11.67	0.0E+00	4306632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10723	23411	36652	2.53	0.0E+00	AB014597.1	NT	Homo sapiens mRNA for KIAA0687 protein, partial cds
10738	23425	36670	1.98	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028219 5'
10744	23439	36683	2.04	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
10753	23447		1.71	0.0E+00	AU124108.1	EST_HUMAN	AU124108.1 NT2RM2 Homo sapiens cDNA clone NT2RM2001675 5'
10771	23454	36697	1.46	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
10771	23454	36698	1.45	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
10778	23459	36702	4.04	0.0E+00	BE702165.1	EST_HUMAN	602142046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3666539 5'
10778	23460		59.14	0.0E+00	BF684061.1	EST_HUMAN	602142046F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
10778	23461	36703	1.3	0.0E+00	BE26928.1	EST_HUMAN	601168342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3644269 6'
10781	23464	36708	5.8	0.0E+00	AU116388.1	EST_HUMAN	AU116388.1 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
10788	23469	36710	6.53	0.0E+00	AU1149608.1	EST_HUMAN	q143c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10788	23469	36711	6.53	0.0E+00	AU1149608.1	EST_HUMAN	q143c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10787	23470	36712	3.04	0.0E+00	AW391937.1	EST_HUMAN	Q1VA-S10234-121189-032-508 ST0234 Homo sapiens cDNA

Page 529 of 536
Table 4
Single Exon Probes Expressed in Brain

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10769	23481	387221	4.39	0.0E+00	AF223391.1	NT	Human sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10768	23481	387222	4.39	0.0E+00	AF223391.1	NT	Human sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10807	23490	387236	9.57	0.0E+00	11424725	EST	Human sapiens insulin receptor (INSR), mRNA
10814	23497	38733	1.42	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00693-170400-191-006 UM00938 Homo sapiens cDNA
10814	23497	387334	1.42	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00693-170400-191-006 UM00938 Homo sapiens cDNA
10814	23498	38735	1.8	0.0E+00	BF243038.1	EST_HUMAN	6020317014F1 NCL CGAP Brn64 Homo sapiens cDNA clone IMAGE:4184979 5'
10817	23500	38738	82.94	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
10821	23504	38743	2.37	0.0E+00	AB028940.1	NT	Human sapiens mRNA for KIAA1117 protein, partial cds
10824	23507	38746	1.59	0.0E+00	AB007932.1	NT	Human sapiens mRNA for KIAA0463 protein, partial cds
10828	23510	38750	3.47	0.0E+00	U50328.1	NT	Human protein kinase C substrate 80K-H (PKRCSH) gene, exon 15-17
10832	23514	38755	1.55	0.0E+00	BE773008.1	EST_HUMAN	RC1-FT0134-470700-012-007 F10134 Homo sapiens cDNA
10832	23514	38756	1.55	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-470700-012-007 F10134 Homo sapiens cDNA
10839	23520	38762	1.47	0.0E+00	W11826.1	EST_HUMAN	57E10 Human retina cDNA 17p5091-cleaved sublibrary Homo sapiens cDNA not directional
10864	23534	38779	138.91	0.0E+00	AA740782.1	EST_HUMAN	ds32a07.s1 NCL CGAP Kid5 Homo sapiens cDNA clone IMAGE:1235412 3' similar to confamil element
10867	23537	38780	2.05	0.0E+00	AW468222.1	EST_HUMAN	hcd4H4.x1 NCL CGAP Kid12 Homo sapiens cDNA clone IMAGE:2812759 3'
10867	23543	38793	2.91	0.0E+00	AF252303.1	NT	Human sapiens signaling lymphocyte activation molecule (SLAM) gene, exon 2
10879	23556	38806	7.34	0.0E+00	Q05095.1	EST_HUMAN	Q35089 Human heart cDNA (Y Nakamura) Homo sapiens cDNA clone 3NH04817
10885	23566	38814	2.31	0.0E+00	AA746375.1	EST_HUMAN	ca55H01.1 NCL CGAP GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10885	23566	38815	2.31	0.0E+00	AA746375.1	EST_HUMAN	ca55H01.1 NCL CGAP GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10895	23575	38826	3.74	0.0E+00	M78448.1	EST_HUMAN	EST70568 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC28
10895	23576	38826	3.74	0.0E+00	M78448.1	EST_HUMAN	EST70568 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC28
10898	23578	38827	6.82	0.0E+00	AL157608.1	EST_HUMAN	DKFZ276112116 T17 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZ276112116 5'
10898	23578	38827	6.82	0.0E+00	AL157608.1	EST_HUMAN	DKFZ276112116 T17 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZ276112116 5'
10910	23580	38836	5.81	0.0E+00	AL111908.1	EST_HUMAN	AUT11898 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10924	23604	38836	1.84	0.0E+00	AV693565.1	EST_HUMAN	AV683656 GKC Homo sapiens cDNA clone GKCNC03 5'
10932	23612	38862	2.09	0.0E+00	BF336553.1	EST_HUMAN	IL3-AT10104-200500-145-007 NT0104 Homo sapiens cDNA
10953	18359	31311	2.73	0.0E+00	AB035266.1	NT	Human sapiens mRNA for neurotin II, complete cds
10955	18369	31312	2.73	0.0E+00	AB035266.1	NT	Human sapiens mRNA for neurotin II, complete cds
10967	23638	38887	2.64	0.0E+00	BE182360.1	EST_HUMAN	PM0-H10645-060500-002-E05 HT0645 Homo sapiens cDNA
10967	23638	38888	2.64	0.0E+00	BE182360.1	EST_HUMAN	PM0-H10645-060500-002-E05 HT0645 Homo sapiens cDNA
10981	23637		1.4	0.0E+00	AV701152.1	EST_HUMAN	601143902F1 NIH_MGC_72 Homo sapiens cDNA clone ADAAAD08 5'
10981	23655	38908	4.07	0.0E+00	BE89423.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAAD08 5'

Page 530 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10989	23683	36919	1.85	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BNC-3q-42-q42.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10989	23683	36920	1.85	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BNC-3q-42-q42.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10992	23686	36923	2.39	0.0E+00	BE018293.1	EST_HUMAN	poly(A) binding protein (MOUSE)
11016	23688	36949	1.77	0.0E+00	BF528807.1	EST_HUMAN	502043377F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181083 5'
11016	23688	36950	1.77	0.0E+00	BF528807.1	EST_HUMAN	502043377F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181083 5'
11018	23688	36951	1.77	0.0E+00	BF528807.1	EST_HUMAN	502043377F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181083 5'
11028	25133	36994	1.27	0.0E+00	AW387768.1	EST_HUMAN	MR4-ST0118-041089-010-A12 ST0118 Homo sapiens cDNA
11028	25133	36995	1.27	0.0E+00	AW387768.1	EST_HUMAN	MR4-ST0118-041089-010-A12 ST0118 Homo sapiens cDNA
11034	23708	36973	1.53	0.0E+00	4758281	NT	Homo sapiens EphA7 (EPHA7) mRNA
11034	23708	36974	8.73	0.0E+00	BE887953.1	EST_HUMAN	60140446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3928403 5'
11037	23708	36977	1.89	0.0E+00	AJ459545.1	EST_HUMAN	ec88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11037	23708	36978	1.89	0.0E+00	AJ459545.1	EST_HUMAN	ec88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11051	23721	36922	2.76	0.0E+00	AL042278.1	EST_HUMAN	DKFZ434L0120_r1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZ434L0120 5'
11058	23763	37028	1.61	0.0E+00	10860882	NT	Homo sapiens ephrin (EPH) mRNA
11058	23763	37031	3.98	0.0E+00	4758827	NT	Homo sapiens neuritin III (NRXN3) mRNA
11058	23756	37032	2.67	0.0E+00	BF206561.1	EST_HUMAN	U1H-B12-agg-h-01-q21.1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11058	23766	37040	4.23	0.0E+00	AS018260.1	NT	Homo sapiens mRNA for KIA00717 protein, partial cds
11058	23766	37041	4.23	0.0E+00	AS018260.1	NT	Homo sapiens mRNA for KIA00717 protein, partial cds
11058	23766	37043	2.69	0.0E+00	BE206946.1	EST_HUMAN	bs0407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
11058	23766	37044	2.69	0.0E+00	BE206946.1	EST_HUMAN	bs0407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
11108	23768	37044	2.69	0.0E+00	BE206946.1	EST_HUMAN	bs0407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
11110	23780	37055	1.9	0.0E+00	11526409	NT	Homo sapiens KIA0426 gene product (KIA0426) mRNA
11124	23793	37069	1.92	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4) mRNA
11127	20052	33133	1.5	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11131	23769	37074	3.84	0.0E+00	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-H04 HT0230 Homo sapiens cDNA
11131	23769	37075	3.84	0.0E+00	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-H04 HT0230 Homo sapiens cDNA
11154	23821	37101	1.96	0.0E+00	AW673499.1	EST_HUMAN	bs6408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11154	23821	37102	1.96	0.0E+00	AW673499.1	EST_HUMAN	bs6408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11176	23843	37128	6.21	0.0E+00	BF507876.1	EST_HUMAN	U1H-B14-ack-b-10-0-U1.1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11176	23843	37128	6.21	0.0E+00	BF507876.1	EST_HUMAN	U1H-B14-ack-b-10-0-U1.1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
11185	23850	37136	1.57	0.0E+00	AJ135170.1	EST_HUMAN	AJ135170 PLACE1 Homo sapiens cDNA clone IMAGE:1001381 5'
11189	23854	37140	1.82	0.0E+00	BF557638.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11189	23855	37141	1.82	0.0E+00	BF557638.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11189	23855	37142	1.67	0.0E+00	BF098811.1	EST_HUMAN	RC3-GN0089-160900-011-008 GN0089 Homo sapiens cDNA
11162	23857	37143	5.5	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11162	23857	37144	5.5	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11189	23864	37144	1.84	0.0E+00	D87082.1	NT	Human mRNA for KIAA0241 gene, partial cds
11204	23869		5.95	0.0E+00	BF240538.1	EST_HUMAN	601870530F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089710 5'
11218	23881	37160	2.04	0.0E+00	AB037787.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11218	23881	37167	2.04	0.0E+00	AB037787.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11222	23885	37170	4.17	0.0E+00	M50983.1	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11222	23885	37171	4.17	0.0E+00	11430968	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11230	23893	37176	1.8	0.0E+00	AA772837.1	EST_HUMAN	607490.61 Stratagene celizo brain S11 Homo sapiens cDNA clone IMAGE:985942 3'
11241	23903	37192	1.62	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11241	23903	37193	1.62	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11244	23906	37198	8.16	0.0E+00	45033544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11251	23913	37205	1.36	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4285502 5'
11254	23918	37209	5.84	0.0E+00	AW328173.1	EST_HUMAN	d02405.01 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11258	23920		71.88	0.0E+00	M50983.1	NT	Human gamma actin-like pseudogene, complete cds
11264	23926	37216	2.83	0.0E+00	BF300998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11264	23926	37217	2.83	0.0E+00	BF300998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11271	23932	37225	105.97	0.0E+00	BF362482.1	EST_HUMAN	QV22-NN0054-230600-333-004 NN0054 Homo sapiens cDNA
11291	23952	37248	2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11291	23952	37249	2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11291	23952	37250	2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11296	23956		3.03	0.0E+00	BE897051.1	EST_HUMAN	601438005F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11296	23957		1.73	0.0E+00	4503786	NT	Homo sapiens tyrosine kinase (FRK) mRNA
11310	23969	37271	3.45	0.0E+00	8923698	NT	Homo sapiens goggin-like protein (GLP), mRNA
11313	23972		2.60	0.0E+00	BF207692.1	EST_HUMAN	601881847F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11314	23973		2.03	0.0E+00	BE25744.1	EST_HUMAN	60116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357394 5'

Page 532 of 536

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11327	24018	37321	4.02	0.0E+00	BE208948.1	EST_HUMAN	ba0407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR-O76022 076022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11327	24018	37322	4.02	0.0E+00	BE208948.1	EST_HUMAN	ba0407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR-O76022 076022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11329	24020	37324	3.88	0.0E+00	AW753028.1	EST_HUMAN	CUO-CT0225-01289-071-408 CT0225 Homo sapiens cDNA
11334	24025		3.06	0.0E+00	AA558707.1	EST_HUMAN	h4208.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M65178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11335	18000	30623	3.84	0.0E+00	AA694954.1	EST_HUMAN	wp09008.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2464094 3'
11336	24026	37330	7.45	0.0E+00	AW327855.1	EST_HUMAN	dn2008.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846918 5'
11355	25134	37348	1.89	0.0E+00	AW252776.1	EST_HUMAN	UI-H-BW0-aj-07-07-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:272509 3'
11352	23173	36401	2.2	0.0E+00	4788027	NT	Homo sapiens neuron III (NRXN3) mRNA
11368	23975	37276	1.73	0.0E+00	BE284068.1	EST_HUMAN	601113903.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3354600 5'
11371	23978	37278	1.74	0.0E+00	BE985909.2	EST_HUMAN	60165908R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:385916 3'
11371	23978	37279	1.74	0.0E+00	BE985909.2	EST_HUMAN	60165908R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:385916 3'
11372	23979	37280	4.52	0.0E+00	BE168666.1	EST_HUMAN	IL5-HT0731-020500-077-003 HT0731 Homo sapiens cDNA
11373	23980		1.29	0.0E+00	BF513960.1	EST_HUMAN	UI-H-BW1-amv-a-08-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11387	23983	37294	7.81	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
11387	23983	37295	7.81	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
11397	24003	37308	5.89	0.0E+00	A923116.1	EST_HUMAN	wp83903.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11401	24050	37353	3.42	0.0E+00	AA760913.1	EST_HUMAN	nc211c07.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11401	24050	37354	3.42	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN. ;
11409	24055	37360	1.94	0.0E+00	BE910546.1	EST_HUMAN	nc211c07.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11418	23183	36413	7.9	0.0E+00	BE576347.1	EST_HUMAN	601581090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3206919 3' similar to TR-O00408 O00409
11419	23186	36416	1.79	0.0E+00	BE616669.1	EST_HUMAN	7021712.x1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:3206919 3' similar to TR-O00408 O00409
11419	23186	36417	1.79	0.0E+00	BE616669.1	EST_HUMAN	CHICKPOINT SUPPRESSOR 1. ;
11428	23193	36424	1.91	0.0E+00	AW575420.1	EST_HUMAN	60127633F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11428	23193	36424	1.91	0.0E+00	AW575420.1	EST_HUMAN	60127633F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11467	24061	37367	1.52	0.0E+00	Y18990.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11461	24064	37371	10.31	0.0E+00	L39891.1	NT	Homo sapiens polykaryotic kidney disease-associated protein (PKD1) gene, complete cds
11461	24064	37371	10.31	0.0E+00	L39891.1	NT	Homo sapiens polykaryotic kidney disease-associated protein (PKD1) gene, complete cds
11478	24077	37387	4.69	0.0E+00	AU138211	EST_HUMAN	AU138211 FLAGE1 Homo sapiens cDNA clone PLACE 1008077 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11481	24092	37404	1.92	0.0E+00	BE622317.1	EST_HUMAN	601441069F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11619	24118	37428	1.42	0.0E+00	AI039634.1	EST_HUMAN	Im94c10.x5 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165778 3'
11629	24126	37434	13.79	0.0E+00	BE748999.1	EST_HUMAN	601672188T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3839012 3'
11629	24126	37436	13.79	0.0E+00	BE748999.1	EST_HUMAN	601672188T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3839012 3'
11639	24130	37447	1.81	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYROT1 Homo sapiens cDNA clone THYROT1001398 5'
11639	24130	37448	1.81	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYROT1 Homo sapiens cDNA clone THYROT1001398 5'
11542	24142	37451	2.08	0.0E+00	AW006022.1	EST_HUMAN	w291h01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F59H10.2 CE11040 ZINC FINGER, C2H2 TYPE:
11546	25135	37485	3.49	0.0E+00	BF002333.1	EST_HUMAN	7022b10.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:3316990 3' similar to TR:Q13458 Q13458 TRIO.1
11571	24170	37485	2.88	0.0E+00	AW387778.1	EST_HUMAN	MR4-ST0118-261089-012-b03 ST0118 Homo sapiens cDNA
11571	24170	37486	2.88	0.0E+00	AW387778.1	EST_HUMAN	MR4-ST0118-261089-012-b03 ST0118 Homo sapiens cDNA
11582	24181	37521	2.41	0.0E+00	AW663777.1	EST_HUMAN	MR3-SN0010-310300-107-b03 SN0010 Homo sapiens cDNA
11601	24200	37521	4.76	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11601	24200	37522	4.78	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11608	24206	37528	5.97	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11612	24210	37533	2.29	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609923 5'
11612	24210	37534	2.29	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609923 5'
11632	24229	37553	2.22	0.0E+00	BE794758.1	EST_HUMAN	601560386F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11634	24231	37554	45.09	0.0E+00	BE879533.1	EST_HUMAN	601491821F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3894220 5'
11640	24237	37560	1.62	0.0E+00	4758927	NT	Homo sapiens neuron III (NRXN3) mRNA
11640	24237	37561	1.62	0.0E+00	4758927	NT	Homo sapiens neuron III (NRXN3) mRNA
11644	24241	37565	1.65	0.0E+00	AF033453.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11648	24243	37572	1.56	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
11653	24250	37572	14.06	0.0E+00	BE409993.1	EST_HUMAN	601268403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11654	24251	37573	1.46	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-02 HT0241 Homo sapiens cDNA Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11655	24252	37574	2.69	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11655	24252	37575	2.69	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11657	18187	30876	1.29	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11657	18187	30879	1.29	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11658	24254	37576	5.6	0.0E+00	BF581641.1	EST_HUMAN	602156722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4256725 5'
11658	24254	37577	5.6	0.0E+00	BF581641.1	EST_HUMAN	602156722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4256725 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11662	24258		1.93	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11664	17605	30503	1.5	0.0E+00	AF272683.1	NT	Homo sapiens gephyrin mRNA, complete cds
11667	24262	37596	1.71	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4: Homo sapiens cDNA clone IMAGE:3956935 5'
11670	24265	37588	1.35	0.0E+00	BE303372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956935 5'
11687	24262	37604	2.5	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11687	24262	37605	2.5	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11729	25193		15.74	0.0E+00	BF309120.1	EST_HUMAN	60189034F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11737	24330	37654	11.68	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
11751	24342	37671	1.3	0.0E+00	BE744311.1	EST_HUMAN	601576636F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11751	24342	37672	1.3	0.0E+00	BE744311.1	EST_HUMAN	601576636F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11757	24348	37678	1.43	0.0E+00	BE267612.1	EST_HUMAN	601173006F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11757	24348	37679	1.43	0.0E+00	BE267612.1	EST_HUMAN	601173006F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11765	24376	37705	1.69	0.0E+00	BE257695.1	EST_HUMAN	601114205F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354872 5'
11765	24376	37706	1.69	0.0E+00	BE257695.1	EST_HUMAN	601114205F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354872 5'
11790	24360	37710	1.68	0.0E+00	AW748184.1	EST_HUMAN	PM1-BT0348-151299-001-c11 BT0348 Homo sapiens cDNA
11790	24360	37711	1.68	0.0E+00	AW748184.1	EST_HUMAN	PM1-BT0348-151299-001-c11 BT0348 Homo sapiens cDNA
11792	24392	37713	2.23	0.0E+00	AW367811.1	EST_HUMAN	MR0-HT0765-271199-005-g03 HT0765 Homo sapiens cDNA
11792	24392	37714	2.23	0.0E+00	AW367811.1	EST_HUMAN	MR0-HT0765-271199-005-g03 HT0765 Homo sapiens cDNA
11797	24387	37720	2.48	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
11797	24387	37721	2.48	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
11808	14848		1.31	0.0E+00	U96264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11821	18691	31659	2.45	0.0E+00	U07223.1	NT	Human beta-chimaerin mRNA, complete cds
11822	24407	37741	5.54	0.0E+00	Z31705.1	NT	H. sapiens GLAST1 gene for glial glutamate transporter, exon6
11835	24419	37780	2.26	0.0E+00	A1663185.1	EST_HUMAN	183802.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2243067 3' similar to SW-62G_HUMAN
11837	24421	37792	2.31	0.0E+00	AU132394.1	EST_HUMAN	PS1959 G2MITOTIC-SPECIFIC CYCLIN G1
11879	25396	30600	2.27	0.0E+00	BE312542.1	EST_HUMAN	AU132394 NT2RP3: Homo sapiens cDNA clone NT2RP3004336 5'
11883	25257		3.89	0.0E+00	A1160063.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3903020 5'
11902	24468		1.6	0.0E+00	A6011396.1	NT	qp17B12.x1 Soares, fetal Lung, NPH-119W Homo sapiens cDNA clone IMAGE:1735231 3'
11902	24468		1.6	0.0E+00	A6011396.1	NT	Homo sapiens gene for AF-6, complete cds
11921	24492		4.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
11929	24489		4.1	0.0E+00	114178823	NT	Homo sapiens calmodulin binding protein 1 (KIA03330), mRNA
11947	24501		3.05	0.0E+00	5602973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11982	25218	30816	2.59	0.0E+00	AF240766.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11993	25226		5.39	0.0E+00	AL041631.1	EST_HUMAN	DXFZp434K0819.t1_434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434K0819 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12015	25369		3.12	0.0E+00	114181818 NT	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12023	24551		3.91	0.0E+00	AL046544.1	EST_HUMAN	DKFZP434G218.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434G218.5
12037	25281		1.68	0.0E+00	AI803497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12076	25390		1.52	0.0E+00	N64464.1	EST_HUMAN	W40603.s1 Soares fetal liver spleen 1NRLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW-PCOL_BAE1M P10272 POL POLYPROTEIN;
12089	24594		5.88	0.0E+00	AF106958.1	NT	Homo sapiens acetylcarnitine lyase gene, complete cds
12092	13593	26282	3.39	0.0E+00	4507800 NT	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12092	13593	26283	3.39	0.0E+00	4507800 NT	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12100	25284		2.21	0.0E+00	10092587 NT	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12129	13318		2.04	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12218	25108	30814	2.83	0.0E+00	AW590382.1	EST_HUMAN	hg31e06.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
12259	25248		1.34	0.0E+00	BE090210.1	EST_HUMAN	RC8-BT0711-250300-011.D05 BT0711 Homo sapiens cDNA
12273	26258		4.43	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (GSTR3) gene, 5' flanking region and pericd cds
12308	24732		3.38	0.0E+00	9635487 NT	EST_HUMAN	Human endogenous retrovirus, complete genome
12351	25252		2.41	0.0E+00	AJ224914.1	EST_HUMAN	en05h04.x1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12353	24778		1.68	0.0E+00	AJ904846.1	EST_HUMAN	QV-BT065-120399-103 BT065 Homo sapiens cDNA
12405	14718	27436	1.51	0.0E+00	6912457 NT	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
12405	14718	27437	1.51	0.0E+00	6912457 NT	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
12423	24769	31039	2.08	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12435	14424	27119	2.76	0.0E+00	H30132.1	EST_HUMAN	Y059e08.r1 Soares breast 3NHBat Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:U64099
12435	14424	27120	2.78	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12448	24818		10.86	0.0E+00	D50659.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12448	24818	31020	2.51	0.0E+00	11418189 NT	EST_HUMAN	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
12448	24818	31021	2.51	0.0E+00	11418189 NT	EST_HUMAN	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P-1), mRNA
12464	14817	27649	1.53	0.0E+00	4758439 NT	EST_HUMAN	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P-1), mRNA
12502	24856		1.5	0.0E+00	AW064959.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12538	14884	26617	2.09	0.0E+00	8622593 NT	EST_HUMAN	H06803.k1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879154 3'
12644	24953	31954	1.88	0.0E+00	11526291 NT	EST_HUMAN	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
12644	24953	31954	1.88	0.0E+00	11526291 NT	EST_HUMAN	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12508	16069	28718	4.24	0.0E+00	4695312 NT	EST_HUMAN	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12576	17605	30562	3.05	0.0E+00	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12562	24905		2.12	0.0E+00	AB029800.1	NT	Homo sapiens CST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
12622	24927	31009	2.06	0.0E+00	9559724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSPF-1), mRNA
12648	25410		2.66	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12654	13390	26021	2.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12729	24999	30972	1.5	0.0E+00	1147862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12735	25004		4	0.0E+00	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
12760	25042	30987	1.76	0.0E+00	AW025032.1	EST, HUMAN	wu63d7.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:2527596 3' similar to TR:Q12844 Q12844
12608	13960	26550	1.37	0.0E+00	9565844	NT	BREAKPOINT CLUSTER REGION PROTEIN, contains TAR1.3 TAR1 repetitive element;
12818	25251		1.39	0.0E+00	AF083824.1	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
							Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 8

1/10

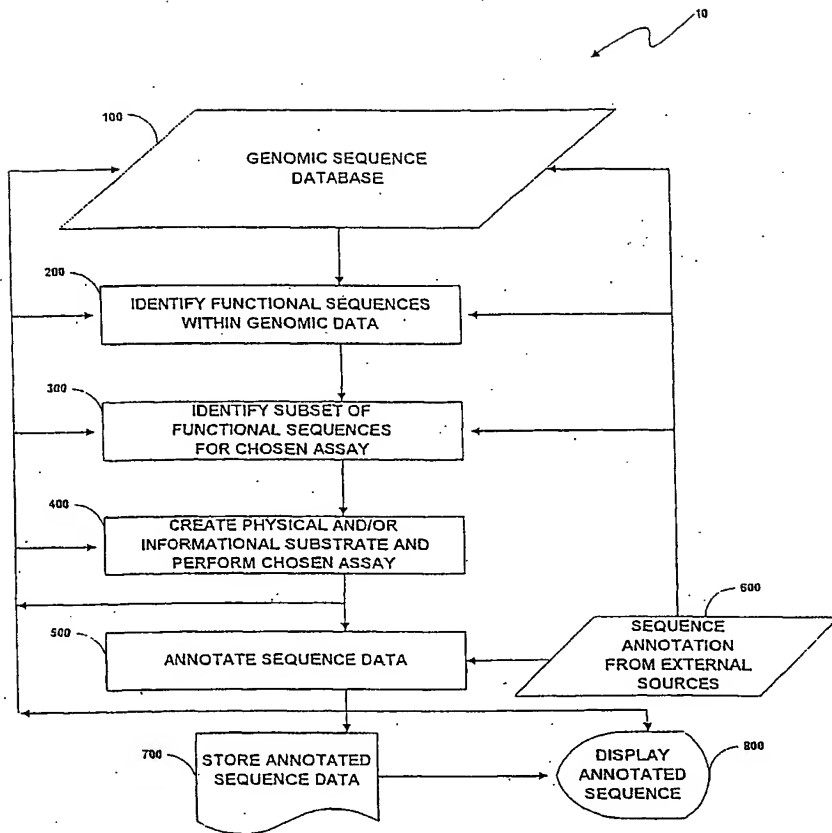


Fig. 1

2/10

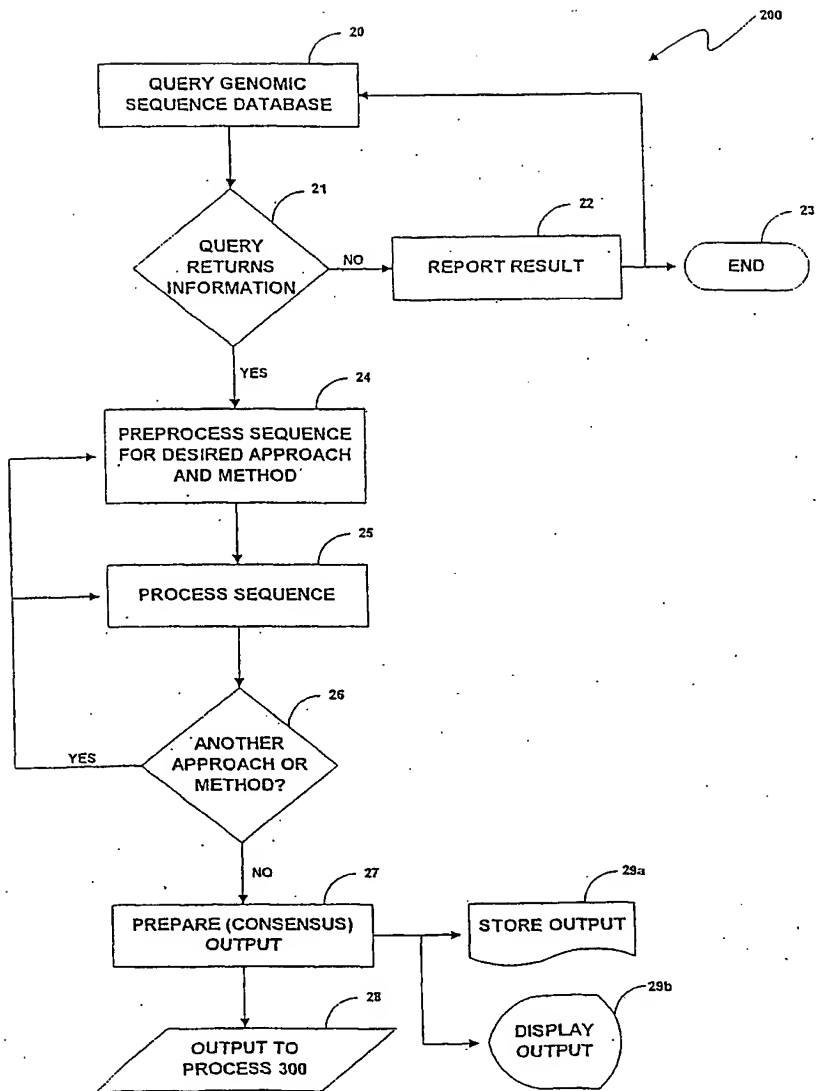


Fig. 2

3/10

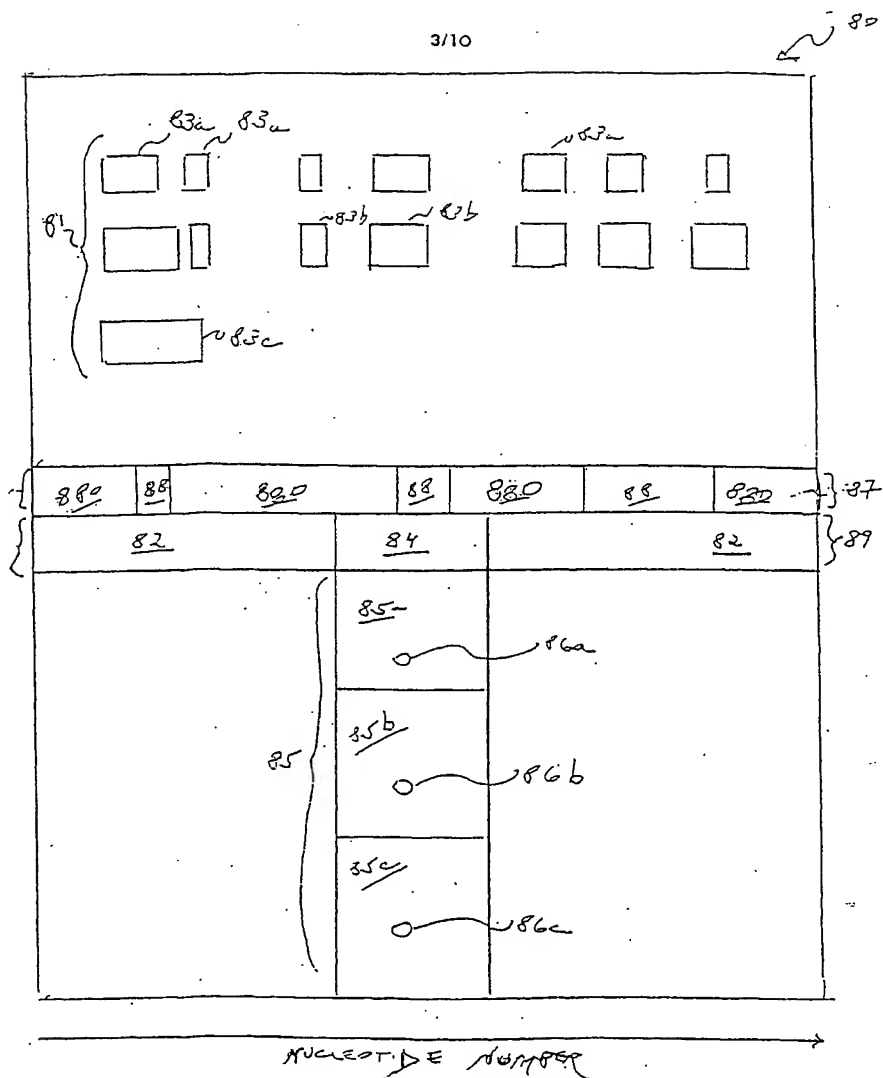


Fig. 3

4/10

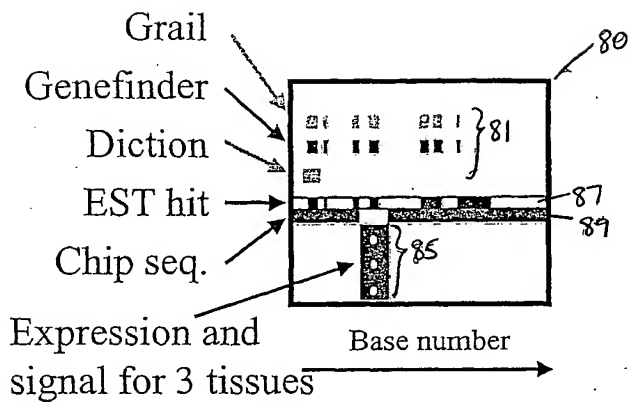


Fig. 4

5/10

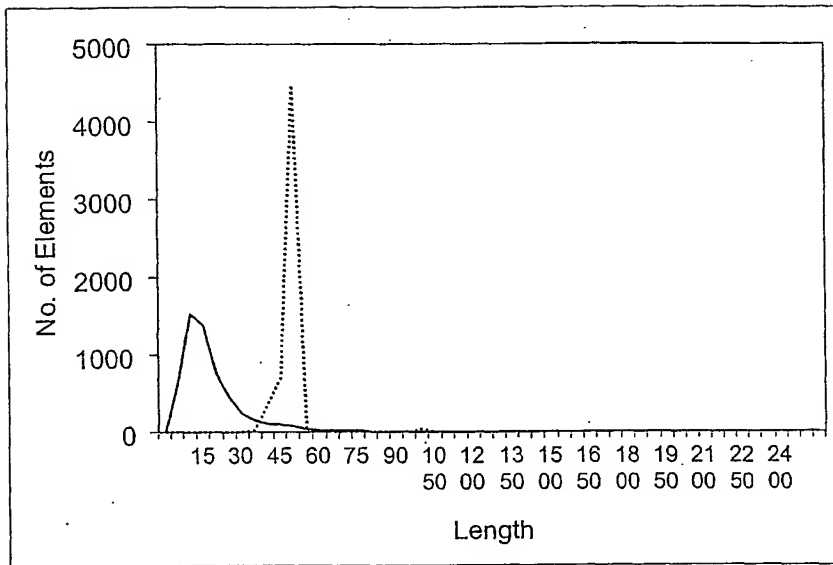


Fig. 5

6/10

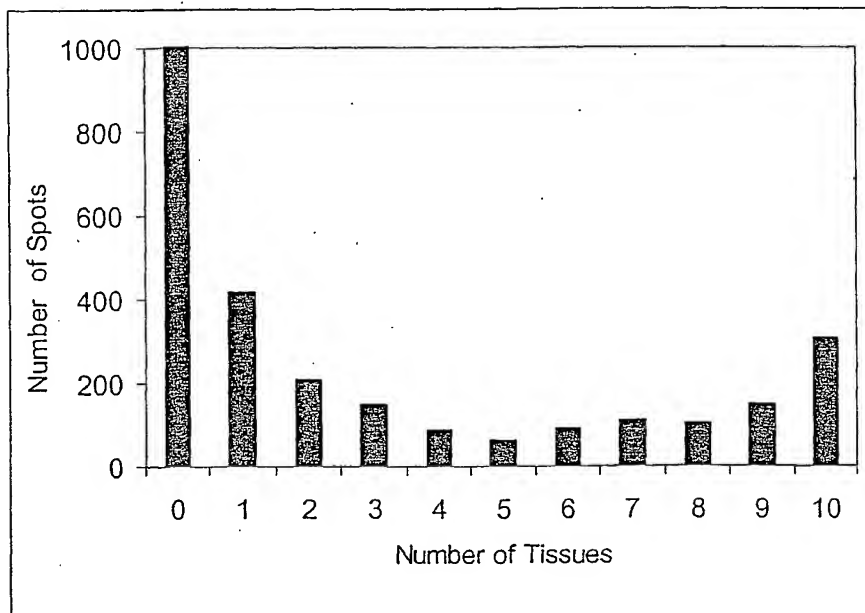


Fig. 6

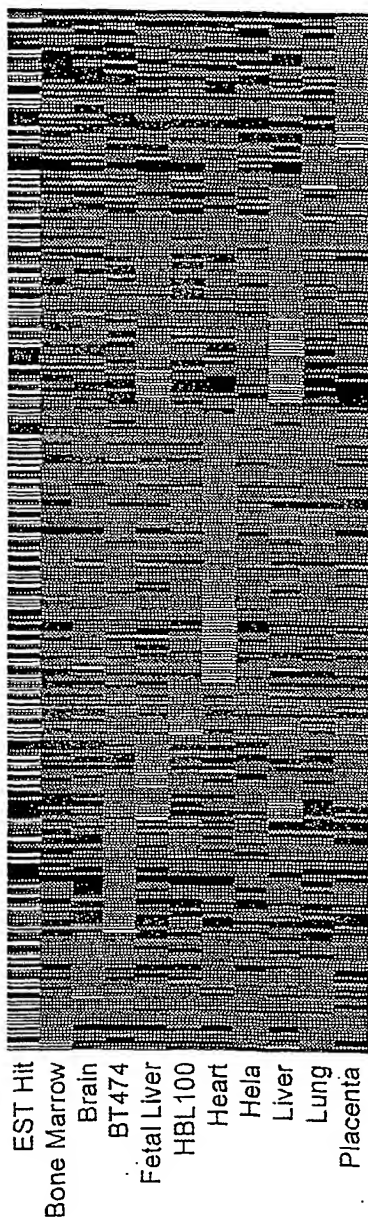


Fig. 7a

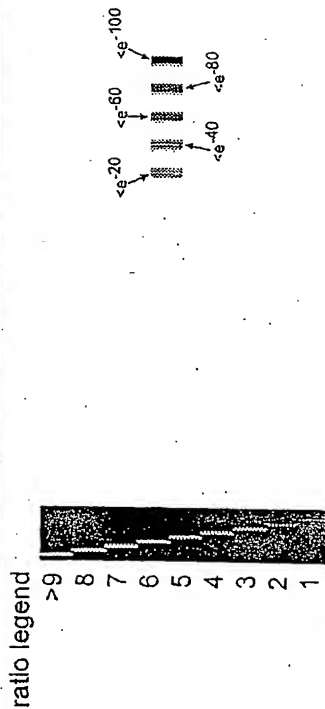


Fig. 7b

Fig. 7c

8/10

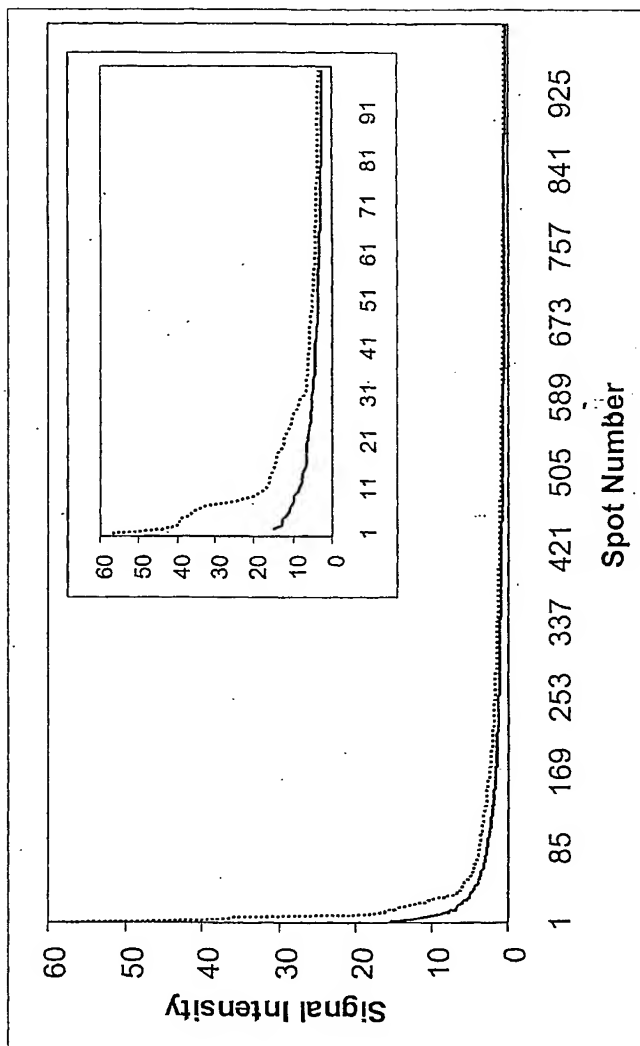


Fig. 8

9/10

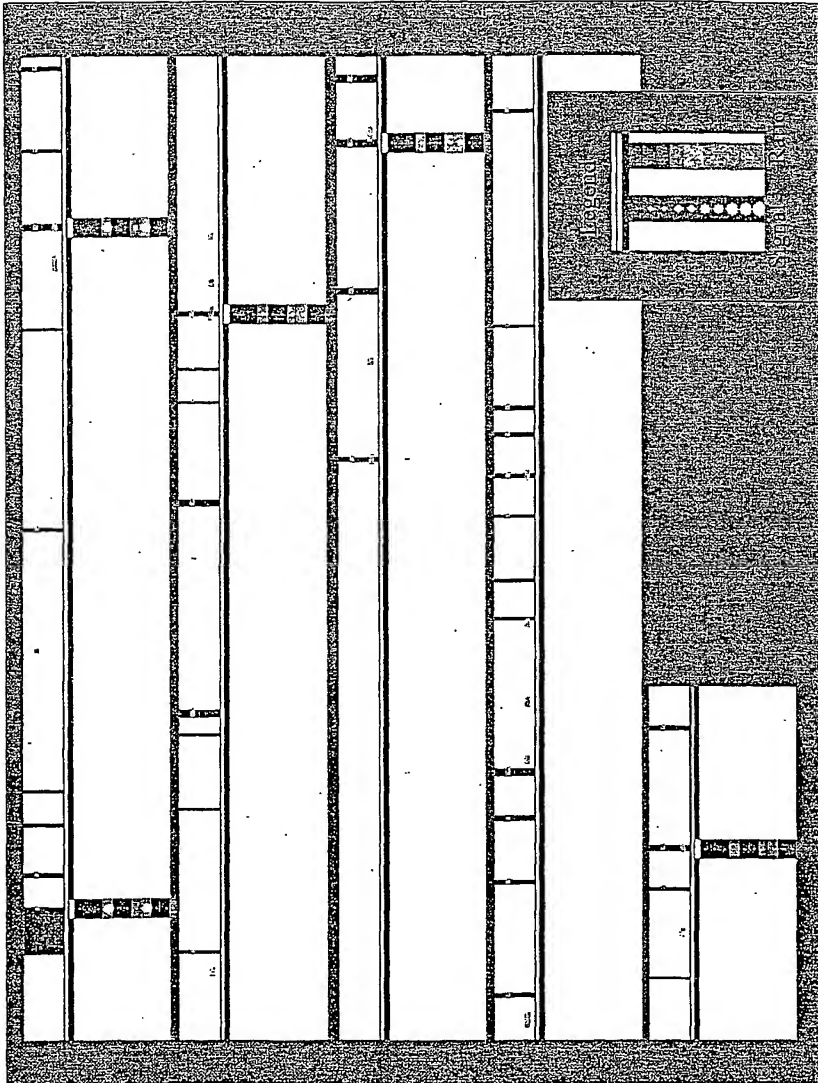
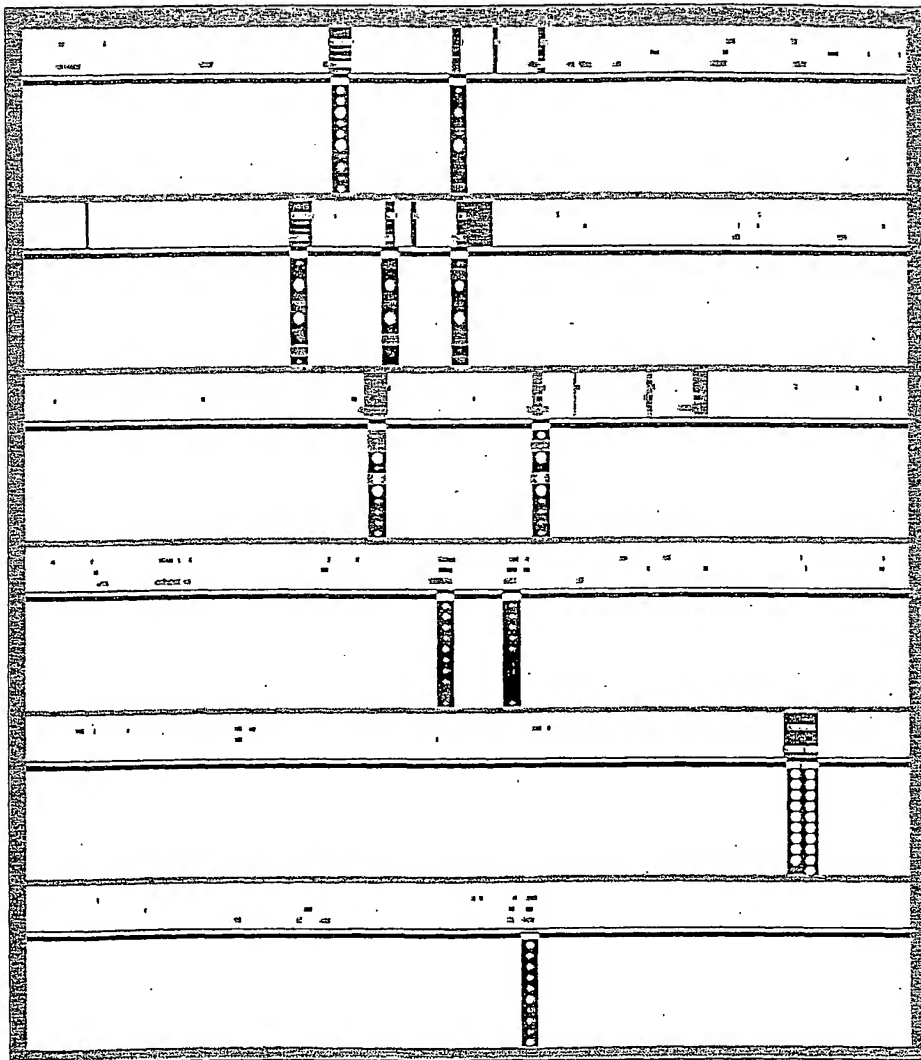


Fig. 9

10/10

Fig. 10



(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/057275 A3

- (51) International Patent Classification⁷: C12Q 1/68, G06F 19/00, C07K 14/47
- (21) International Application Number: PCT/US01/00667
- (22) International Filing Date: 30 January 2001 (30.01.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|------------|--------------------------------|----|
| 60/180,312 | 4 February 2000 (04.02.2000) | US |
| 60/207,456 | 26 May 2000 (26.05.2000) | US |
| 09/608,408 | 30 June 2000 (30.06.2000) | US |
| 09/632,366 | 3 August 2000 (03.08.2000) | US |
| 60/234,687 | 21 September 2000 (21.09.2000) | US |
| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6 | 4 October 2000 (04.10.2000) | GB |
- (71) Applicant (for all designated States except US): AEOM-ICA, INC. [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
- (88) Date of publication of the international search report:
17 April 2003
- (15) Information about Correction:
Previous Correction:
see PCT Gazette No. 42/2002 of 17 October 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/057275 A3

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the brain and their use in methods for detecting gene expression.

INTERNATIONAL SEARCH REPORT

International Application No.

.../US 01/00667

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68 G06F19/00 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, EMBASE, CHEM ABS Data, EMBL, BIOSIS, INSPEC

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! ID:AC007372, April 1999 (1999-04) DICKHOFF ET AL.: "Homo sapiens chromosome 14 BAC containing gene for type 2 iodothyronine deiodinase (DIO2) gene" XP002186078	13-21,25
Y	abstract	1-12, 22-24, 26,27
X	DATABASE EMBL 'Online! ID:CNS0000F, 11 May 1999 (1999-05-11) HEILIG ET AL.: "Sequencing of the human chromosome 14" XP002186079	13-21,25
Y	abstract	1-12, 22-24, 26,27

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

26 September 2002

Date of mailing of the international search report

08. 10. 2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00667

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! ID: AQ750225, 20 July 1999 (1999-07-20) MAHAIRAS ET AL.: "Construction of a Characterized Clone Resource for Genomic Sequencing" XP002186080	13-21,25
Y	abstract	1-12, 22-24, 26,27
Y	WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) the whole document	1-12, 22-24, 26,27
Y	WO 99 67422 A (SMITHKLINE BEECHAM CORP ;LEARY JEFFREY J (US); TAL SINGER RUTH (US) 29 December 1999 (1999-12-29) the whole document	1-12, 22-24, 26,27
Y	BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document	1-12, 22-24, 26,27
Y	CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document	1-12, 22-24, 26,27
Y	TAKAHASHI N ET AL: "High-density cDNA filter analysis of the expression profiles of the genes preferentially expressed in human brain" GENE, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, NL, vol. 164, no. 2, 27 October 1995 (1995-10-27), pages 219-227, XP004041878 ISSN: 0378-1119 the whole document	1-12, 22-24

-/--

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 01/00667

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>YASOJIMA K ET AL: "TANGLED AREAS OF ALZHEIMER BRAIN HAVE UPREGULATED LEVELS OF EXON 10 CONTAINING TAU MRNA" BRAIN RESEARCH, AMSTERDAM, NL, vol. 831, no. 1/2, 1999, pages 301-305, XP000929899 ISSN: 0006-8993 the whole document</p>	1-12, 22-24
Y	<p>ERMAK G ET AL: "RESTRICTED PATTERNS OF CD44 VARIANT EXON EXPRESSION IN HUMAN PAPILLARY THYROID CARCINOMA" CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD, US, vol. 56, no. 1, 1 March 1996 (1996-03-01), pages 1037-1042, XP002063388 ISSN: 0008-5472 the whole document</p>	1-12, 22-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00667

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-24, 26 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (all partially)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-24,26 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first invention in form 206 PCT. If additional fees are paid for the (one or more) as yet unsearched inventions, similar statements about incomplete searches could be issued.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq.Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 25443. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 12830).

Likewise, claim 26, which refers to peptides encoded by Seq. Ids. 1 or 2 and 12830, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 25443.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

national Application No

PCT/US 01/00667

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9830722	A	16-07-1998	AU 6035698 A	03-08-1998
			EP 0973939 A1	26-01-2000
			JP 2001508303 T	26-06-2001
			US 6303301 B1	16-10-2001
			WO 9830722 A1	16-07-1998
			US 2002028454 A1	07-03-2002
			US 2002039739 A1	04-04-2002
WO 9967422	A	29-12-1999	CA 2330731 A1	29-12-1999
			EP 1090144 A1	11-04-2001
			JP 2002518064 T	25-06-2002
			WO 9967422 A1	29-12-1999